PIRSA_PS_080462

Towards optimising the spatial scale of abalone fishery management

May 2008

Wild Fisheries

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Towards optimising the spatial scale of abalone fishery management

FRDC Project No. 2004/019

SARDI Aquatic Sciences Publication No. F2008/000082-1
SARDI Research Report Series No. 273

S. Mayfield and T.M. Saunders (Editors)

SARDI Aquatic Sciences, 2 Hamra Avenue West Beach SA 5024

May 2008

ABALONE Industry Association of South Australia Inc.

Working for a sustainable future

Government of South Australia

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Australian Government
Fisheries Research and Development Corporation

Towards optimising the spatial scale of abalone fishery management

S. Mayfield and T.M. Saunders (Editors)

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Final Report for the Fisheries Research and Development Corporation

FRDC Project No. 2004/019

SARDI Aquatic Sciences Publication No. F2008/000082-1

SARDI Research Report Series No. 273

ISBN 978-0-7308-5386-2

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Printed in Adelaide: May 2008

Reviewers: Dr Mike Steer and Mr Greg Ferguson (SARDI Aquatic Sciences)
Anonymous (FRDC)

Approved by: Dr Tim Ward, Principal Scientist: Wild Fisheries, SARDI Aquatic Sciences

Signed: 

Date: 22 May 2008
Circulation: Public Domain

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NON-TECHNICAL SUMMARY

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OBJECTIVES:

1. To identify and investigate the utility of a 'morphometric marker' as a rapid, non-destructive approach for determining boundaries among blacklip populations;
2. To evaluate the spatial variation in the fisheries biology, morphology and population genetics of blacklip populations in the Southern Zone of the South Australian abalone fishery;
3. To evaluate approaches for effective compliance at finer spatial scales;
4. To establish a framework that will assist in the development of 'management units' appropriate to the spatial variation observed and in accordance with both management and compliance limitations; and
5. To model populations of blacklip at a scale appropriate to the spatial variation observed.

Fine-scale population structure is common in many inshore marine species. This is particularly the case for sedentary invertebrates, like abalone, for which the component populations are characterised by a complex spatial structure evident at fine spatial scales. Populations are effectively isolated from conspecifics, and typically have variable life-history parameters (*e.g.* rates of growth, size at sexual maturity and fecundity) that strongly influence their productivity. Consequently, these populations (or stocks) respond independently to the effects of fishing. Broad-scale management, that does not identify or account for variability among stocks in these fisheries, places fast-growing populations at risk of being over-exploited, while leaving slow-growing components under utilised. The increased recognition of their complex spatial structure has led to renewed calls for the scales of abalone fishery management to be more closely aligned with those of the component populations (*i.e.* creation of 'management units' (MUs)). However, precisely that same complex spatial structure, and associated variability, makes reducing the scales of management in these fisheries challenging. Consequently, management operates over large spatial scales.

In concert with the initiative by the Western Abalone Divers Association Inc. and two concurrent Fisheries Research and Development Corporation projects (2005/024 and 2007/066), this project is among the first to provide a mechanism to facilitate a reduction in the spatial scale of abalone fishery assessment and management. The project focussed on (1) developing a simple, practical and cost-effective measure to discriminate among, and estimate key life-history parameters of, blacklip abalone (*Haliotis rubra*; hereafter referred to as blacklip) stocks; (2) identifying potential MUs and their associated life-history characteristics; and (3) outlining an initial framework, including consideration of population genetics, fisheries compliance and stock-assessment modelling, for MU implementation.

A principal outcome of this project was the identification of a 'morphometric marker', based on the ratio between shell length and shell height, which could both discriminate among blacklip stocks and predict their biological characteristics. Thus, this tool can be used as a basis for

identifying and managing MUs for blacklip at relevant ecological scales that are difficult to detect with genetic approaches. Importantly, it can be applied at any spatial scale, thereby overcoming the observed mix of variability and lack of predictability of the size and location of blacklip populations. When used within a suitable management framework, it can provide the necessary information to enable practical reductions in the scale of blacklip fishery management, which have previously been hampered by the inability to gather detailed demographic data at appropriate spatial scales. This approach will aid optimisation of blacklip fishery management because individual stocks can now be identified and then separately managed on the basis of their key life-history characteristics. This provides the opportunity for better resource use and, consequently, a reduction in the risk of fishery collapse.

Such stock identification is an integral component of modern fisheries science. It underpins effective fisheries management because management then occurs at spatial scales that reflect the actual population structure of the species. The tool that we have developed here provides an important opportunity to re-visit the stock structure of blacklip in the Southern Zone of the South Australian abalone fishery (SZ). We applied the 'morphometric marker' to >100 commercial shell samples from throughout the fishery. Our data suggest that only two current fishing areas constitute potential MUs and that the creation of at least six additional MUs is warranted. Subsequently, we estimated the biological characteristics of each MU, providing initial information (*e.g.* on size limits) to underpin their appropriate management. Further sampling from the commercial catch, which is relatively easy and inexpensive, is likely to suggest more MUs in the future. Consequently, this 'morphometric marker' is a powerful tool for identifying and distinguishing among blacklip stocks, and for estimating some of their important life-history characteristics – *i.e.* this marker is fundamental to the practical determination (*e.g.* size and location) of MUs along with their life-history characteristics, at relevant spatial scales. We suggest that in the absence of this tool, cost-effective application of the principals underpinning MUs, and thus practical identification and management of individual abalone stocks, is unlikely to be achievable.

We also suggest that a framework for successful implementation of MUs for species with spatially-complex population structures requires a holistic approach. Seven steps were identified as necessary to move from a sub-regional to MU-based spatial scale in this fishery. These were (1) clear and relevant management objectives; (2) transparency through effective and ongoing stake-holder engagement and consultation; (3) robust, reliable and accurate measures for discriminating among, and estimating the biological parameters of, component stocks; (4) practical selection, clear definition and appropriate scales for MUs; (5) clear management (and compliance) arrangements; (6) robust reporting systems; and (7) reliable, cost-effective data underpinning defendable assessments, including the use of suitable performance measures.

Finally, this report deliberately makes no recommendations about changing management arrangements in the SZ. Rather, it provides a tool for stakeholders in the fishery to use, in conjunction with Primary Industries and Resources South Australia, Abalone Management South Australia Inc. and the South Australian Research and Development Institute, in re-considering and, where appropriate, amending current arrangements for the fishery. This reflects the strong, interactive, collaborative ('co-management') approach to managing the valuable resource supporting this fishery. Application of this approach to other Haliotid fisheries may realise similar benefits.

KEYWORDS: abalone, spatial variation, 'morphometric marker', fisheries management

ACKNOWLEDGEMENTS

This project would never have begun, let alone be completed, without the inspiration, dedication and support from a large number of individuals and organisations.

Bob Pennington (President: Abalone Industry Association of South Australia Inc. (AIASA)), Michael Tokley (AIASA), Dr Tim Ward (South Australian research and Development Institute (SARDI)), Dr Harry Gorfine (Primary Industries and Research Victoria (PIRVic)), Merilyn Nobes (Primary Industries and Resources South Australia (PIRSA) and the South Australian (SA) Fisheries Research and Advisory Board provided advice and guidance in the development of the project.

We gratefully acknowledge the Fisheries Research and Development Corporation (FRDC) for providing the base funds, and for their ongoing support throughout the course of the project. SARDI (Aquatic Sciences) provided substantial in-kind support. This included considerable logistical and administrative support through the course of the project and, along with the Commonwealth Scientific and Industrial Research Organisation, provision of access to a range of facilities including laboratories and associated equipment.

We thank Bob Pennington, Michael Tokley, Dr Tim Ward, Sean Sloan (PIRSA), Dr Craig Noell (PIRSA), Will Zacharin (PIRSA), Martin Smallridge (PIRSA) and Arthur Martel (AIASA), along with all SA Southern Zone Abalone Fishery licence holders, divers and deckhands for advice, guidance and support through the life of the project.

Many people gave up their time to attend and contribute meaningfully to the six workshops held during the course of the project. We are particularly grateful to Charlie Cooper (Fisheries Victoria), A/Professor Rob Day (University of Melbourne), Sean Dowdell (PIRSA), Paul Faithow (PIRSA), Tania Wurst (PIRSA), David Forbes (Western Abalone Divers Association Inc. (WADA)), Patrick Gilmour (University of Melbourne), Drew Laslett (PIRSA), Luke McAvaney (University of Melbourne), Len McCall (WADA), Dr Craig Noell, Dr Jeremy Prince (Biospherics Pty Ltd), Harry Peeters (WADA), Bob Pennington, Peter Riddle (WADA), Bill Sinnott (Fisheries Victoria), Martin Smallridge, Melanie Snart (PIRSA), Rona Spicer (Strategic Management Consultants Pty Ltd), Michael Tokley, Ian Westhorpe (Fisheries Victoria), Duncan Worthington (NSW Abalone Industry Association) and all SA Southern Zone Abalone Fishery licence holders, divers and deckhands in this regard. Further, we acknowledge the reciprocal invitations from Harry Peeters and Len McCall to attend WADA workshops that further facilitated exchange of information, thereby benefiting the ongoing development of this project.

Numerous individuals assisted in the field and in the laboratory. We acknowledge assistance in this regard from Neal Chambers, Steve Coe, Byron Deak, Peter Hawthorne, Matthew Hoare, Alan Jones, and David Sturges. In addition, we thank Sou-west Seafoods, Dover Fisheries, Southern Canning, Jo Austin, Steven Bayley, Gary Boyle, Michael Buhlmann, Chris Carrison, Brad Clarke, Jim Cope, Jim Godden, Robert Itzerott, Peter Kelly, Dwayne Kelly, Leigh Kent, Dick Perry, Graham Pollard and Stan Sunderland for providing shell samples for measurement.

We acknowledge the support and assistance from Dr Rick McGarvey (SARDI) and Dr Jason Tanner (SARDI) for advice with statistical analyses. Ian Carlson (SARDI) and Annette Doonan (SARDI) provided many of the maps. Suzanne Bennett (SARDI) chased a large number of elusive references on our behalf. Erin Sautter assisted with editing the report. We are grateful to Rowan Chick (SARDI), A/Professor Sean Connell (University of Adelaide), Cameron Dixon (SARDI), Daniel Gorman (University of Adelaide), Dr Reyn Naylor (NIWA), Dr Jeremy Prince, Dr. Bayden Russell (University of Adelaide), Dr Michael Steer (SARDI) and Dr Tim Ward for taking the time to provide helpful reviews and suggestions on the draft chapters. We also acknowledge the contributions by an anonymous reviewer nominated by the FRDC.

This report was reviewed by Greg Ferguson and Dr Mike Steer (SARDI Aquatic Sciences), and an anonymous reviewer nominated by the FRDC. The report was formally approved for release by Dr Tim Ward, Wild Fisheries Principal Scientist, SARDI Aquatic Sciences.

LIST OF ACRONYMS

AIASA	Abalone Industry Association of South Australia Inc.
AMSA	Abalone Management South Australia Inc.
ANCOVA	Analysis of co-variance
CI	Confidence interval
CPUE	Catch-per-unit effort
DFA	Discriminant function analysis
DF	Discriminant function
FDA	'Fish-down' area
FMC	Fishery Management Committee
FRAB	Fisheries Research Advisory Board
FRDC	Fisheries Research and Development Corporation
GPS	Global positioning system
MLL	Minimum legal length
MtDNA	Mitochondrial DNA
MU	Management unit
NIWA	National Institute of Water & Atmospheric Research Ltd
Non-FDA	Non 'fish-down' area
NSW	New South Wales
PCA	Principal components analysis
PIRSA	Primary Industries and Resources South Australia
PIRVic	Primary Industries and Research Victoria
SA	South Australia
SAAF	South Australian abalone fishery
SARDI	South Australian Research and Development Institute
SE	Standard error
SH	Shell height
SL	Shell length
SV	Shell volume
SW	Shell width
SWt	Shell weight
SZ	Southern Zone of the SAAF
TACC	Total allowable commercial catch
WADA	Western Abalone Divers Association Inc.

CHAPTER 1. General Introduction

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1.1 Overview

This is the final report to the Fisheries Research and Development Corporation (FRDC) on FRDC project 2004/019 "*Towards optimising the spatial scale of abalone fishery management*". The report is divided into eight Chapters. Chapter 1 is the General Introduction that outlines the structure of the report, summarises the need to reconsider the spatial scales of abalone fishery management as a consequence of the spatial complexity and variability in abalone stock structure, documents the aims and objectives of the project and provides a description of the Southern Zone of the South Australian abalone fishery (SZ) within which the project was undertaken.

Chapter 2 describes and documents the morphological variation of blacklip abalone (*Haliotis rubra*; hereafter referred to as blacklip) across the SZ and the identification of a simple 'morphometric marker', based on the relationship between shell length and shell height, for distinguishing among blacklip populations. Spatial variation in several key biological parameters, including rates of growth and size at sexual maturity, and the relationships between these parameters and the 'morphometric marker' are provided in Chapter 3. The strength of these relationships enable this marker to be used to re-evaluate the spatial scale of abalone fishery management in the SZ, including the development of 'management units' (MUs; Chapter 6), supported by appropriate and effective fine-scale fisheries compliance approaches (Chapter 5).

The molecular analyses of blacklip population structure that were based on both microsatellite loci and mtDNA are presented in Chapter 4. Preliminary outputs from a length structured stock assessment model that was used to assess the status of blacklip in two possible MUs, Ringwood Reef and Middle Point, are provided in Chapter 7.

Chapter 8 is the General Discussion. It synthesises the information presented in the previous Chapters and outlines future research directions.

1.2 Background

Fine-scale population structure is common in many inshore marine species because they are structured by static coast scapes (Sponaugle *et al.* 2002; Strathmann *et al.* 2002; Swearer *et al.* 2002; Orensanz *et al.* 2005). This is particularly the case for sedentary invertebrates with limited larval dispersal, for which the populations (or stocks) tend to be characterised by their complex spatial structure that is typically evident across fine spatial scales (Sponaugle *et al.* 2002; Strathmann *et al.* 2002; Orensanz *et al*. 2005). Aggregations of such species form discrete populations, that are more or less isolated from conspecifics by reproduction and migration (Berryman 2002; Morgan and Shepherd 2006), often with variable life history parameters (McShane *et al.* 1988; Orensanz and Jamieson 1995; Withler *et al.* 2003; Orensanz *et al.* 2005).

Assessment and management of such spatially complex stocks is challenging (Prince 2005), primarily because (1) the scale at which the biology of the target species varies is far smaller than the scale at which data are commonly acquired; and (2) the high costs of separately assessing and managing numerous component populations within a given fishery. These difficulties lead to assessment and management processes occurring at spatial scales considerably greater than those suggested by the spatial complexity of the stocks (Prince 2005). This consequent mismatch between the scale of the component units of stock within a fishery and the scale of assessment and management has been termed the 'tragedy of scale' (Prince and Hilborn 2003) and has been blamed for the failure to maintain a sustainable resource in numerous sedentary invertebrate fisheries (Perry *et al.* 2002; Orensanz *et al.* 2005) including abalone (Sloan and Breen 1988; Davis *et al*. 1996, 1998; Farlinger and Campbell 1992; Haaker *et al*. 1996; Tegner 2000; Prince 2004).

Abalone (Genus *Haliotis*) are a typical group of sedentary invertebrate species with limited larval dispersal that have numerous populations across their geographical extent (Prince 2005; Morgan and Shepherd 2006). These populations frequently show a high degree of variability in morphology, rates of growth, fecundity and size at sexual maturity (Breen and Adkins 1982; Shepherd and Hearn 1983; McShane *et al.* 1988b, 1994; Nash 1992; Worthington *et al*. 1995; Worthington and Andrew 1997, 1998; Tarbath 2003; Prince 2005; Naylor *et al*. 2006). There is also increasing evidence that abalone larvae generally disperse only short distances (Prince *et al*. 1987; McShane *et al*. 1988a; Nash 1992; Shepherd and Brown 1993; McShane

1995; Temby *et al*. 2007). In combination, the patterns of localised recruitment and the biological and morphometric differences observed across fine spatial scales have led to increasing calls for explicit spatial management (*e.g*. Prince and Shepherd 1992; McShane 1995; Worthington and Andrew 1998; Prince 2005) to overcome the many problems of managing abalone stocks using traditional, regional-scale management approaches (Prince 2003, 2004, 2005).

Management of abalone fisheries in Australia generally occurs over large spatial scales (from 100 – 1000 km) on a State-by-State basis through the use of individual quotas, minimum harvest lengths and total allowable catches (Prince and Shepherd 1992). Such regional-scale management approaches afford limited consideration of the spatial complexity in the abalone stocks, and thus fail to consider spatial variability in key life-history parameters among populations (Prince 2005). Persistence with this approach may ultimately compromise the sustainability of Australia's abalone resources, and suggests the need for consideration and development of MUs (Taylor and Dizon 1999; Pallsbøll *et al*. 2006). Nevertheless, even though there is growing evidence of the need for fine-scale assessment and management, strategies and programs to move beyond broad-scale management are rare.

One of the earliest examples of a reduction in the spatial scale of abalone fishery management was the introduction of four, separately-managed, 'fish-down' areas (FDAs) in the SZ in 1994 (see section 1.4). This recognised the biological and morphological variability among blacklip populations in this Zone, in that the FDAs were designed to encompass components of the fishery within which the blacklip populations were considered to be 'stunted' (Tyrer 1995; Mayfield *et al.* 2007). Collectively, there is a total allowable commercial catch (TACC) for these four areas that is harvested at a minimum legal length (MLL) which is 15 mm shell length (SL) smaller than that which applies across the remainder of the fishery. However, despite these relatively 'novel' management arrangements it is widely acknowledged that FDAs do not encompass all of the 'stunted' blacklip populations in this fishery and their large size ensures they also contain populations of 'non-stunted' blacklip.

More recently, in 2002, the Western Abalone Divers Association Inc. (WADA), the industry association representing divers and licence holders in the Western Zone of the Victorian abalone fishery, began assessing and managing their fishery at a reef-code scale. To achieve this, they use a harvest policy framework underpinned by a "rapid assessment" of abalone population "health", visually determined from the shape and appearance of abalone shells from the commercial catch (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). Evolution of this process has led to increasingly complex, spatial management of the

resource, including reef-specific catch limits and MLL and, for some reefs, daily catch limits (Mr Harry Peeters, WADA, personal communication). Largely undertaken through a series of workshops, the WADA initiative is being augmented, and extended into other jurisdictions through a concurrent FRDC project (FRDC 2005/024 "*Abalone industry development: local assessment and management by industry*").

Alongside the WADA initiative and FRDC 2005/024, this project is among the first to provide a mechanism to more closely align the scale of assessment and management with the scale of the biological and morphological variability across the component populations. The project was conducted in the SZ because (1) the fishery is small (<200 km of effective fishing area); (2) the Zone already has four separately managed FDAs that are regulated by their own TACC and MLL (see Section 1.4); and (3) the licence holders and divers in the Zone have experience with and accept fine-scale management.

The overarching goal of this project was to develop a means to facilitate assessment and management of abalone fisheries at finer spatial scales to provide the opportunity for (1) better resource use through the assessment of component stocks; and (2) reducing the risk of fishery collapse through the setting of multiple, spatially-specific TACC and MLL. It was based on the premises that (1) morphological variation in blacklip across the SZ would inform the development of a 'morphometric marker' that, in turn, would reflect variability in key biological parameters; and (2) application of the 'morphometric marker' on commercial shell samples could generate a 'morphometric map' of the fishery to aid consideration of alternative spatial management strategies, including the development of MUs.

1.3 Project objectives

There were five objectives. These were:

1. To identify and investigate the utility of a 'morphometric marker' as a rapid, non-destructive approach for determining boundaries among blacklip populations (Chapter 2);
2. To evaluate the spatial variation in the fisheries biology, morphology and population genetics of blacklip populations in the Southern Zone of the South Australian abalone fishery (Chapters 3 and 4);
3. To evaluate approaches for effective compliance at finer spatial scales (Chapter 5);
4. To establish a framework that will assist in the development of 'management units' appropriate to the spatial variation observed and in accordance with both management and compliance limitations (Chapter 6); and
5. To model populations of blacklip at a scale appropriate to the spatial variation observed (Chapter 7).

1.4 Description of the Southern Zone abalone fishery

The South Australian abalone fishery began in 1964, with management arrangements evolving since its inception (see Table 1.1). The fishery expanded rapidly in the late 1960s, with the number of entrants exceeding 100 by 1970. In 1971 licences were made non-transferable to reduce the number of operators, and the fishery was divided into three zones (Western, Central and Southern) to facilitate more effective management (Figure 1.1).

The SZ includes all coastal waters of South Australia east of Meridian 139°E, with the exception of the Coorong and waters inside the Murray River mouth (Figure 1.2). The fishing season in the Zone extends from 1 September to 31 August. Most (98%) of the TACC is comprised of blacklip (Figure 1.3; Table 1.2a,b). In 2006/07 the blacklip TACC was 144 t shell weight (Table 1.2b). A small amount of greenlip abalone is also harvested (*H. laevigata*; hereafter referred to as greenlip). The greenlip TACC in 2006/07 was 6 t shell weight (Table 1.2b). The TACC for greenlip and blacklip have generally been stable in recent years (Figure 1.3). Levels of recreational and illegal harvest are considered small (Mayfield *et al*. 2007).

A MLL of 130 mm SL was imposed on both species in 1971. Size limits were reviewed in the early 1980s, and the minimum size of blacklip was reduced to 120 mm SL in 1984. It was then changed again to 125 mm SL in 1988. The MLL for greenlip has remained unchanged at 130 mm SL since 1971. Quotas were introduced in 1988.

To monitor catches and facilitate compliance with quota limits, fishers must complete a 'Catch and Disposal Record' form upon landing. In addition, a research logbook must also be completed for each fishing day and submitted to SARDI Aquatic Sciences at the end of each month. Commercial catch and effort data on this fishery have been collected since 1968.

Unique to the SZ are four FDAs (Figure 1.4). Within these FDAs, the blacklip were considered to be 'stunted' when compared to the remainder of the fishery. 'Stunted' blacklip have a smaller maximum length, and/or a slower growth rate, when compared to other populations (Wells and Mulvay 1995). The licence holders and divers in the fishery developed and managed the FDAs between 1984/85 and 1988/89, without regulation. Formal management arrangements for harvesting of 'stunted' (110.0 – 124.9 mm SL) blacklip from the FDAs were developed from 1989/90 through the former Abalone Management Liaison Committee and the later Abalone Fishery Management Committee. These arrangements included ministerial exemption notices issued under Section 59 of the *Fisheries Act 1982*.

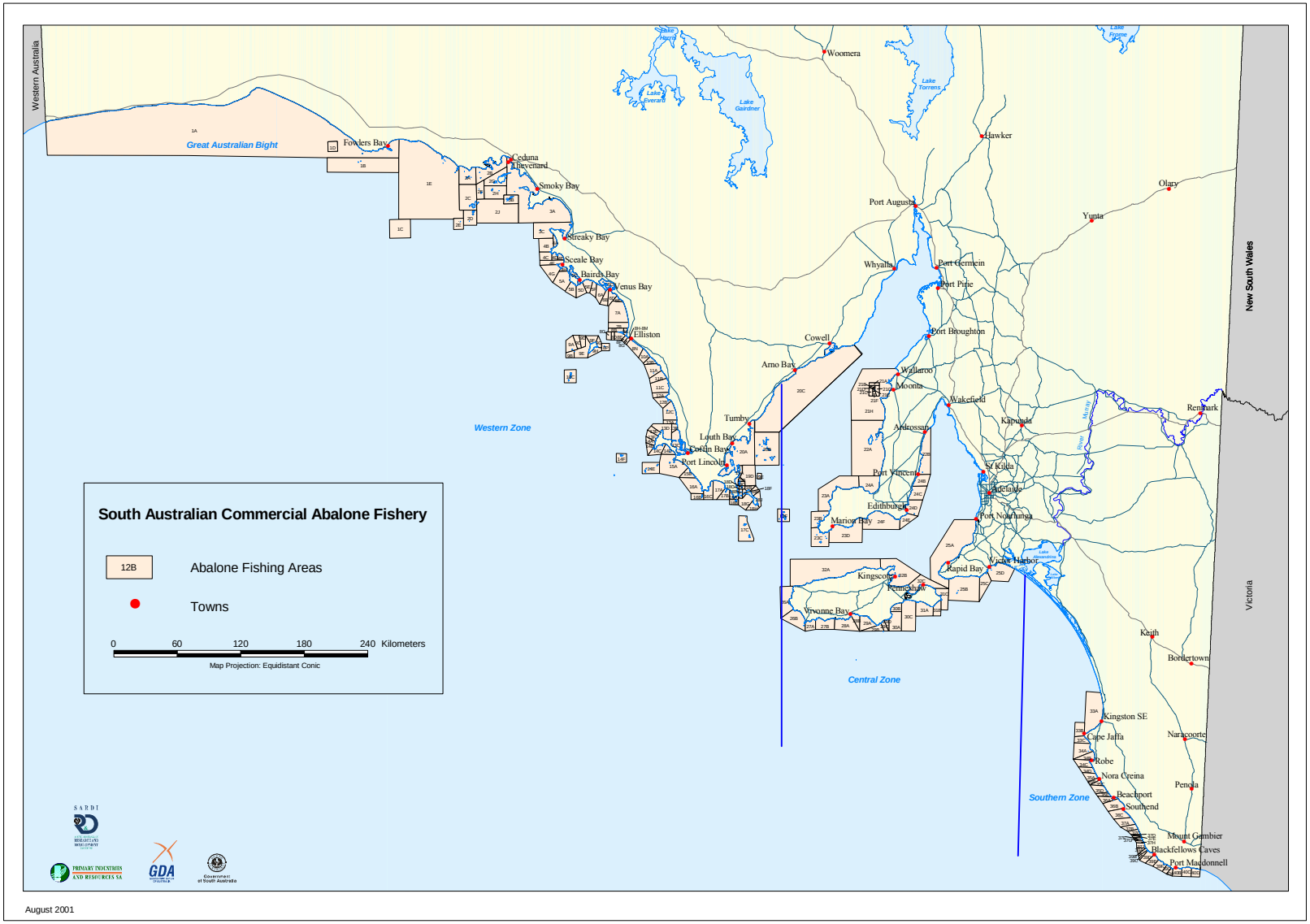

Figure 1.1: Fishing zones and fishing areas of the South Australian abalone fishery.

Figure 1.2: Fishing areas of the SZ.

Table 1.1: Management milestones in the SZ.

Date	Milestone
1964	Fishery started
1971	Licences made non-transferable
	Fishery divided into three zones
	MLL set at 130 mm SL for both species
1976	30 Licences remained; 5 additional licences issued
1978	Sub Zones and fishing blocks replaced by map numbers and codes
1984	Blacklip MLL amended to 120 mm SL in the SZ
1988	Quota introduced to the SZ
	Blacklip MLL amended to 125 mm SL in the SZ
1993	Abolition of owner-operator regulation
1994	Four FDAs defined in the SZ
1997	Management Plan implemented
2003	SZ separated into FDAs and non-'fish-down' areas (non-FDAs) with separate TACC
2004	Management Plan Revised
	Fishery assessed against the principles of ecologically sustainable development
2005	Greenlip TACC increased from 3 to 6 t
	Blacklip TACC in the non-FDA increased from 96 to 99 t
	Blacklip TACC in the FDA reduced from 51 to 45 t

Table 1.2a: Total allowable commercial catches (tonnes, shell weight) for the SZ from 1988/89 to 2002/03.

Fishing season	Greenlip SL ≥ 130 mm	Blacklip SL ≥ 125 mm	Blacklip 110 mm ≤ SL ≤ 125 mm
1988/89	3	108	-
1989/90	3	108	-
1990/91	3	108	-
1991/92	3	108	-
1992/93	6	108	-
1993/94	6	108	-
1994/95	6	108	36
1995/96	6	84	60
1996/97	6	96	48
1997/98	6	108	36
1998/99	6	108	36
1999/00	6	108	36
2000/01	3	108	39
2001/02	3	108	39
2002/03	3	108	39

Table 1.2b: Total allowable commercial catches (tonnes, shell weight) for the SZ from 2003/04 to 2006/07.

Fishing season	Greenlip SL ≥ 130 mm	Blacklip (Non-FDA) SL ≥ 125 mm	Blacklip (FDA) SL ≥ 110 mm
2003/04	3	96	51
2004/05	3	96	51
2005/06	6	99	45
2006/07	6	99	45
2007/08	6	99	45

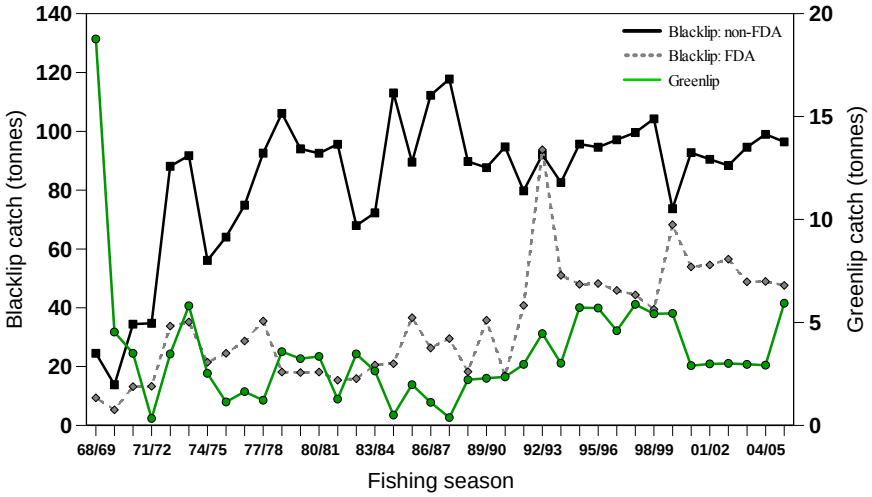

Figure 1.3: Estimated catch (tonnes) of blacklip (FDA and non-FDA) and reported catch of greenlip in the SZ from 1968/69 to 2005/06.

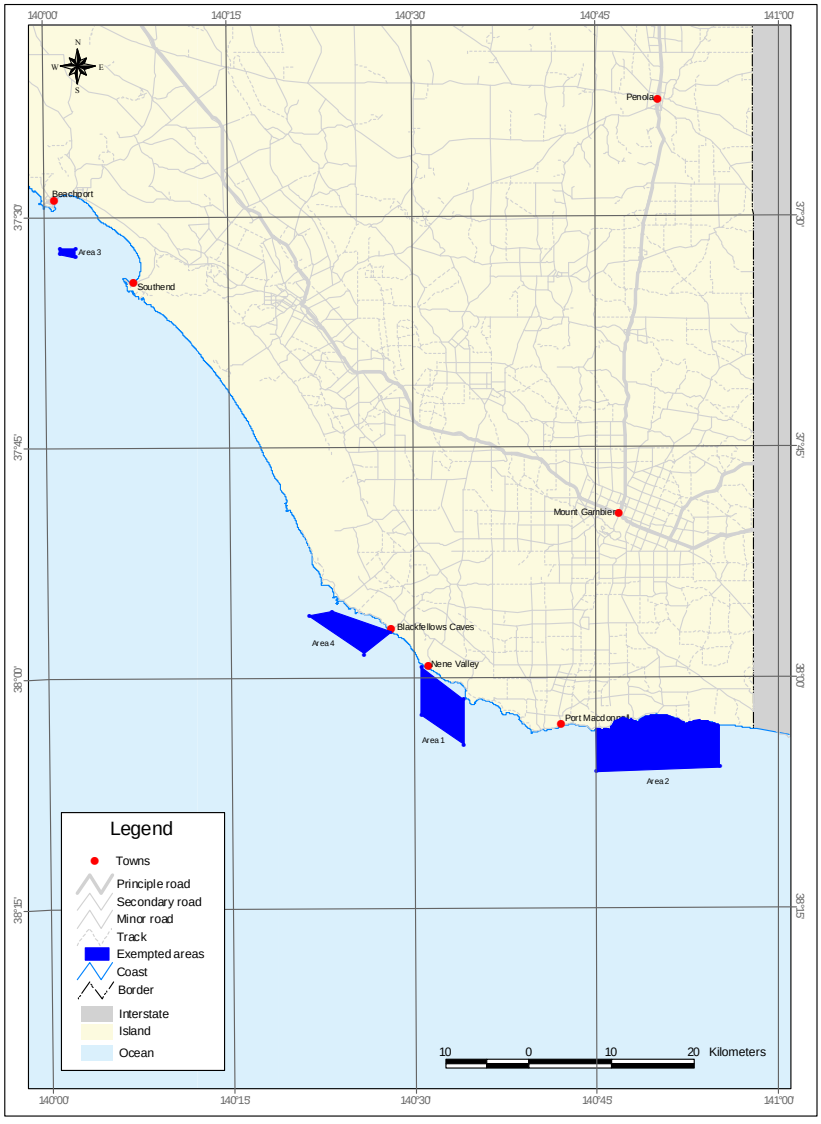

Figure 1.4: Locations of the four FDAs in the SZ within which the MLL of blacklip is 110 mm SL.

Recent changes to the Fisheries (*Scheme of Management – Abalone Fisheries*) Regulations 1991 formally provided for the harvesting of blacklip above a MLL of 110 mm SL in the four FDAs from 2003/04. Prior to 2003/04 the TACC of 'stunted' blacklip from the FDAs ranged between 36 and 60 t. Fishers were also permitted to harvest blacklip >125 mm SL from the FDA as part of the 'normal' blacklip TACC.

The management arrangements were amended from 1 September 2003. The SZ was divided into two sub-regions – non-FDAs and FDAs. In 2003/04 and 2004/05 the blacklip TACC in the two sub-regions was 96 and 51 t, respectively. Since 2005/06 the blacklip TACCs in the non-FDAs and FDAs have been 99 and 45 t, respectively (Table 1.2b).

Since 1997, the fishery has operated under the control of a formal Management Plan (Zacharin 1997; Nobes *et al*. 2004). This Plan ensures that the fishery is managed through a regime of input (*e.g.* limited entry) and output (*e.g*. MLL, TACC) controls. The Management Plan identifies biological, economic, environmental and social management objectives. Each of these has associated strategies that, in turn, are linked to a range of performance measures and indicators.

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CHAPTER 2. Identification of a 'Morphometric Marker' for Distinguishing among Blacklip Populations.

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2.1 Introduction

Fine-scale population structure is common in many inshore marine species because they are structured by static coast scapes (Sponaugle *et al.* 2002; Strathmann *et al.* 2002; Swearer *et al.* 2002; Orensanz *et al.* 2005). This is particularly the case for sedentary invertebrates with limited larval dispersal, for which the populations (or stocks) tend to be highly structured across small spatial scales (Sponaugle *et al.* 2002; Strathmann *et al.* 2002; Orensanz *et al*. 2005). Aggregations of such species form discrete populations, that are more or less isolated from conspecifics by reproduction and migration (Berryman 2002; Morgan and Shepherd 2006), often with variable life-history parameters (McShane *et al.* 1988; Orensanz and Jamieson 1995; Withler *et al.* 2003; Orensanz *et al.* 2005). The high degree of population structuring in these species has been historically unrecognised in their management, leading to serial depletion of populations and in many cases stock collapse (*e.g.* Tegner *et al.* 1996; Perry *et al.* 2002; Orensanz *et al.* 2005). This is because acquiring information on the boundaries between separate populations is impeded by the difficulties of tracking minute larva (Swearer *et al.* 2002; Gilg and Hilbish 2003) and there are high costs of collecting biological information across a range of spatial scales (Prince 2005).

The study of morphometric variation among populations may offer a cost-effective way to identify separate populations of marine species (Cadrin 2005). While this approach has been commonly used (Cadrin 2000; Kong *et al.* 2007), spatial patterns in morphology may be environmentally induced, and not reflect demographically isolated units (Swain and Foote 1999; Swain *et al*. 2005). However, the highly localised populations formed by sedentary invertebrates with limited larval dispersal are likely to exist at similar scales to this environmental variation, making studies on morphology an extremely useful tool for

population identification. In addition, morphological differences among populations are likely to indicate differences in growth, maturation and fecundity (Cadrin 2005), so can potentially provide biological information to support effective management (Cadrin and Friedland 1999).

Abalone (Genus *Haliotis*) are a typical group of sedentary invertebrate species with limited larval dispersal that have numerous discrete populations across their geographical extent (Prince 2005; Morgan and Shepherd 2006). These populations often differ in their biology and morphology (Shepherd and Hearn 1983; McShane *et al.* 1988; Worthington *et al*. 1995; Worthington and Andrew 1997, 1998; Tarbath 2003; Tarbath *et al.* 2003), resulting in the presence of so-called 'stunted' areas of abalone that have a slower growth rate and/or a smaller maximum length compared to adjacent populations (Shepherd and Cannon 1988; Nash 1992). 'Stunted' populations typically form dense aggregations in sheltered areas with lower wave exposure (McShane and Naylor 1995a). It is suggested that abalone in these protected areas grow more slowly than individuals in more exposed habitats as a result of lower water movement providing less food in the form of drift algae (Day and Fleming 1992; Shepherd and Steinberg 1992; McShane and Naylor 1995a). However, density-dependent processes may also contribute to relatively lower rates of growth in 'stunted' areas (Emmett and Jamieson 1988; McShane and Naylor 1995b; Dixon and Day 2004).

The current broad-scale (100 – 1000 km of coastline; McShane *et al*. 1994) management of most abalone fisheries fails to account for the finer-scale variability in population structure evident in abalone stocks. This leaves fast-growing populations prone to overfishing and slower-growing populations under utilised (Strathmann *et al.* 2002; Prince 2005). In response to this localised variability, the spatial scale of management in the South Australian abalone fishery has decreased steadily since 1985. Notably, in the Southern Zone of this fishery (SZ) there are four, separately managed, 'fish-down' areas (FDAs) within which the blacklip abalone (*H. rubra*; hereafter referred to as blacklip) populations are considered 'stunted'. These areas were formally introduced during 1994/95 following *ad hoc* fishing at a variety of minimum legal lengths (MLL) between September 1989 and October 1994 (Tyrer 1995; Mayfield *et al.* 2007). Collectively, the FDAs have a separate total allowable commercial catch (TACC) that is harvested at a MLL of 110 mm shell length (SL), 15 mm smaller than that in the remainder of the fishery. Nevertheless, despite these relatively 'novel' management arrangements it is acknowledged that FDAs do not encompass all of the 'stunted' blacklip in this fishery and their size ensures they also contain populations of 'non-stunted' blacklip.

Studies on the spatial variability of abalone morphology have shown differences among sites separated by as little as 200 m (Breen and Adkins 1982; McShane *et al.* 1988, 1994;

Worthington *et al*. 1995). Consequently, phenotypic variation in morphometric traits may be an effective method for discriminating among 'stunted' and 'non-stunted' abalone populations. The objective of this Chapter was to investigate the potential of identifying a 'morphometric marker' that could be used as a tool to discriminate between 'stunted' and 'non-stunted' populations of blacklip in the SZ. This was achieved by examining the spatial variability in the morphology of blacklip among 'stunted' and 'non-stunted' sites at broad (10 km's) and fine (100 m's) spatial scales within the fishery. The 'morphometric marker' developed was applied to the fine-spatial-scale samples to assess the spatial extent of 'stunted' and 'non-stunted' populations, and management arrangements in one current FDA.

2.2 Methods

2.2.1 Study site

This study was conducted in the SZ, which includes all coastal waters of South Australia east of Meridian 139°E, with the exception of the Coorong and waters inside the Murray River mouth. After consultation with divers and licence holders, all of the sites were distributed in the waters between the Salmon Hole and the South Australia/Victoria border (Figure 2.1).

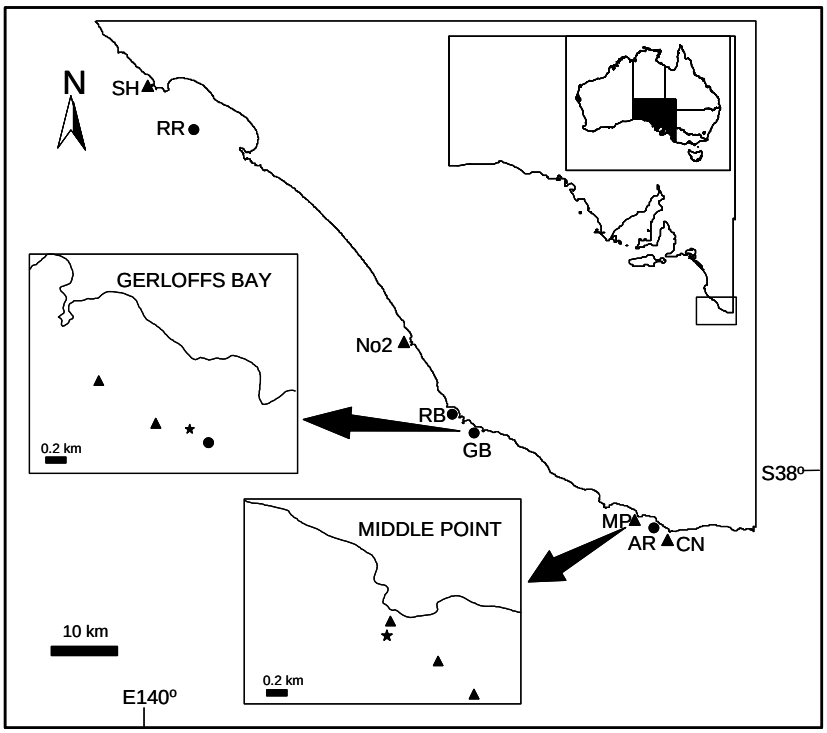

Figure 2.1: Map of study area showing locations of the eight broad-scale sites and the sub-sites within GB and MP (inserts). Circles and triangles represent 'stunted' and 'non-stunted' broad-scale sites, respectively. Stars indicate the location of the broad-scale sites in these areas. Comprehensive details for each site are provided in Table 2.1.

2.2.2 Broad-scale

Data to evaluate the broad-scale variation in morphology were obtained from eight sites (Gerloffs Bay (GB), Ringwood Reef (RR), Acis Reef (AR), Red Rock Bay (RB), Salmon Hole (SH), Number 2 Rocks (No2), Middle Point (MP) and Cape Northumberland (CN)) distributed along ~100 km of coastline (see Table 2.1a). The first four sites were located in areas with 'stunted' blacklip while the latter four were in areas with 'non-stunted' blacklip (Figure 2.1). 'Stunted' and 'non-stunted' sites were selected on the basis that they represented two common growth forms in the SZ, and other abalone fisheries, so the development of a 'morphometric marker' would have to at least have the ability to separate blacklip from these sites. Furthermore, these sites were also chosen as they were regularly targeted by commercial fishers. Between 120 (SH) and 236 (GB) blacklip were collected from each of these sites between October 2004 and February 2005 (see Table 2.1a).

Table 2.1: Summary of blacklip morphometric collection data from the broad- (a) and fine-scale (b) sites in the SZ. Sites arranged from north to south. Bold indicates a 'stunted' broad-scale site.

	Site	Descriptor	Latitude	Longitude	Date	n	Size range
a	Salmon Hole	SH	37°29.2' S	139°59.8'E	17/10/2004	120	51-167
	Ringwood Reef	**RR**	37°31.9' S	140°02.6'E	17/10/2004	203	37-141
	Number 2 Rocks	No2	37°48.8' S	140°19.5'E	27/11/2004	168	11-158
	Red Rock Bay	**RB**	37°54.6' S	140°23.2'E	28/11/2004	131	28-148
	Gerloffs Bay	**GB**	37°55.7' S	140°24.4'E	11/02/2005	236	27-122
	Middle Point	MP	38°02.5' S	140°37.0'E	31/10/2004	128	30-170
	Acis Reef	**AR**	38°02.8' S	140°37.9'E	31/10/2004	215	15-147
	Cape Northumberland	CN	38°03.6' S	140°39.7'E	31/10/2004	173	39-159
b	**Gerloffs Bay**	**GB**	37°55.7' S	140°24.4'E	23/05/2006	153	49-124
	Gerloffs Bay 150	GB150	37°55.8' S	140°24.2'E	23/05/2006	187	53-130
	Gerloffs Bay 400	GB400	37°55.7' S	140°24.5'E	23/05/2006	162	49-160
	Gerloffs Bay 1000	GB1000	37°55.4' S	140°23.9'E	23/05/2006	167	48-145
	Middle Point	MP	38°02.5' S	140°37.0'E	21/05/2006	134	54-156
	Middle Point 150	MP150	38°02.4' S	140°37.0'E	26/05/2006	164	50-151
	Middle Point 400	MP400	38°02.6' S	140°37.3'E	21/05/2006	138	74-153
	Middle Point 1000	MP1000	38°02.9' S	139°37.5'E	26/05/2006	161	71-158

2.2.3 Fine-scale

To assess finer-scale patterns in blacklip morphology, Gerloffs Bay and Middle Point were re-sampled in conjunction with the collection of additional samples from sub-sites located approximately 150 (GB150, MP150), 400 (GB400, MP400) and 1000 m (GB1000, MP1000) from each of these two sites (Figure 2.1; Table 2.1b). Gerloffs Bay and Middle Point were

chosen for re-sampling as blacklip from these sites showed substantial differentiation in morphology. In addition, information on the spatial extent of 'stunted' populations in Gerloffs Bay and 'non-stunted' populations in Middle Point was important as they receive high levels of fishing pressure from commercial fishers. The sub-sites were determined by moving the prescribed distance along a randomly selected compass bearing from the original site whereupon divers were deployed to locate the nearest aggregation of blacklip. Between 134 (MP) and 187 (GB150) blacklip were collected from Gerloffs Bay and Middle Point and each of the six sub- sites during May 2006 (see Table 2.1b).

2.2.4 Morphometric sampling

At all sites, samples of blacklip were collected using SCUBA within approximately a 10 x 10 m^2 area. Divers moved haphazardly among blacklip aggregations and collected every individual observed. This methodology was assumed to provide a relatively unbiased sample of the size range of blacklip present as samples were typically collected from 3 to 4 aggregations. In comparison, a strictly random approach to sampling would have relied on identifying all of the aggregations within each site which would have been difficult to achieve given the time limitations of SCUBA diving.

Numerous 'morphometric measurements' including SL, shell width (SW), shell height (SH), shell weight (SWt), shell volume (SV) and whole wet weight (WW) were obtained from each blacklip collected. All of the linear shell measurements were obtained using vernier callipers to 0.1 mm (Tissot 1988) and weight measurements were obtained using an electronic balance to 0.1 g. Shell volume was measured by sealing the respiratory pores with a latex glove, filling the shell with water and then weighing the water from the shell.

2.2.5 Data analysis

As a result of the considerable variation in SL among sites (Table 2.1; Figure 2.2), SW and SH were transformed by dividing SL with each of these variables to provide an index that was independent of SL. The effect of SL on the rest of the morphometric measures was removed using the relationship described by (Thorpe 1975) that adjusts each variable to that expected for the overall mean SL. In addition, this transformation removed the non-linearity of these relationships, satisfying the assumptions underlying the principle components analysis (PCA; Quinn and Keough 2002). Furthermore, only blacklip greater than 90 mm SL were used due to the similarity in juvenile morphology among sites (Figure 2.2). The morphometric data included in the multivariate analysis were SL/SW, SL/SH, SWt, SV and (WW). PCA was then used to reduce the dimensionality of the transformed morphometric data.

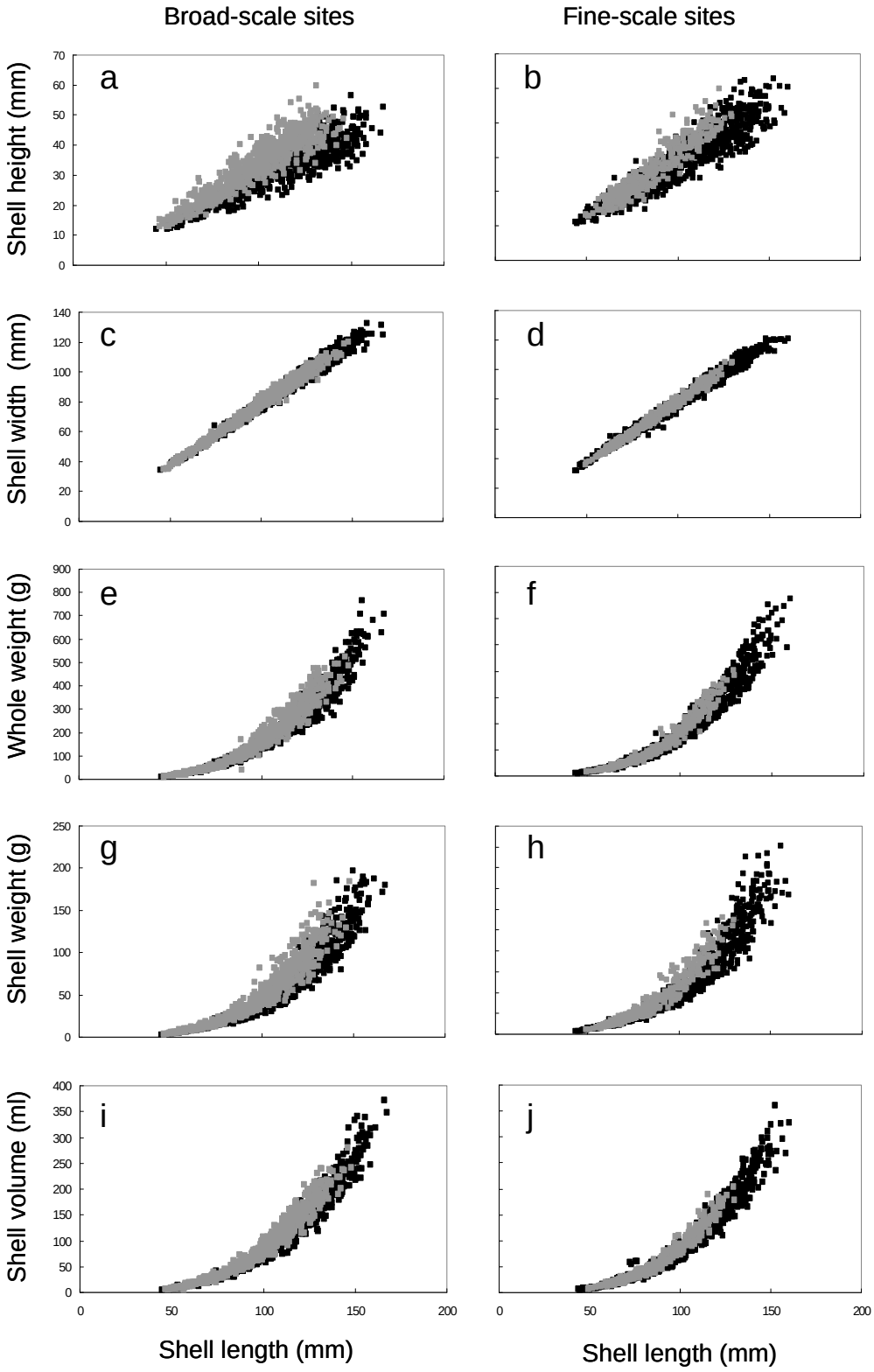

Figure 2.2: Relationships between SH (a & b), SW (c & d), WW (e & f), SWt (g & h), SV (i & j) and SL for all sites. Grey and black points indicate data from 'stunted' and 'non-stunted' sites, respectively.

Thereafter, discriminant function analysis (DFA) was used to determine which morphometric character contributed most to the observed variation among sites. This was achieved by initially including all the variables, then sequentially removing the variable with the lowest 'F-to-remove' value. The 'F-to-remove' value indicates the statistical significance of a variable in the discrimination between groups, that is, it is a measure of the extent to which a variable makes a unique contribution to the prediction of group membership. The discriminant function (DF) was developed from the retained variable with the highest 'F-to-remove' value. The success of the discrimination among sites was assessed by determining the proportion of the various groups of blacklip that were correctly assigned to their respective site of origin. The assumptions of linearity between relationships of the variables for the PCA and homogeneity of the within-group variance-covariance matrices for the DFA (Quinn and Keough 2002) were met through the above transformations of the data.

To assess the suitability of using the SL/SH ratio as a 'morphometric marker' to differentiate among sites, analysis of variance (ANOVA) was used with site as a random factor. Tukey's HSD *post hoc* tests were conducted to assess where the differences existed. Plots of residuals against group means revealed that these data satisfied the assumptions of normality and homogeneity of variance (Quinn and Keough 2002). Statistica version 6.1 (StatSoft; www.statsoft.com) was used for all ANOVA and DFA. PC-ORD was used to conduct all PCA's (McCune and Mefford 1999).

2.3 Results

2.3.1 Broad-scale

Blacklip from the 'stunted' sites generally had higher and heavier shells compared to those in 'non-stunted' sites while the rest of the morphometric measures tended to overlap between the two classifications (Figure 2.2). Principal components analysis showed that blacklip from Acis Reef and Red Rock Bay, and from Cape Northumberland, Middle Point and Number 2 Rocks exhibited similar morphometric characteristics (Figure 2.3). Blacklip from Salmon Hole tended to separate from the other 'non-stunted' sites while those from Gerloffs Bay and Ringwood Reef grouped separately to the other sites (Figure 2.3). Further, the PCA reduced the number of axes from 5 to 2 as the first two axes explained almost 95% of the variation.

The DF, based on the SL/SH ratio (Table 2.2) further supported these results. Samples of blacklip from Gerloffs Bay, Salmon Hole and Ringwood Reef showed high levels of 'correct classification' (>60%; Table 2.3). However, lower proportions (<35%) of samples from

Number 2 Rocks and Red Rock Bay were correctly classified, primarily due to the data from these sites overlapping with those from other sites (Figure 2.3).

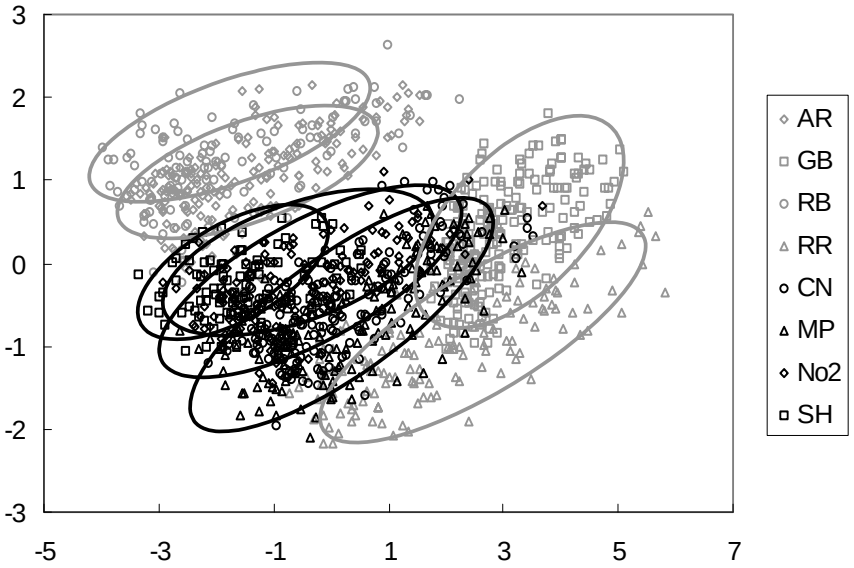

Figure 2.3: Ordination of the PCA on the morphometric characteristics from each of the eight broad-scale sites. Black and grey symbols indicate blacklip from 'non-stunted' and 'stunted' sites, respectively. Ellipses indicate 95% confidence intervals. Comprehensive details for each site are provided in Table 2.1.

The SL/SH ratio differed significantly among sites ($F_{7,772}$ = 37.65, P = <0.0001) with the Tukey's HSD tests revealing significant differences between 'stunted' and 'non-stunted' areas. Furthermore, within 'non-stunted' areas, Cape Northumberland had a significantly lower SL/SH ratio compared to the other sites (Figure 2.4). These data suggest that a SL/SH ratio >3.25 reflects blacklip from 'non-stunted' populations and <3.25 reflects individuals from 'stunted' populations.

Table 2.2: Summary outputs from the DFA on all morphometric characters for the broad- and fine- scale sites. Morphometric characters in bold indicate the DF with the highest F-to-remove value.

Scale	Morphometric character	F-to-remove
Broad-scale	**Length/height**	**58.43**
Broad-scale	Length/width	6.79
Broad-scale	Whole weight	36.65
Broad-scale	Shell weight	7.23
Broad-scale	Shell volume	40.37
Fine-scale	**Length/height**	**44.63**
Fine-scale	Length/width	3.63
Fine-scale	Whole weight	33.71
Fine-scale	Shell weight	29.77
Fine-scale	Shell volume	24.57

Table 2.3: Outputs from the DFA examining the percentage of successful discrimination among sites based on the SL/SH ratio for each of the eight broad-scale sites. Comprehensive details for each site are provided in Table 2.1.

Site	Percent correct	SH	RR	No2	RB	GB	MP	AR	CN
Salmon Hole	64.7	**55**	1	17	2	1	2	3	4
Ringwood Reef	63.8	0	**51**	3	3	17	1	2	3
Number 2 Rocks	27.7	13	8	**38**	0	14	32	0	32
Red Rock Bay	31.8	2	2	3	**28**	7	2	30	14
Gerloffs Bay	60.2	0	11	3	1	**59**	0	8	16
Middle Point	36.8	10	1	18	2	4	**43**	13	26
Acis Reef	47.6	9	2	11	13	15	3	**70**	24
Cape Northumberland	36.5	4	2	25	3	12	23	30	**57**
Total	**44.2**	**93**	**78**	**118**	**52**	**129**	**106**	**156**	**176**

2.3.2 Fine-scale

Blacklip had higher shells that were heavier in both shell and whole weight at two sub-sites (GB and GB150) compared to the other sub-sites. This variability was reflected in the PCA outputs as samples from these two sub-sites tended to group away from those of the other sub-sites (Figure 2.5), and was a result of differences observed in the SL/SH ratio (Table 2.2). However, the DFA showed that two sub-sites (GB and GB150) had low levels of correct classification as a result of samples from these two sites overlapping in the PCA (Table 2.4; Figure 2.5). MP1000 had the highest level of correct classification (62.8%) as it tended to group away from the other sites that all overlapped strongly (Table 2.4; Figure 2.5).

The SL/SH ratio varied significantly among sites ($F_{7,601}$ = 23.5, P = <0.0001). In Gerloffs Bay, the Tukey's HSD test revealed that GB and GB150 had a significantly lower SL/SH ratio compared to the other sites while MP1000 had a significantly lower SL/SH ratio compared to the other sites in Middle Point (Figure 2.6). Application of the 3.25 SL/SH ratio value identified above suggests blacklip at two sub-sites within Gerloffs Bay (GB and GB150) are 'stunted' while blacklip at the remainder of the sub-sites are 'non-stunted'. These results suggest that the spatial extent of 'stunted' blacklip populations in Gerloffs Bay is up to 400 m compared to 1000 m for 'non-stunted' populations in Middle Point.

2.4 Discussion

The collection of morphometric data across both broad and fine spatial scales enabled identification of a simple 'morphometric-marker' to distinguish among 'stunted' and 'non-stunted' blacklip populations. The substantial, small-scale spatial variation in morphology of blacklip observed in this study was most evident in differences in the SL/SH ratio of

individuals among sites. The DFA revealed that this ratio was primarily responsible for the variation observed in the PCA among sites and was consistent across broad and fine spatial scales. The spatial differentiation in blacklip morphology observed here is probably a result of spatial variability in environmental factors acting at multiple spatial scales. However, abalone morphology has been shown to vary at the finest spatial scales measured (Worthington *et al.* 1995). Given that abalone probably disperse over scales of 10-100 m's (Prince *et al.* 1987), populations formed under these conditions, that are demographically isolated from conspecifics, exist at very fine spatial scales (Temby *et al.* 2007) and would be similar to that at which environmental variability operates. Consequently, we argue that the SL/SH ratio is likely to be a useful tool for differentiating among separate abalone populations.

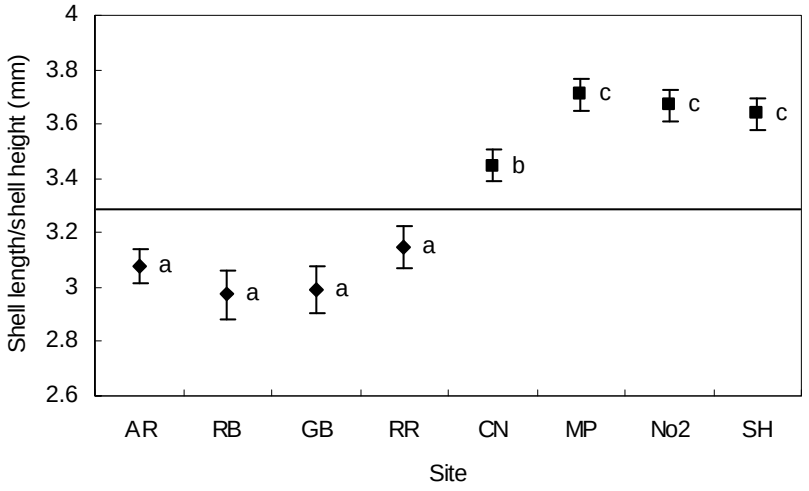

Figure 2.4: SL/SH ratio for all blacklip measured from the 'stunted' (diamonds) and 'non-stunted' (squares) broad-scale sites. Letters indicate groups classified by the Tukey's HSD test. Horizontal line indicates SL/SH ratio value that separates 'stunted' from 'non-stunted' sites. Error bars are ±1 SE. Comprehensive details for each site are provided in Table 2.1.

Table 2.4: Outputs from the DFA examining the percentage of successful discrimination among sites based on the SL/SH ratio for the GB and MP broad-scale sites and the six sub-sites. Comprehensive details for each site are provided in Table 2.1.

Site	Percent	GB	GB150	GB400	GB1000	MP	MP150	MP400	MP1000
GB	40.0	**22**	25	0	3	1	0	0	4
GB150	48.5	14	**32**	0	14	0	3	1	2
GB400	38.5	1	1	**20**	15	0	6	6	3
GB1000	62.8	2	5	7	**49**	0	5	9	1
MP	5.6	0	3	1	6	**4**	19	26	12
MP150	56.1	0	2	6	5	1	**46**	14	8
MP400	54.1	2	1	3	6	5	13	**53**	15
MP1000	54.1	3	4	1	4	7	5	15	**46**
Total	**46.3**	**44**	**73**	**38**	**102**	**18**	**97**	**124**	**91**

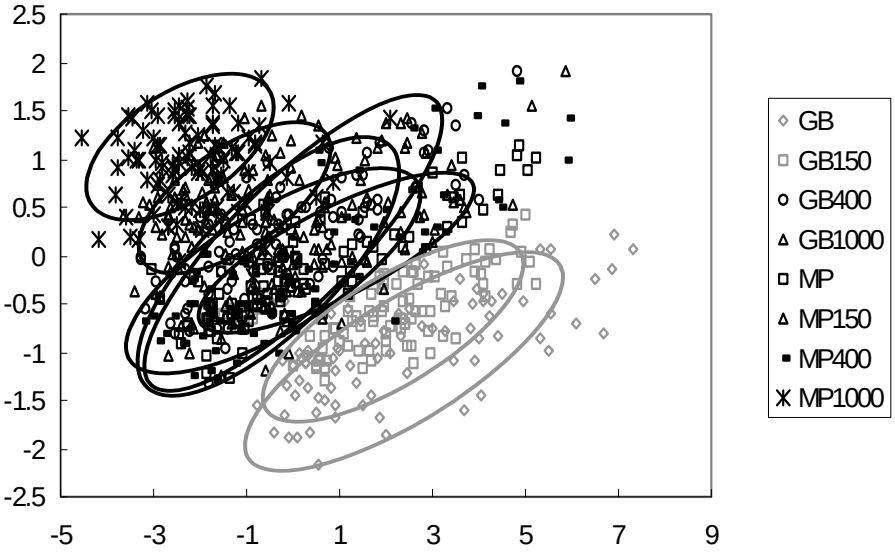

Figure 2.5: Ordination of the PCA on the morphometric characteristics from GB, MP and the six sub-sites. Black and grey symbols indicate blacklip from 'non-stunted' and 'stunted' sites, respectively. Ellipses indicate 95% confidence intervals. Comprehensive details for each site are provided in Table 2.1.

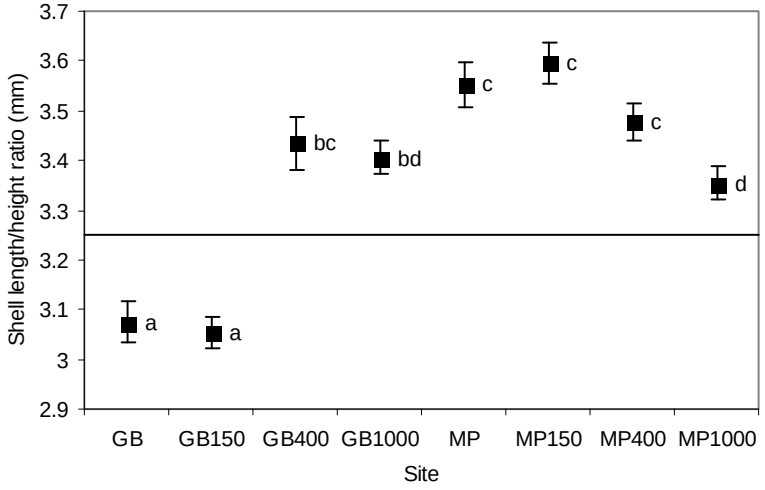

Figure 2.6: SL/SH ratio for all blacklip measured from GB, MP and the six sub-sites. Letters indicate groups classified by the Tukey's HSD test. Horizontal line indicates SL/SH ratio value that separates 'stunted' from 'non-stunted' sites. Error bars are ±1 SE. Comprehensive details for each site are provided in Table 2.1.

Broad-scale differences in morphology were greatest among sites in 'stunted' areas compared to 'non-stunted' areas, with a SL/SH ratio of 3.25 separating all of the 'stunted' and 'non-stunted' sites. However within the 'non-stunted' sites, Cape Northumberland had a significantly lower SL/SH ratio compared to the others suggesting blacklip from this site may comprise an intermediate morphological classification between the two we have presented here. The fact that the SL/SH ratio was able to identify this variability indicates that it is a sensitive measure of morphometric differentiation among blacklip populations. The

morphometric samples collected at finer scales revealed that the 'stunted' population of blacklip in Gerloffs Bay occupied a smaller area compared to the 'non-stunted' one in Middle Point. 'Stunted' individuals were only found within 400 m of the original Gerloffs Bay site while all of the samples within 1000 m of the Middle Point site were classified as 'non-stunted'. Consequently, these data suggest that the scale of differentiation between 'stunted' and 'non-stunted populations ranges from up to 400 m (Gerloffs Bay) to at least 1000 m (Middle Point). These results might imply that the population at Middle Point could potentially extend to 10's – 100's km if similar values of the SL/SH ratio were observed continuously over this range. However, the mixture of 'stunted' and 'non-stunted' populations among the broad-scale sites suggests that the environmental conditions that are probably causing the variability in the ratio are acting at finer scales. In addition, the population at Middle Point is probably nearing its boundary at this distance, as MP1000 had a significantly lower SL/SH ratio compared to the other sites in Middle Point. Alternatively, blacklip at MP1000 could represent the beginning of a separate population within Middle Point that is an intermediate classification similar to that of Cape Northumberland above.

These results are supported by those in previous studies where abalone inhabiting areas of slower rates of growth tend to have heavier, wider and higher shells compared to those located in areas with faster growth rates (Breen and Adkins 1982; McShane *et al.* 1988; Tissot 1988; Worthington *et al*. 1995). Breen and Adkins (1982) found slower-growing *H. kamatsakana* populations could be differentiated on the basis of SH. Similarly, in New South Wales, Worthington *et al*. (1995) found that slower-growing abalone populations had significantly wider shells. In their study, SH was not measured but could also have potentially separated these populations. However, neither of these studies collected samples of abalone at appropriate spatial scales to identify the spatial extent of separate populations. Our data, in combination with these studies suggest that the principles underpinning the 'morphometric marker' we have developed may be more broadly applicable to other abalone fisheries.

While the SL/SH ratio was able to discriminate between 'stunted' and 'non-stunted' populations of blacklip in the SZ so was the variability in SL. The blacklip in all of the 'non-stunted' sites had substantially greater SLs compared to those in 'stunted' sites. However, using SL as a tool to discriminate between these populations is problematic as 'non-stunted' populations that are heavily fished will have very few large abalone and the length frequencies will be similar to 'stunted' populations that are unfished. Nevertheless, length frequencies of populations in conjunction with the SL/SH ratio would be extremely useful in discriminating between 'lightly fished' and 'stunted' populations. 'Lightly fished' populations could potentially be classified as 'stunted' according to the SL/SH ratio as they tend to have

many larger abalone that have reached their maximum size and have grown substantially in shell height due to their age (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). Given that these populations will still have a higher average SL compared to that for 'stunted' populations, length frequency distributions for each of these populations would reveal this difference.

Patterns of morphometric variation among populations are likely to indicate differences in growth and maturation rates (Cadrin 2005) and will determine how they respond to exploitation (Wells and Mulvay 1995). Therefore, for the purpose of fishery stock assessment, morphologically distinct populations should be modelled and managed as separate management units (Cadrin and Friedland 1999; Cadrin 2000, 2005). While this has been attempted in the SZ with the implementation of FDAs, where stunted stocks of blacklip were thought to exist, the boundaries of these fishing areas were based on ease of geographical identification due to the limited information on the extent of these populations. The location and boundaries of these FDAs can now be re-considered by using the 'morphometric marker' we have developed as a tool to ensure they encompass only 'stunted' blacklip. For example, data presented here suggest that FDA 4, that encompasses all of Gerloffs Bay, could be reduced in size to exclude 'non-stunted' blacklip. Further, two sites (Acis Reef and Red Rock Bay) not located in any of the current FDAs were classified as 'stunted' indicating the potential for additional FDAs across the SZ. In addition, our data indicate that 'non-stunted' blacklip may exist as larger populations compared to 'stunted' blacklip. Consequently, management units for the former could potentially be much larger in size compared to those for the latter. However, further morphometric samples of blacklip are required to determine the consistency and confirm the location and extent of the 'stunted' and 'non-stunted' populations across this fishery. If individual populations of abalone can be identified using this approach then managing these separately according to their specific morphological characteristics would assist in guarding against serial depletions of abalone stocks.

The development of this approach provides a cost-effective tool to provide a wealth of data, through the measurement and analysis of shell samples to inform changes (*i.e*. a reduction) in the spatial scale of abalone management. This is timely as the concept of finer scale management of abalone fisheries has effectively become the orthodox position (Naylor *et al.* 2006) but its application has been restricted by the inability to gather detailed demographic data at useful spatial scales (Prince 2005; Naylor *et al.* 2006). Thus, use of the 'morphometric marker' developed in this Chapter provides an opportunity to bridge the traditional disconnect between scales of ecological variation and fisheries management. While these ideas are particularly pertinent for abalone given their history of stock collapse, fine-scale population

structuring is common for most sedentary invertebrates and probably for many teleosts and chondrichthyans (Prince 2005). Consequently, developing a 'morphometric marker' may be able to assist with the conservation and management of many marine species.

2.5 Conclusions

From a range of morphological measurements obtained from samples of 'stunted' and 'non-stunted' blacklip collected from two spatial scales, we identified that the ratio between shell length and shell height showed clear and significant differences among samples from these two groups. The 'morphometric marker' developed in this Chapter has the potential to be used as a tool to rapidly and cost-effectively identify individual populations that can then be managed separately. This approach is likely to be applicable to other species of abalone, as well as other sedentary invertebrates with limited larval dispersal because the ability to identify and separately manage component populations is becoming increasingly important in guarding against over-exploitation of many marine species.

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CHAPTER 3. Spatial Variation in the Biology of Blacklip Abalone and its Relationship to the 'Morphometric Marker'

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3.1 Introduction

It is becoming increasingly evident that many sedentary marine invertebrates demonstrate fine-scale population structure across their range (Strathmann *et al*. 2002; Orensanz *et al*. 2005). These individual populations (or stocks) are isolated from conspecifics by reproduction and migration (Berryman 2002) and often vary in their life-history parameters (McShane *et al*. 1988; Orensanz and Jamieson 1995; Steffani and Branch 2003; Orensanz *et al*. 2005), typically as a consequence of environmental variability (Begg *et al*. 1999).

While this variability has long been recognised, the spatial scale at which it exists is poorly understood, due to biological data being typically collected from study sites that inadequately represent the variation that occurs across the distribution of the species (Prince 2005). The lack of appropriate data to inform marine scientists and managers has resulted in many of these species becoming serially depleted across their range, with stock collapses occurring in some extreme cases (Tegner *et al*. 1996; Perry *et al*. 2002; Orensanz *et al*. 2005). Thus, while there is a clear need to acquire information on the biological variability among separate populations, this process has been restricted by the high costs and difficulties of collecting these data across the required range of spatial scales (Prince 2005).

The collection of morphometric data may offer a cost-effective alternative for inferring key biological parameters for individual populations. This is a result of patterns in morphometric variation reflecting differences in growth, maturation rates and fecundity, as body form is a product of ontogeny (Begg *et al*. 1999; Cadrin 2005). For example, individuals in populations characterised by slower growth tend to be smaller in body form, mature at smaller sizes and produce less eggs compared to those in populations with faster growth (Campbell *et al*. 2003;

Campbell and Ming 2003). If biological variability can be linked to a simple morphometric measure, inferring the biology of a species at appropriate spatial scales, using morphological variability as a surrogate becomes practicable.

In addition, these relationships enable spatial variability in morphology to be used to identify separate populations of these species (Chapter 2; Cadrin and Silva 2005; Saunders *et al*. 2008), based on their different biological characteristics. While this approach has been commonly used in teleosts (Worthington *et al.* 1995b; Berg *et al*. 2005; Cadrin and Silva 2005) it can be applied to sedentary marine invertebrates that have easily-measurable, hard-body parts that reflect their ontogenetic history. Although these morphological characteristics may be environmentally induced (Swain and Foote 1999; Alunno-Bruscia *et al*. 2001; Swain *et al*. 2005), the highly localised populations formed by sedentary invertebrates with limited adult movement and larval dispersal are likely to exist at similar scales to this environmental variation.

Abalone (genus *Haliotis*) are a typical sedentary invertebrate species, having numerous discrete populations across their range (Prince 2005; Morgan and Shepherd 2006) that often differ in their biology and morphology (McShane *et al*. 1988; Worthington *et al*. 1995b; Worthington and Andrew 1997, 1998; Tarbath 2003). This variability commonly results in the presence of so-called 'stunted' areas of abalone that have a slower growth rate and/or a smaller maximum length compared to adjacent populations (Nash 1992; Wells and Mulvay 1995). 'Stunted' populations typically form dense aggregations in sheltered areas with lower wave exposure (McShane and Naylor 1995). It is suggested that abalone in these protected areas grow more slowly, mature at smaller sizes and produce fewer eggs compared to individuals in more exposed habitats (Shepherd *et al*. 1991; Wells and Mulvay 1995; Worthington and Andrew 1997; Campbell *et al*. 2003). This variability is considered to be primarily a result of lower water movement providing less food in the form of drift algae (Day and Fleming 1992; Shepherd and Steinberg 1992; McShane and Naylor 1995). However, density-dependent processes, or genetic variability, may also contribute to lower rates of growth in 'stunted' areas, compared to other fished populations (Emmett and Jamieson 1988; Dixon and Day 2004).

The current broad-scale (100 – 1000 km; McShane *et al*. 1994a) management of most abalone fisheries fails to account for the finer-scale variability in their population structure, leaving fast-growing populations prone to overfishing and slower-growing populations under utilised (Strathmann *et al*. 2002; Prince 2005). In response to this localised variability, the spatial scale of management in Australian abalone fisheries has decreased substantially over recent

years. Notably, in the Southern Zone of the South Australian abalone fishery (SZ), separately managed, 'fish-down' areas (FDAs) within which the blacklip abalone (*H. rubra*, hereafter referred to as blacklip) populations are considered 'stunted' were introduced between 1989 and 1994. Despite these attempts to reduce the spatial scale of management, it is widely acknowledged that the current management areas still encompass numerous populations of abalone that vary in their life-history parameters.

To overcome this challenge, stakeholders in the Victorian Western Zone abalone fishery use a qualitative assessment of the shape (*i.e.* flat or domed) and appearance (*i.e.* clean or fouled) of shells from commercial catches to aid reef-specific assessment (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). This has led to increasingly complex spatial management of the resource, with current management arrangements including reef-specific catch limits and minimum legal lengths. However, these assessments of shell shape and appearance need to be calibrated with key biological parameters to ensure that individual populations of abalone are being managed on the basis of their biological characteristics.

Obtaining biological information for individual populations of abalone is unlikely to be achievable by traditional research methods, given the high costs of conducting tag-recapture and reproductive studies across the scale of current fisheries. However, the substantial spatial variation in abalone morphology (Chapter 2; Breen and Adkins 1982; McShane *et al*. 1994b; Worthington *et al*. 1995a; Saunders *et al*. 2008) may offer a proxy through which biological variability among populations can be inferred. For example, identification of a simple 'morphometric marker' (Chapter 2; Saunders *et al*. 2008), based on the ratio of shell length to shell height (SL/SH ratio), enabled differentiation between 'stunted' and 'non-stunted' populations in the SZ. Linking this simple measure to key biological parameters has the potential to enhance the utility of the 'morphometric marker' as a tool to support fine-scale, spatial management of abalone fisheries.

In this Chapter, we investigated the spatial variability in the rate of growth, size at maturity and fecundity among populations of blacklip in the SZ. This was achieved by collecting biological information from 'stunted' and 'non-stunted' sites at broad (10 km's) and fine (100 m's) spatial scales within this fishery. Further, to assess whether spatial variation in morphology was reflected in the biological variation, we examined the strength of the relationships between key biological parameters and the simple 'morphometric marker' developed previously (Chapter 2; Saunders *et al*. 2008). This enabled evaluation of the utility of this 'morphometric marker' to infer biological characteristics of blacklip populations.

3.2 Methods

3.2.1 Study site

This study was conducted in the SZ, which includes all coastal waters of South Australia east of Meridian 139°E, with the exception of the Coorong and waters inside the Murray River mouth. After consultation with divers and licence holders, all of the sites were distributed between Beachport and the South Australia/Victoria border (Figure 3.1). Data to evaluate the spatial variation in the rate of growth, size at maturity and fecundity were obtained from eight sites (Gerloffs Bay (GB), Ringwood Reef (RR), Acis Reef (AR), Red Rock Bay (RB), Salmon Hole (SH), Number 2 Rocks (No2), Middle Point (MP) and Cape Northumberland (CN)) distributed along ~100 km of coastline. The first four sites were located in areas with 'stunted' blacklip while the latter four were in areas with 'non-stunted' blacklip (Figure 3.1). 'Stunted' and 'non-stunted' sites were selected on the basis that they represented two common growth forms in the SZ, and other abalone fisheries. To assess finer-scale patterns in blacklip biological parameters Gerloffs Bay and Middle Point were re-sampled in conjunction with the collection of additional samples from sub-sites located approximately 150 (GB150, MP150), 400 (GB400, MP400) and 1000 m (GB1000, MP1000) from each of the two sites (Figure 3.1). Gerloffs Bay and Middle Point were chosen for re-sampling as blacklip from these sites showed biological traits that were typical of 'stunted' and 'non-stunted' populations, respectively. The sub-sites were determined by moving the prescribed distance along a randomly selected compass bearing from the original site whereupon divers were deployed to locate the nearest aggregation of blacklip.

3.2.2 Growth

Between 368 (SH) and 404 (RR) blacklip were tagged at each of the eight broad-scale sites between November 2004 and January 2005 (Table 3.1). This process required that they be removed from the water to tag and measure the shell length (SL) of individuals to the nearest 0.5 mm before they were replaced in the area from where they were collected. Individuals were collected in a haphazard manner to obtain a representative sample of the size range present in each site. Small (12 mm), individually numbered, plastic disc tags were attached to blacklip by fixing a nylon rivet to the proximal pore hole of the shell (Prince 1991). These individuals were then recaptured and re-measured for SL during January and February 2006. Recaptures from the Gerloffs Bay and Middle Point sites were returned to the site from which they were recaptured so that growth data could be collected at these sites during the same time period as the sub-sites. At the sub-sites, between 158 (GB1000) and 288 (GB150) blacklip were tagged and measured as described above between January and May 2006 and were recaptured and re-measured between November 2006 and April 2007 (Table 3.1).

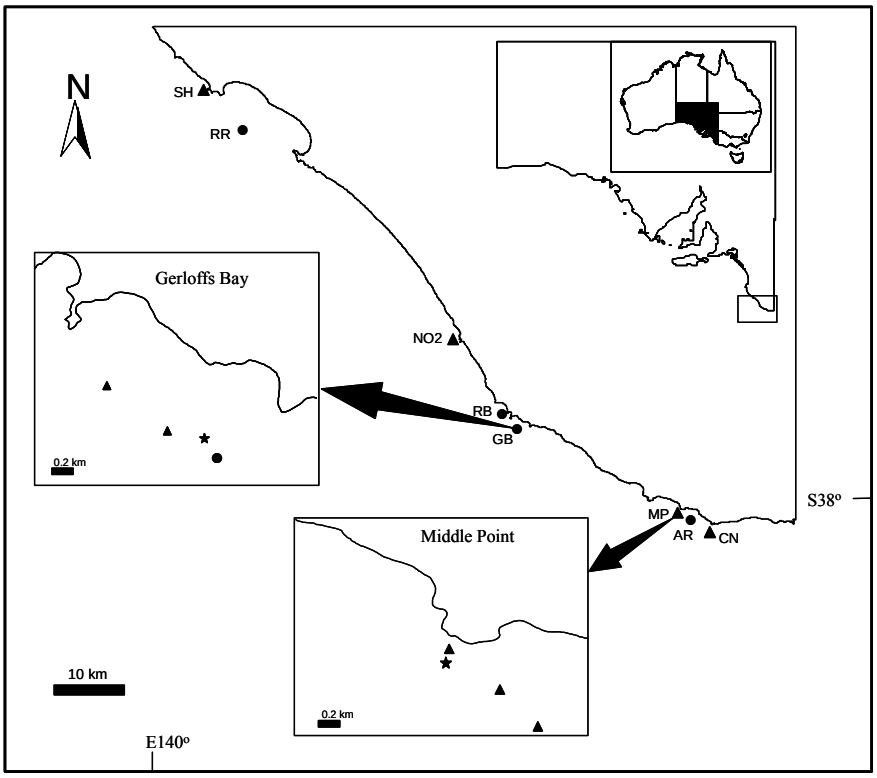

Figure 3.1: Map of study area showing locations of the eight broad-scale sites and the sub-sites within GB and MP (inserts). Circles and triangles represent 'stunted' and 'non-stunted' sites, respectively. Comprehensive details for each site are provided in Table 3.1.

3.2.3 Size at maturity

Between 120 (SH) and 236 (GB) blacklip (> 30 mm SL) were collected by SCUBA divers from the broad-scale sites between October 2004 and February 2005. Blacklip have advanced gonadal development between October and April in the SZ (Mayfield *et al*. 2002) so the blacklip sampled during this study should not have their size at maturity skewed to higher size classes as a result of having recently spawned. In addition, between 131 (MP150) and 187 (GB150) blacklip were collected between December 2006 and January 2007 from the sub-sites within Gerloffs Bay and Middle Point (Table 3.1). Each blacklip was measured and the reproductive state (immature, male or female) determined macroscopically, based on gonad colour (immature-brown, male-creamy and female-pale green; Shepherd and Laws 1974).

3.2.4 Fecundity

The entire visceral mass of approximately 30 mature female blacklip were retained from the size-at-maturity samples from all sites. Individuals ranged in size from 55 to 157 mm SL. To preserve the visceral mass for subsequent egg counting, each sample was labelled and preserved in 100% ethanol for at least one month.

Table 3.1: Summary of blacklip tagging and collection data from the broad- (a) and fine-scale (b) sites in the SZ. Sites arranged from north to south. Bold indicates a 'stunted' site.

	Location				Tagging data						Collection data		
	Site	Descriptor	Latitude	Longitude	Date tagged	Number tagged	Size range tagged (mm SL)	Date recaptured	Number recaptured (%)	Size range recaptured (mm SL)	Date collected	Number collected	Size range collected (mm SL)
a	Salmon Hole	SH	37°29.2' S	139°59.8'E	13/12/2004	368	54-181	19/01/2006	76 (20.6)	85-181	17/10/2004	120	51-167
	Ringwood Reef	**RR**	37°31.9' S	140°02.6'E	25/11/2004	404	36-147	19/01/2006	63 (15.6)	55-147	17/10/2004	203	37-141
	Number 2 Rocks	No2	37°48.8' S	140°19.5'E	27/11/2004	398	41-164	20/01/2006	97 (24.4)	75-166	27/11/2004	168	11-158
	Red Rock Bay	**RB**	37°54.6' S	140°23.2'E	03/12/2004	397	60-150	20/01/2006	74 (18.6)	78-150	28/11/2004	131	28-148
	Gerloffs Bay	**GB**	37°55.7' S	140°24.4'E	29/01/2005	402	28-124	05/02/2006	58 (14.4)	41-124	11/02/2005	236	27-122
	Middle Point	MP	38°02.5' S	140°37.0'E	10/11/2004	399	38-167	21/01/2006	59 (14.8)	38-167	31/10/2004	128	30-170
	Acis Reef	**AR**	38°02.8' S	140°37.9'E	11/11/2004	398	34-148	21/01/2006	65 (16.3)	67-148	31/10/2004	215	15-147
	Cape Northumberland	CN	38°03.6' S	140°39.7'E	26/11/2004	396	21-148	06/02/2006	75 (18.9)	60-148	31/10/2004	173	39-159
b	**Gerloffs Bay**	**GB**	37°55.7' S	140°24.4'E	29/01/2006	58	41-124	22/11/2006	39 (67.2)	36-112	04/01/2007	153	49-124
	Gerloffs Bay 150	GB150	37°55.8' S	140°24.2'E	16/05/2006	288	37-142	16/04/2007	34 (8.3)	37-120	04/01/2007	187	53-130
	Gerloffs Bay 400	GB400	37°55.7' S	140°24.5'E	17/05/2006	179	63-160	25/04/2007	45 (25.1)	63-149	10/01/2007	162	49-160
	Gerloffs Bay 1000	GB1000	37°55.4' S	140°23.9'E	16/05/2006	158	41-186	16/04/2007	32 (20.3)	53-160	10/01/2007	168	48-145
	Middle Point	MP	38°02.5' S	140°37.0'E	21/01/2006	59	75-156	13/04/2007	28 (47.5)	63-154	10/12/2006	135	48-156
	Middle Point 150	MP150	38°02.4' S	140°37.0'E	26/04/2006	207	53-160	13/04/2007	70 (33.8)	61-161	10/12/2006	131	44-150
	Middle Point 400	MP400	38°02.6' S	140°37.3'E	27/04/2006	201	49-155	14/04/2007	35 (17.4)	57-140	10/12/2006	138	59-153
	Middle Point 1000	MP1000	38°02.9' S	139°37.5'E	26/04/2006	209	40-152	13/04/2007	51 (24.4)	56-141	10/12/2006	161	50-158

Following preservation, the ovary was excised from the visceral mass and weighed to the nearest 0.01 g. Estimates of the number of eggs per gram of ovary were obtained from three sub-samples taken from three regions of the gonad (tip of the conical appendage, top of the body whorl and anterior gonad; after Wells and Keesing 1989). Sub-sample wet weights ranged from 0.4 to 2.5 mg. Each sub-sample was separated, and the eggs flushed into a plankton-counting chamber with 70% ethanol and counted using a dissecting microscope at 40x magnification. The total number of eggs for each blacklip was calculated by multiplying the average egg number per gram of gonad, by the total weight of the gonad.

3.2.5 Data analysis

To test for differences in rates of growth among sites an analysis of covariance (ANCOVA) was carried out on the regression slopes of annual growth rate against length at tagging.

The percentage of mature blacklip was determined for individual 5 mm size classes. These data were fitted to a two parameter logistic curve (after Schnute and Richards 1990) of the form:

$$P(L) = (1 + \exp[-(L - L_{50}) / \delta])^{-1}$$

Where $P(L)$ represents the proportion of mature blacklip from length class L, L_{50} the length at 50% maturity and δ the steepness of the ogive. The model parameters were estimated by minimising the negative binomial likelihoods. The confidence intervals for L_{50} were determined using profile likelihood methods (Haddon 2001). Likelihood ratio tests were used to test for differences in L_{50} among sites.

Egg number was log transformed and differences among the slopes and Y-intercepts of the resultant linear relationships (log egg number = m·SL + c) were investigated using ANCOVA. Site was a random factor and shell length a covariate for these analyses.

Given the assumption of ANCOVA that the covariate is similarly distributed between treatments for each analysis (Quinn and Keough 2002), data were truncated to examine the robustness of the test. Truncating the growth and log transformed fecundity data did not alter the significance of the test so all data were retained in the analyses. To determine where the significant differences lay between factors, *t*-tests on adjusted means were calculated for each combination of factors with a sequential Bonferonni adjustment of significance levels to correct for multiple testing (Quinn and Keough 2002).

Relationships between each biological parameter (residuals of growth, L_{50} and residuals of fecundity) and the SL/SH ratio were evaluated by plotting the biological parameters against the average SL/SH ratio for each of the collections at the broad-scale sites and the sub-sites separately, and for all sites combined. The average growth residuals were calculated by using multiple linear regression for the eight broad-scale sites. The residuals from this analysis indicated whether a shell was longer or shorter than expected compared to the average growth relationship. Residuals were calculated in the same way for the sub-sites. This residual analysis was used in a similar way on the log-transformed fecundity relationship among sites. The maximum likelihood estimates calculated for L_{50} above were used in these plots. Relationships among these variables were investigated through correlation analyses.

3.3 Results

3.3.1 Growth

There was a significant linear relationship between SL at tagging and rate of growth at all sites, with larger individuals growing more slowly compared to smaller ones (Table 3.2; Figures 3.2 and 3.3). There was significant variation among the broad-scale sites ($F_{7,533}$ = 20.05, $P < 0.0001$). This variation was primarily a result of blacklip in the 'non-stunted' sites (CN, MP, No2 and SH) having significantly higher rates of growth when compared to those in 'stunted' sites (AR, GB, RB and RR; Figure 3.2). Furthermore, blacklip at two 'non-stunted' sites, Number 2 Rocks and Salmon Hole, had significantly faster rates of growth compared to Cape Northumberland and Middle Point (Figure 3.2). There was also significant variation among the blacklip tagged within Gerloffs Bay ($F_{3,145}$ = 8.84, $P < 0.0001$) and Middle Point ($F_{3,179}$ = 22.90, $P < 0.0001$). Multiple comparisons revealed that blacklip at three locations (GB, GB150 and MP1000) had significantly slower rates of growth compared to the other sites (Figure 3.3).

3.3.2 Size at maturity

Among the broad-scale sites, the likelihood ratio test revealed that L_{50} was generally significantly lower for blacklip in 'stunted', compared to 'non-stunted' sites (Figure 3.4). The exception was Red Rock Bay, at which blacklip had a similar L_{50} compared to those for most of the 'non-stunted' sites (Figure 3.4). Blacklip at Salmon Hole had a significantly higher L_{50} compared to all of the other sites (Figure 3.4). There were also differences in L_{50} within Gerloffs Bay as a result of individuals at two sites (GB and GB150) having a significantly lower L_{50} compared to those at other sites (Figure 3.5). The L_{50} for blacklip at MP1000 was significantly lower when compared to the rest of the sites in this area (Figure 3.5).

Table 3.2: Sample size (n), correlation coefficient (*r*) and *P* value from the relationship between blacklip SL at tagging and annual growth rate for all broad- (a) and fine-scale (b) sites in the SZ. Values for a and b are the constants of the linear relationship. Comprehensive details for each site are provided in Table 3.1.

	Site	n	a	b	*r*	*P*
a	Salmon Hole	76	0.257	39.98	0.898	<0.001
	Ringwood Reef	63	0.191	24.49	0.916	<0.001
	Number 2 Rocks	82	0.225	36.01	0.845	<0.001
	Red Rock Bay	74	0.184	24.27	0.858	<0.001
	Gerloffs Bay	58	0.157	18.84	0.855	<0.001
	Middle Point	59	0.225	32.01	0.904	<0.001
	Acis Reef	62	0.212	27.12	0.921	<0.001
	Cape Northumberland	75	0.217	30.07	0.885	<0.001
b	Gerloffs Bay	39	0.114	15.61	0.527	<0.001
	Gerloffs Bay 150	31	0.060	11.98	0.381	<0.001
	Gerloffs Bay 400	44	0.239	34.75	0.813	<0.001
	Gerloffs Bay 1000	33	0.169	28.26	0.669	<0.001
	Middle Point	28	0.225	31.34	0.937	<0.001
	Middle Point 150	70	0.333	47.66	0.898	<0.001
	Middle Point 400	35	0.296	39.85	0.816	<0.001
	Middle Point 1000	51	0.268	38.12	0.784	<0.001

3.3.3 Fecundity

Samples among the broad-scale sites showed significant variability in fecundity ($F_{7,254} = 2.31$, $P < 0.03$). However, the multiple comparisons revealed that these were a result of blacklip within Gerloffs Bay and Red Rock Bay having significantly lower fecundity compared to the other sites, rather than differences between 'stunted' and 'non-stunted' sites (Figure 3.6). There were also significant differences in the fecundity of blacklip within Gerloffs Bay ($F_{3,82} = 6.00$, $P < 0.001$) and Middle Point ($F_{3,80} = 4.41$, $P < 0.001$) as a result of blacklip at three sites (GB, GB150 and MP1000) having significantly lower fecundity when compared with that for blacklip at the remaining sites (Figure 3.7).

3.3.4 Relationships between biology and morphology

There were significant positive relationships between the SL/SH ratio and growth (broad-scale sites: $r = 0.804$, df = 7, $P < 0.01$; sub-sites: $r = 0.868$, df = 7, $P < 0.005$), L_{50} (broad-scale sites: $r = 0.761$, df = 7, $P < 0.02$; sub-sites: $r = 0.925$, df = 7, $P < 0.001$) and fecundity (broad-scale sites: $r = 0.673$, df = 7, $P < 0.05$; sub-sites: $r = 0.717$, df = 7, $P < 0.05$; Figure 3.8). Furthermore, when data from the broad-scale and sub-sites were combined, there were significant correlations between the SL/SH ratio and each of the biological parameters (growth: $r = 0.826$, df = 15, $P < 0.001$; L_{50}: $r = 0.807$, df = 15, $P < 0.001$; fecundity: $r = 0.647$, df = 15, $P < 0.005$; Figure 3.8).

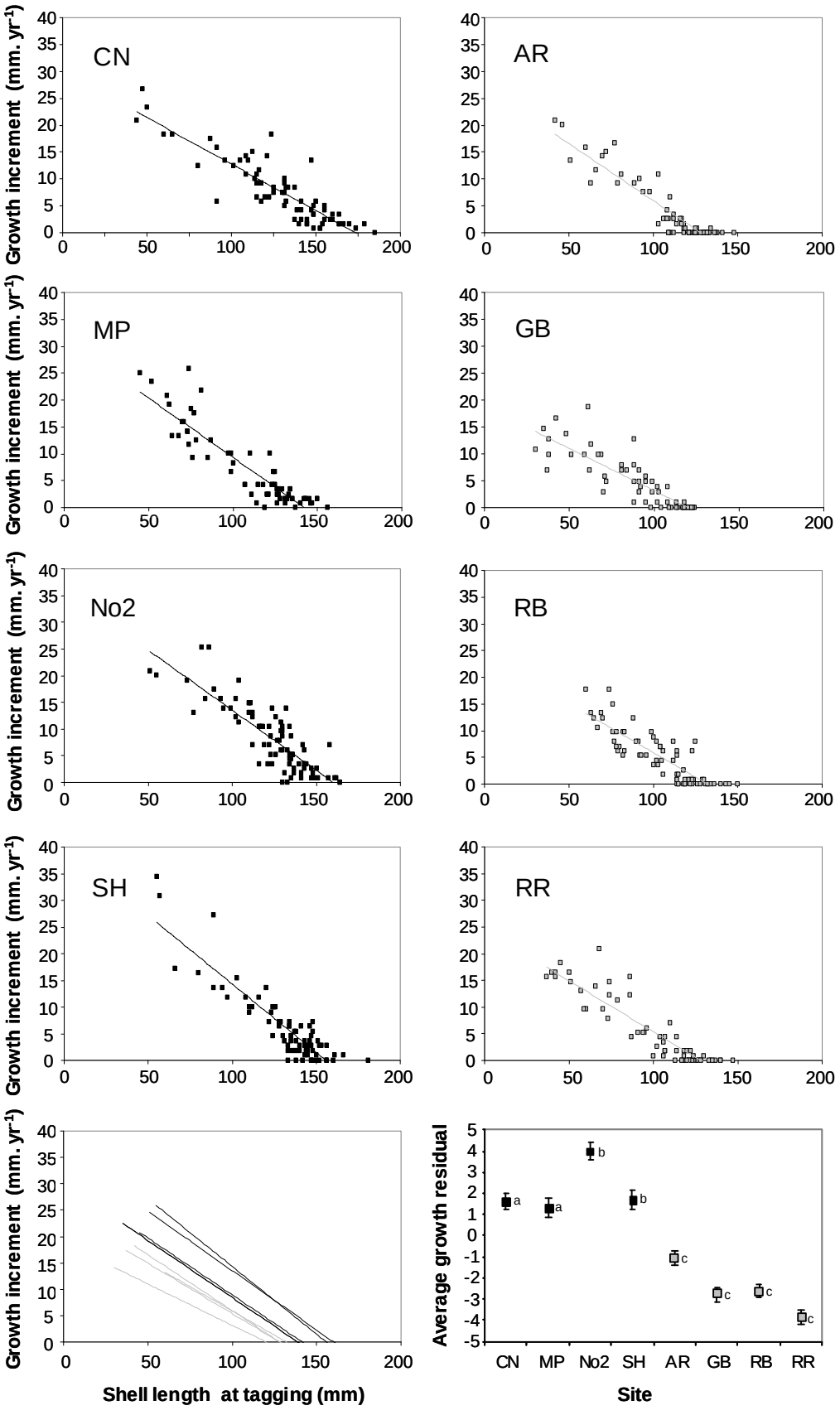

Figure 3.2: Relationship between SL at tagging and growth increment for blacklip at the broad-scale sites. The bottom two plots are the trend lines for each of these relationships and the average growth residuals for all sites. Letters indicate similar groups classified by the multiple comparisons. Black and grey symbols indicate 'non-stunted' and 'stunted' sites, respectively. Error bars are ±1 SE. Comprehensive details for each site are provided in Table 3.1.

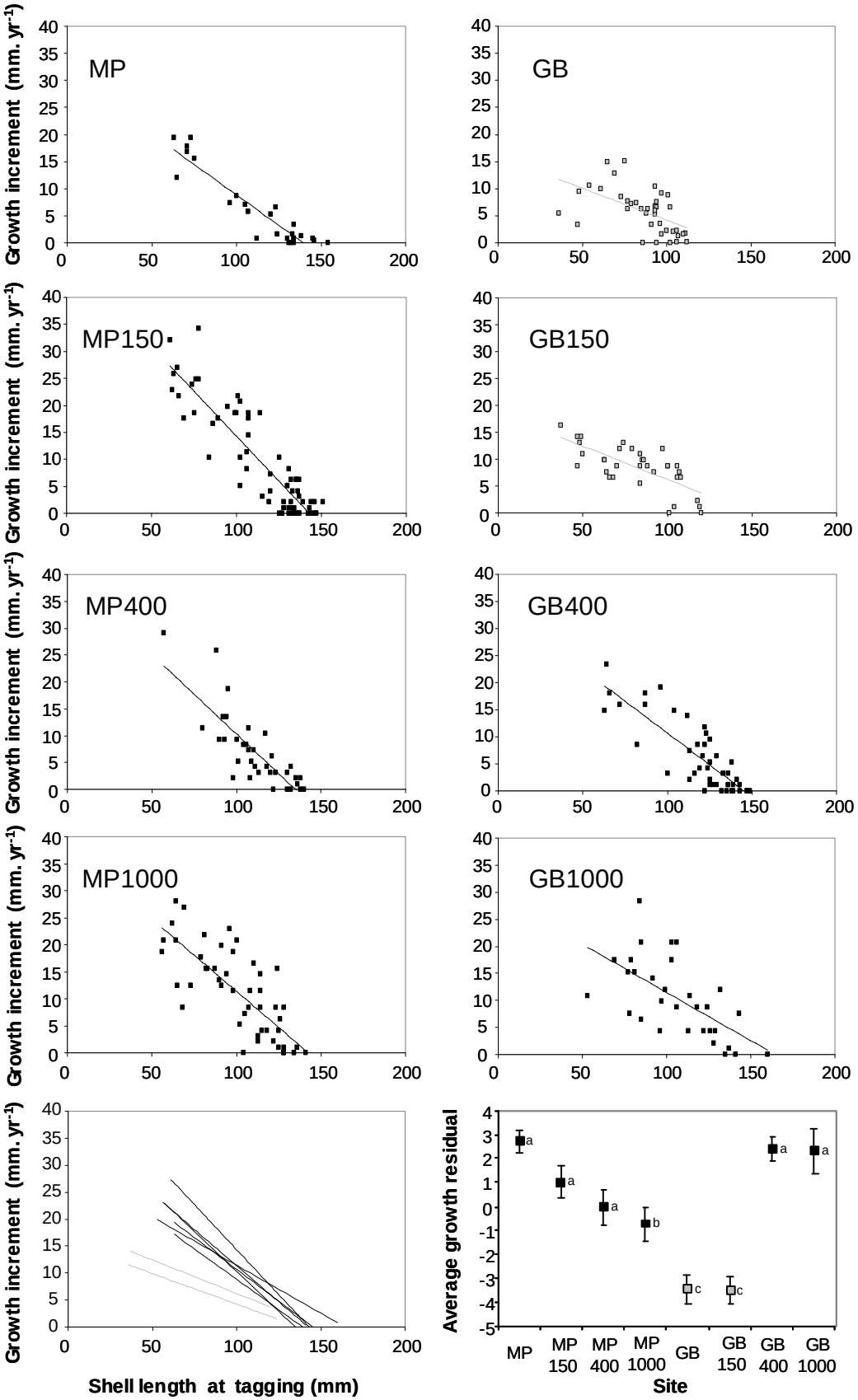

Figure 3.3: Relationship between SL at tagging and growth increment for blacklip at the MP and GB broad-scale sites and sub-sites. The bottom two plots are the trend lines for each of these relationships and the average growth residuals for all sites. Letters indicate similar groups classified by the multiple comparisons. Black and grey symbols indicate 'non-stunted' and 'stunted' sites, respectively. Error bars are ±1 SE. Comprehensive details for each site are provided in Table 3.1.

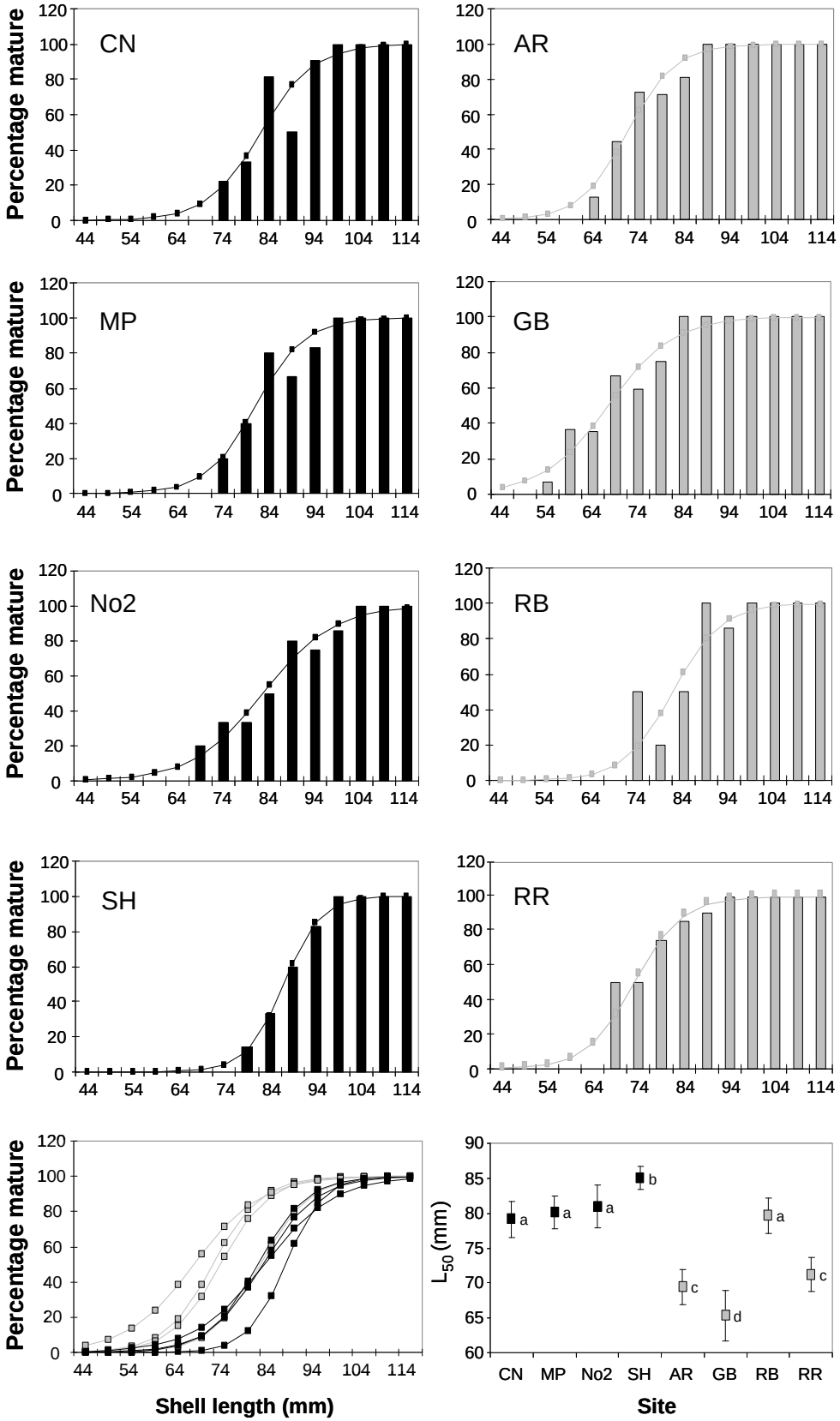

Figure 3.4: Percentage of mature blacklip within each size class at the broad-scale sites. The bottom two plots are the trend lines for each of these relationships and the estimates of L_{50} for all sites. Letters indicate similar groups classified by the likelihood ratio test. Black and grey symbols indicate 'non-stunted' and 'stunted' sites, respectively. Error bars indicate 95% confidence intervals. Comprehensive details for each site are provided in Table 3.1.

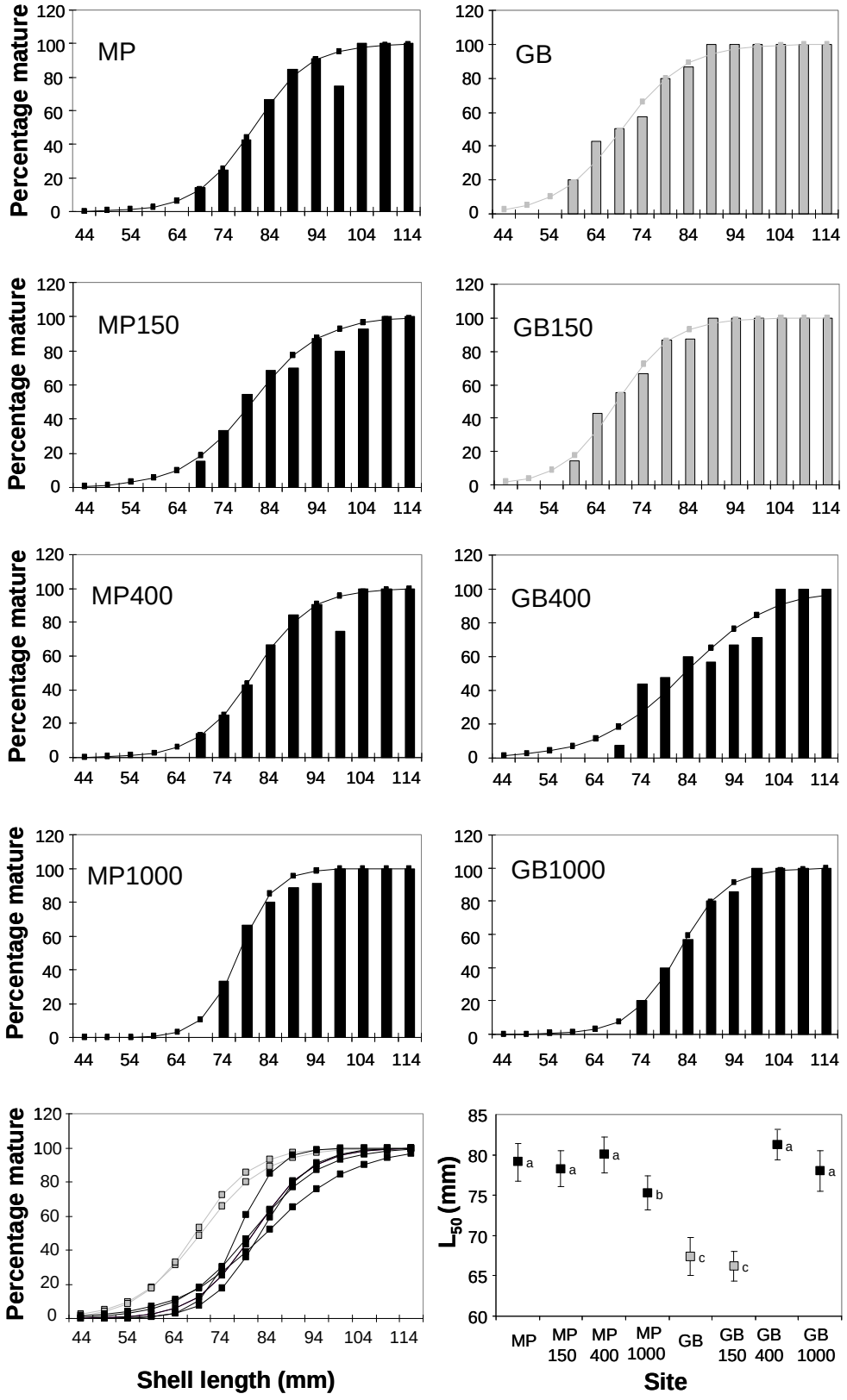

Figure 3.5: Percentage of mature blacklip within each size class at the MP and GB broad-scale sites and sub-sites. The bottom two plots are the trend lines for each of these relationships and the estimates of L_{50} for all sites. Letters indicate similar groups classified by the likelihood ratio test. Black and grey symbols indicate 'non-stunted' and 'stunted' sites, respectively. Error bars indicate 95% confidence intervals. Comprehensive details for each site are provided in Table 3.1.

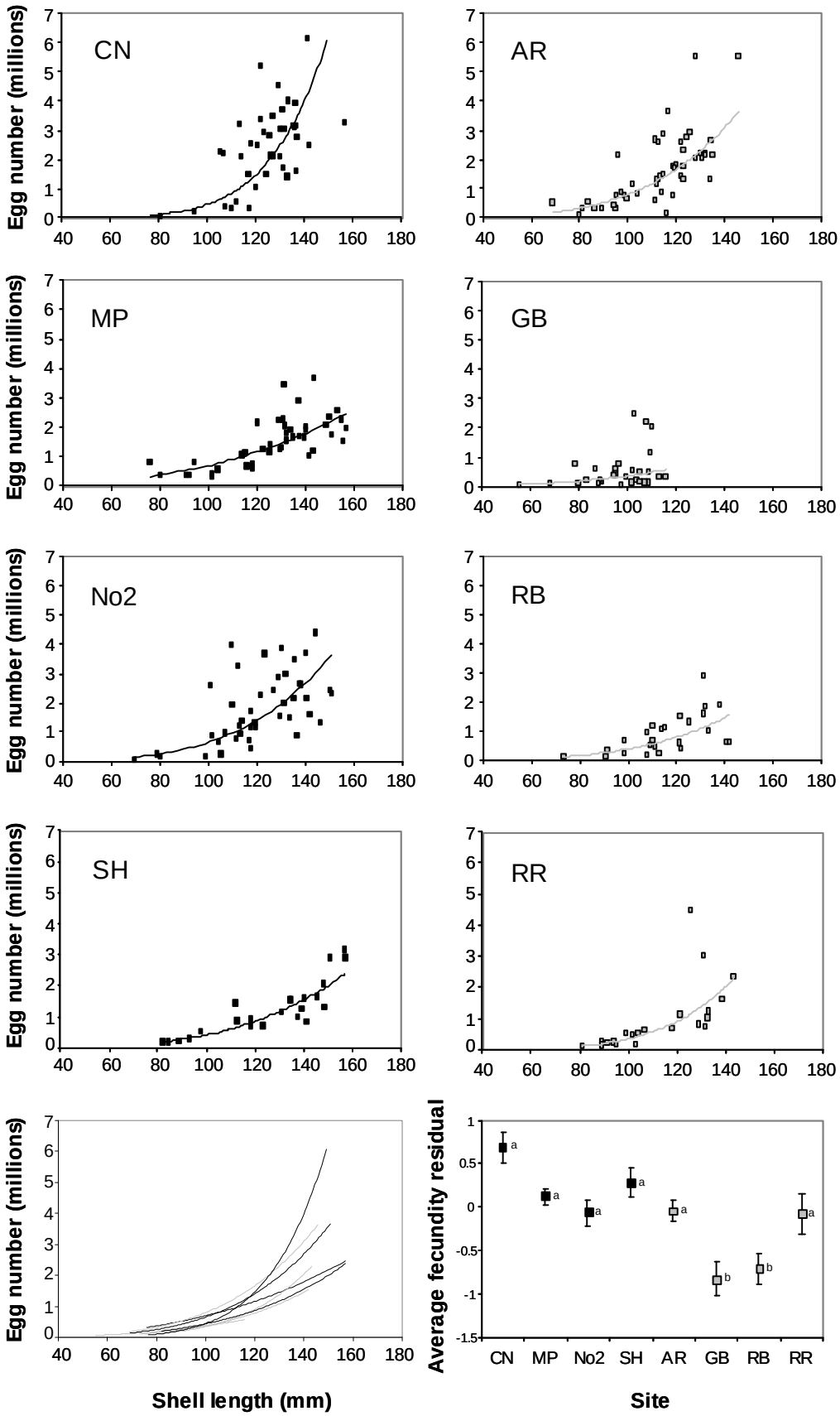

Figure 3.6: Relationship between number of eggs and SL for blacklip at the broad-scale sites. The bottom two plots are the trend lines for each of these relationships and the average fecundity residuals for all sites. Letters indicate similar groups classified by the multiple comparisons. Black and grey symbols indicate 'non-stunted' and 'stunted' sites, respectively. Error bars are ±1 SE. Comprehensive details for each site are provided in Table 3.1.

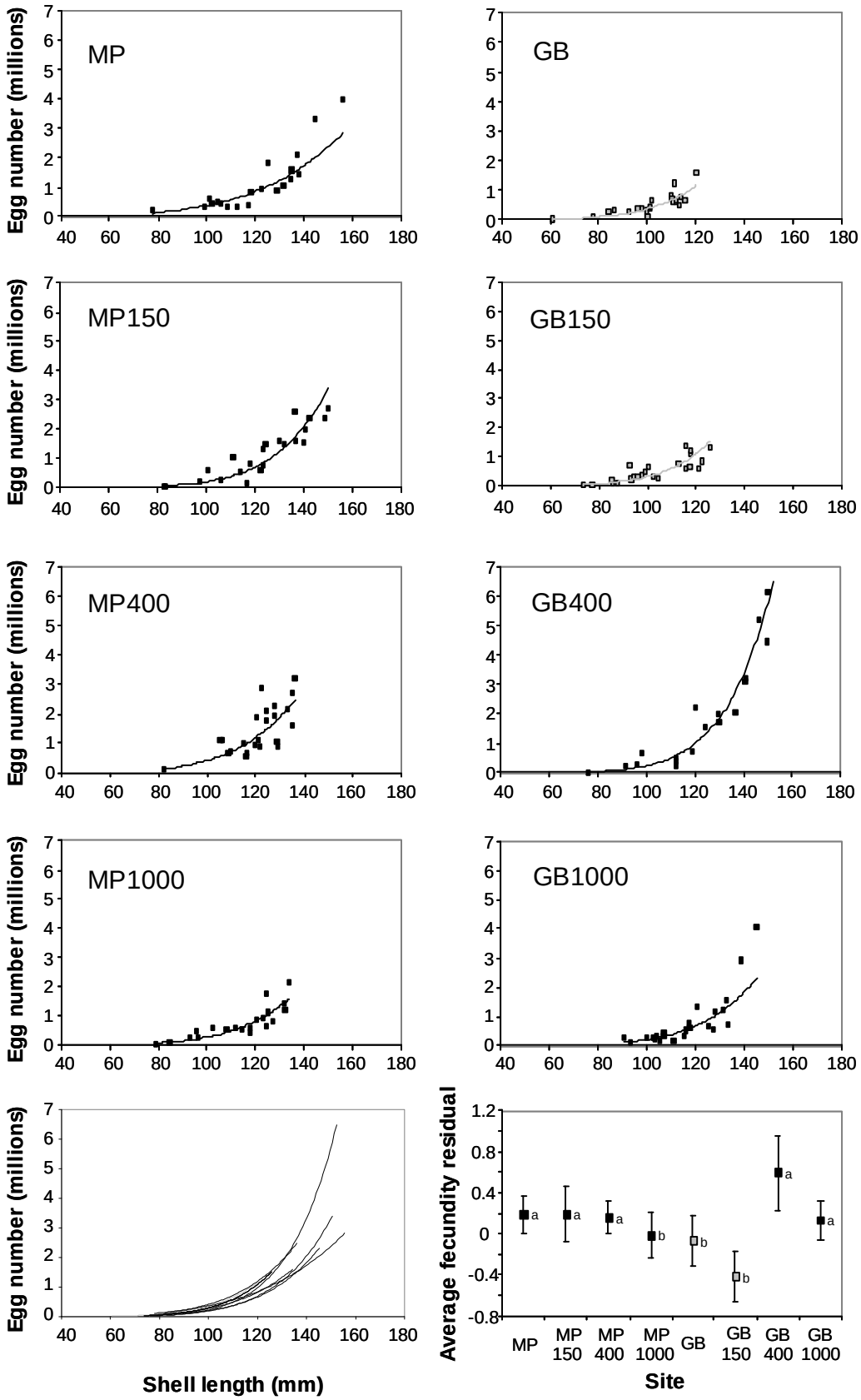

Figure 3.7: Relationship between number of eggs and SL for blacklip at the MP and GB broad-scale sites and sub-sites. The bottom two plots are the trend lines for each of these relationships and the average fecundity residuals for all sites. Letters indicate similar groups classified by the multiple comparisons. Black and grey symbols indicate 'non-stunted' and 'stunted' sites, respectively. Error bars are ±1 SE. Comprehensive details for each site are provided in Table 3.1.

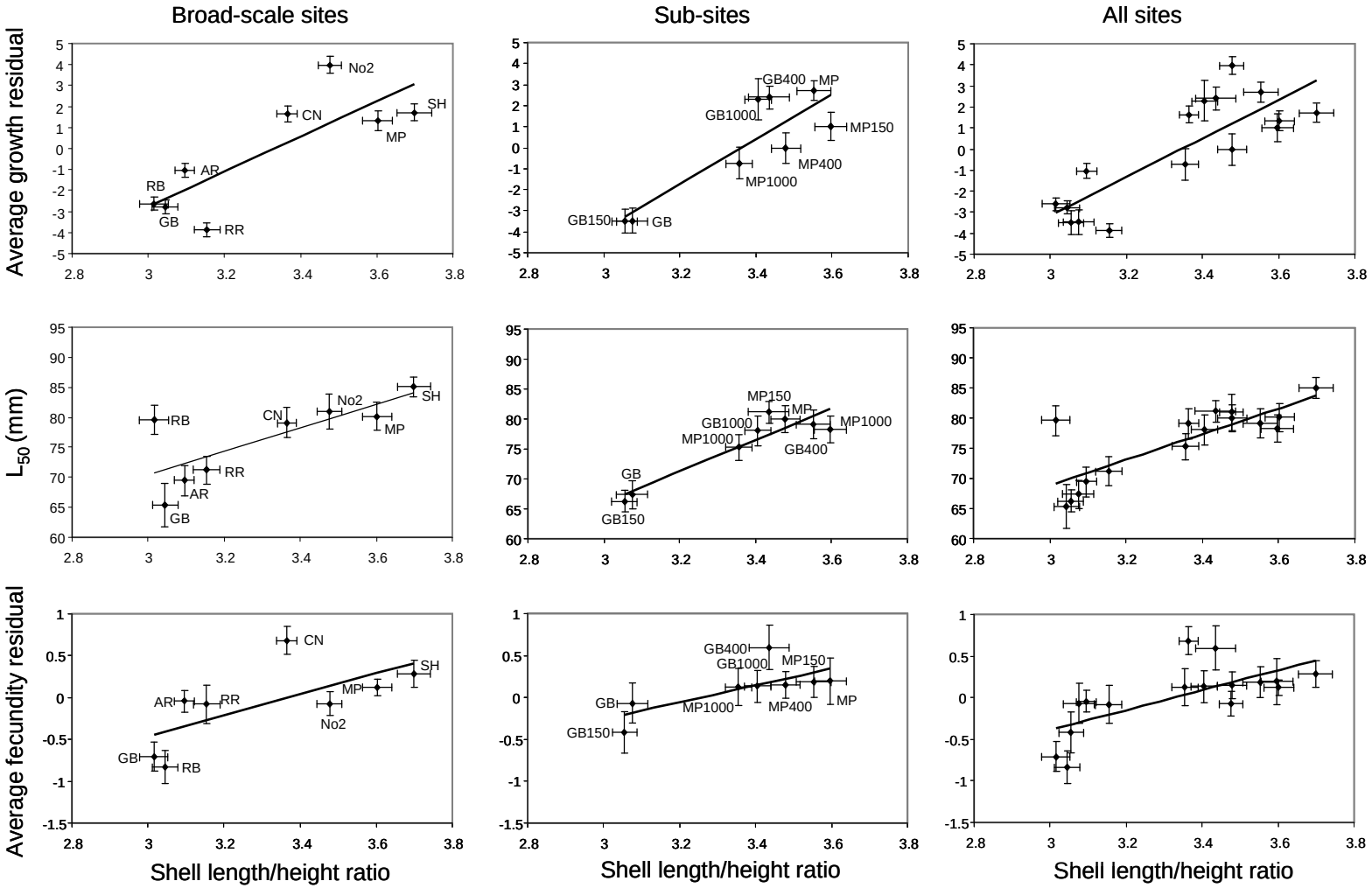

Figure 3.8: Relationship between the SL/SH ratio and average growth residuals, estimates of L_{50} and average fecundity residuals for the broad-scale and sub-sites separately, and for all sites combined. Error bars are ±1 SE (growth and fecundity) or 95% confidence intervals (L_{50}). Comprehensive details for each site are provided in Table 3.1.

3.4 Discussion

The collection of information on growth, size-at-maturity and fecundity from throughout the SZ demonstrated that these parameters vary at both broad (10's km) and fine (100's m) spatial scales. Moreover, we were able to demonstrate that these parameters were significantly correlated to a simple 'morphometric marker' (Chapter 2; Saunders *et al*. 2008). The spatial variability in the biology of blacklip observed is likely a result of fine-scale spatial variability in environmental factors (Swain *et al*. 2005). However, the dispersal of abalone probably only occurs at scales of 10-100 m's (Prince *et al*. 1987). Therefore, populations formed under these conditions exist at very fine spatial scales (Temby *et al.* 2007) and would be similar to that at which environmental variability operates. Consequently, the 'morphometric marker' could provide a valuable tool to aid fine-scale management of abalone fisheries by inferring the key biological parameters of individual populations, and through using this information to discriminate among these.

The substantial spatial variation in growth that we observed for blacklip in the SZ appears to be characteristic of abalone populations world-wide (McShane *et al*. 1988; Day and Fleming 1992; Worthington *et al*. 1995a). Differences in growth among the broad-scale sites were primarily determined by the site being within a 'stunted' or 'non-stunted' area. Within Gerloffs Bay, the 'stunted' pattern of growth was only observed within 400 m of the original site; the sites beyond this distance had significantly higher growth rates, that were similar to those in the 'non-stunted' sites. In contrast, growth patterns of blacklip at Middle Point were consistent across a broader area, up to 1000 m from the original site. These differences are likely to be attributed, in part, to abalone in 'stunted' sites being exposed to lower food availability as a result of less water movement and hence less drift algae, compared to 'non-stunted' populations (McShane *et al*. 1988; Day and Fleming 1992; Worthington *et al*. 1995b). Furthermore, higher densities of conspecifics may have also contributed to differences in the rate of growth among sites (Dixon and Day 2004) as abundances of blacklip were about seven times higher within 'stunted' sites compared to those in 'non-stunted' (Saunders *et al*. in review). In addition to these factors, genetic variability among populations may be influencing the growth of abalone (Worthington *et al*. 1995a). To delineate the affect these environmental or genetic factors have on this observed spatial variation in growth, reciprocal transplant experiments need to be conducted (Swain and Foote 1999).

The spatial variability in size at maturity closely matched that observed for growth. At broad spatial scales, sites that contained 'stunted' blacklip generally had a smaller size at maturity compared to those in 'non-stunted' sites. The exception to this was the blacklip in one 'stunted' site (RB) where they grew slowly but matured at a similar size to individuals in the

'non-stunted' sites. Anecdotal evidence from fishers suggests that blacklip in this area grow quickly, but this manifests itself in changes in shell width and height as opposed to length. Importantly, within Gerloffs Bay and Middle Point the spatial variability in size at maturity mimicked that for growth. These results are unsurprising as growth rate reflects both individual size at age and the rate at which that size is attained and will affect size/age of maturity for individuals (Begg *et al*. 1999; Cadrin 2005). Indeed, these patterns in growth and size at maturity are commonly observed in abalone populations in Tasmania (Tarbath 2003), New South Wales (Worthington *et al*. 1995a), Victoria (McShane *et al*. 1988) and elsewhere in South Australia (Shepherd and Hearn 1983). These observations are probably a result of maturity being related to age, with abalone in 'stunted' areas maturing at the same age, but at a smaller size, compared to those in 'non-stunted' areas (Shepherd and Laws 1974; Prince *et al*. 1988; Shepherd *et al*. 1991; Nash 1992; McShane and Naylor 1995). However, as we have no data on the age of individual blacklip in this study, the observation of smaller size at maturity at 'stunted' compared to 'non-stunted' sites may reflect plasticity in the life-history strategy of abalone among these areas (McAvaney *et al*. 2004; Naylor *et al*. 2006).

Among the broad-scale sites, blacklip at the 'stunted' sites that exhibited the lowest growth rates (GB, RB) also had the lowest levels of fecundity. However, individuals at the 'stunted' sites that had slightly higher growth rates tended to have similar levels of fecundity compared to those in the 'non-stunted' sites. The fact that fecundity was not as tightly linked to growth, when compared to size-at-maturity, is probably due to the substantial individual variation that was observed in egg-count data in this study. This variability is most likely caused by the low sample sizes not accounting for the highly variable timing and duration of spawning of blacklip (Shepherd and Laws 1974). Consequently, at the time of collection all blacklip may have appeared to be fully gravid, despite some individuals having spawned and only having a fraction of their eggs. Importantly, within Gerloffs Bay and Middle Point, spatial patterns in fecundity were consistent with those observed for growth and L_{50}. Similar spatial variability in growth and fecundity have been observed, with abalone generally producing fewer eggs in 'stunted' compared to 'non-stunted' areas (Shepherd *et al*. 1992; Wells and Mulvay 1995; Campbell *et al*. 2003).

The spatial variability in the biology of blacklip we have observed at multiple scales in the SZ was not unexpected, as it has been documented in numerous studies in Australia and elsewhere around the world. However, we have taken the identification of this variability in the SZ three additional steps forward. Firstly, we have demonstrated that growth, size-at-maturity and fecundity tend to covary together across these spatial scales. Previous studies have typically focussed on the spatial variability of these parameters in isolation. Secondly,

we were able to identify the scale at which biological variability exists within two locations in the SZ. In Gerloffs Bay, populations of blacklip that exhibited 'stunted' characteristics (low growth, small size at maturity and low fecundity) were observed to occupy an area of approximately 400 m compared to 1000 m for the 'non-stunted' population of blacklip in Middle Point. Thirdly, and most importantly, we have demonstrated that the SL/SH ratio developed previously (Chapter 2; Saunders *et al*. 2008) is highly correlated to key life-history parameters among populations of blacklip at both broad (100 km) and fine (100's m) spatial scales. Therefore, even though the biological classifications of the populations we have examined were not always consistent, these strong relationships allow for the biological characteristics of other populations of abalone to be inferred simply and inexpensively by applying the SL/SH ratio to spatially-resolved, commercial-catch samples. Furthermore, the value of the SL/SH ratio can be used to determine the growth, size at maturity and fecundity for any population based on these relationships. Assessment of samples from across the fishery will ultimately enable these populations to be mapped, with fine-scale systematic sampling facilitating determination of the boundaries of individual populations within and between these areas. The biological information inferred by the SL/SH ratio could then be used to assign individual populations of abalone with appropriate size limits that reflect their biological characteristics.

3.5 Conclusions

The information presented in this Chapter provides an important step towards practical implementation of fine-scale management strategies for abalone fisheries. Identifying the strong correlation between a simple 'morphometric marker' and estimates of key biological parameters provides a potential tool to infer biological variability among populations of abalone and to separate them on this basis. Obtaining this information by traditional research methods remains challenging due to the high costs of obtaining demographic data at appropriate spatial scales. Thus, use of the 'morphometric marker' provides a simple, cost-effective opportunity to bridge the traditional disconnect between scales of ecological variation and fisheries management. While this approach is particularly pertinent for abalone, given their stock structure and history of sudden collapse, it could also be applied to many other sedentary invertebrates that have fine-scale population structure and easily measurable hard-body parts that reflect their ontogenetic history. Consequently, being able to predict biological variation using a 'morphometric marker' is broadly applicable and can assist with the conservation and management of many sedentary invertebrate species.

3.6 References

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CHAPTER 4. Molecular Analysis of Blacklip Abalone Population Structure

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4.1 Introduction

Abalone (Genus *Haliotis*) are patchily distributed, typically forming discrete populations (or stocks), with differing life-history characteristics across their distribution (Shepherd and Brown 1993; Morgan and Shepherd 2006). A key issue for ensuring sustainable abalone fisheries is identifying the appropriate scale at which they should be managed (Shepherd and Brown 1993; Prince 2005) because regional scale management may compromise the sustainability of component populations by failing to account for spatial variability in life-history parameters (Prince 2005). In Australia, management of abalone fisheries occurs over large spatial scales (from 100 – 1000 km) on a State-by-State basis through individual quotas, minimum harvest lengths and total allowable catches (Prince and Shepherd 1992), despite evidence that abalone larvae generally disperse only short distances (Prince *et al*. 1987; McShane *et al*. 1988; Nash 1992; Shepherd and Brown 1993; McShane 1995). There is also a high degree of variability in growth rates, fecundity and size at sexual maturity among populations within Australian States (Shepherd and Hearn 1983; McShane *et al*. 1988; Worthington *et al*. 1995; Worthington and Andrew 1997, 1998; Tarbath 2003; Tarbath *et al*. 2003) and adults are unlikely to migrate or move far following settlement (Shepherd 1973).

In Victoria and South Australia, management of abalone fisheries is evolving from the broad-scale, regional approach towards explicit consideration of spatial variability. Concerns over the sustainability of blacklip abalone (*H. rubra*; hereafter referred to as blacklip) stocks in the Western Zone of the Victorian abalone fishery resulted in an industry-based initiative that has reduced the scale of management to that of individual reefs, each with a separate total allowable commercial catch (TACC) and size limit (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). In the Southern Zone of the South Australian abalone fishery (SZ), the collection of fine-scale data on blacklip morphology (Chapter 2; Saunders *et al*. 2008) and biology (Chapter 3; Saunders and Mayfield in press) suggests these vary significantly among

populations, with a simple morphometric marker, based on the ratio between shell length and shell height (Chapter 2; Saunders *et al*. 2008), able to discriminate among stocks and identify 'management units' (Chapter 6; Taylor and Dizon 1999). Application of this tool suggests a shift to numerous 'management units' is warranted in the SZ (Chapter 6).

One of the key elements missing from management approaches in the move towards finer-scale management of blacklip in Victoria and South Australia, is consideration of whether or not separate populations classified by biological or morphometric methods reflect ecological populations that are self sustaining (Day and Shepherd 1995; Berryman 2002). Given the difficulties of tracking tiny larvae over potentially large distances, examination of molecular markers offers a potential tool to provide this information (Hamm and Burton 2000).

Previous researchers have estimated the connectedness of blacklip populations or the 'genetic neighbourhood/range' of populations at approximately 500 km (Brown 1991; Brown and Murray 1992), although there is minimal information on the level of gene flow among populations. To date, researchers have examined genetic variation and population structure of blacklip collections from Australian waters using allozymes, random amplified polymorphic DNA (RAPDs), mitochondrial DNA (mtDNA) and genotypic repeat sequences. Studies have reported conflicting results (see Huang *et al*. 2000; Conod *et al*. 2002; Evans *et al*. 2004a; Li *et al*. 2006), but have generally revealed restricted gene flow among populations in different Australian States with higher levels of homogeneity within State waters.

This Chapter presents the results from the molecular investigations examining the genetic connectedness of blacklip in the SZ. This was achieved by sampling blacklip from seven sites distributed throughout the fishery, separated by between 2 and 80 km. Genetic connectivity among samples was analysed using both microsatellite and mtDNA markers. Microsatellites are co-dominant, bi-parental nuclear markers that display high levels of polymorphism. They are used widely in fisheries and aquaculture studies (O'Connell and Wright 1997 and references within) and have been used to assess the population structure for a number of abalone species (*e.g.* Conod *et al*. 2002; Evans *et al*. 2004b; Li *et al*. 2006). Notably, this is the first large-scale study to employ a set of newly identified microsatellite loci developed for blacklip (see Baranski *et al*. 2006) in a population context.

In contrast, mtDNA is haploid and generally inherited (or transmitted) through the maternal line. It is a closed circular molecule and, consequently, effective population sizes estimated from mtDNA data are smaller than those estimated from nuclear, single copy DNA. This increases the sensitivity of mtDNA to genetic drift and population bottleneck effects (Brown

et al. 1979; Avise 1994 and references within; Moore 1995). Mitochondrial DNA is a powerful molecular tool for investigating population genetic diversity and species identification, reflecting rapid sequence substitutions and changes. Like microsatellites, mtDNA has been used to investigate population structure in several abalone species (*e.g.* Brown 1995; Burton and Tegner 2000).

4.2 Materials and methods

4.2.1 Samples and DNA extraction

Samples (hereafter referred to as collections) comprised frozen (-20°C) blacklip muscle tissue from seven sites distributed throughout the SZ (Figure 4.1; Table 4.1). Collections comprised whole juveniles (70 – 80 mm shell length) obtained over an area of <10m^2 at each site. Total genomic DNA was extracted from ~20 mg of foot muscle tissue using a Wizard SV96 Genomic DNA Purification System (Promega; USA) as per the manufacturer's instructions, except for elution volumes, which were reduced to 200 µl. Remaining tissue samples and an aliquot of the extracted DNA were stored at –80°C. The genomic DNA for each individual was diluted to 100 ng.µl^{-1} for mtDNA applications and a second aliquot of 10 – 25 ng.µl^{-1} was used for microsatellite loci. These aliquots were stored at 4°C for working applications.

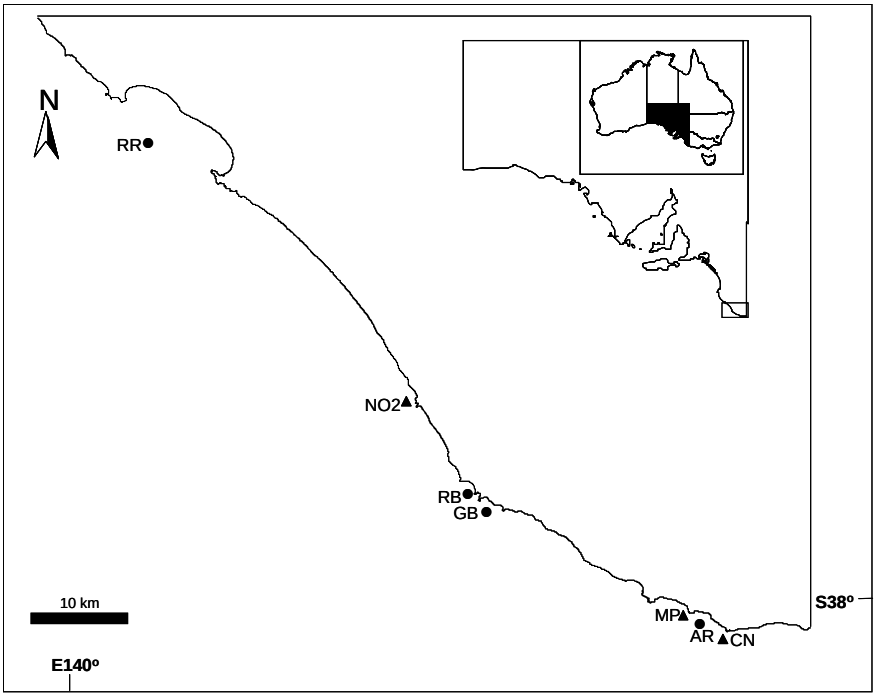

Figure 4.1: Map of study area showing locations of the seven sites from which collections were obtained. Circles and triangles represent 'stunted' and 'non-stunted' sites, respectively. Comprehensive details for each site are provided in Table 4.1.

Table 4.1: Summary of blacklip collection data from the seven sites in the SZ. Sites arranged from north to south. Bold indicates a 'stunted' site (see Chapters 2 and 3).

Site	Descriptor	Latitude	Longitude	Date collected	Sample size
Ringwood Reef	**RR**	37°31.9' S	140°02.6'E	24/03/06	48
Number 2 Rocks	No2	37°48.8' S	140°19.5'E	25/03/06	48
Red Rock Bay	**RB**	37°54.6' S	140°23.2'E	24/03/06	48
Gerloffs Bay	**GB**	37°55.7' S	140°24.4'E	24/03/06	48
Middle Point	MP	38°02.5' S	140°37.0'E	25/03/06	48
Acis Reef	**AR**	38°02.8' S	140°37.9'E	25/03/06	48
Cape Northumberland	CN	38°03.6' S	140°39.7'E	25/03/06	48

4.2.2 MtDNA-RFLP digests

The polymerase chain reaction (PCR) was used to amplify an approximately 1500 base pair gene fragment from the mtDNA genome. This fragment (*ND3/COIII* region) consists of a large portion of the NADH subunit 3 gene, the complete COIII gene (Sweijd 1999) and five transfer RNA genes (Maynard *et al*. 2005).

The primers used were P3: 5'-AAAGTGATCACAGAAATGACCCG-3' and P4: 5'-GATAAGAAGAAAGCAAAGAACCCC-3' (Sweijd 1999). PCR reactions were undertaken in an Eppendorf Mastercycler® EP gradient thermal cycler (Eppendorf; Germany) and a Perkin Elmer GeneAmp® System 9600 thermal cycler (Applied Biosystems; USA). Reactions consisted of 1 µl of 10 mM dNTPs (Promega; USA), 3 µl of 25 mM $MgCl_2$ (Applied Biosystems), 5 µl of 10× AmpliTaq Gold Buffer (Applied Biosystems), 1 µl of 10 µM P3 and P4 (Geneworks; South Australia), 0.25 µl of AmpliTaq Gold (Applied Biosystems) and 100 – 150 ng of template DNA, adjusted to a final volume of 50 µl with ddH_2O. The PCR cycling conditions were as follows: initial denaturation at 93°C for 10 min, 35 cycles of 93°C for 30 s, 60°C for 1 min, and 72°C for 2 min 30 s. A final extension cycle of 72°C for 10 min was followed by an indefinite 4°C hold.

Restriction fragment length polymorphism (RFLP) haplotypes were assessed by digesting the *ND3/COIII* fragment with five restriction enzymes (*DdeI*, *DpnII*, *HaeIII*, *MspI* and *RsaI* (New England Biolabs; USA) as described by Conod *et al*. 2002). Enzyme digests were undertaken separately and fragments were run on a 2.5% TBE (Tris, Boric acid, EDTA) buffer agarose gel containing ethidium bromide at 120V for 1 hr against a Hyperladder size standard (Bioline; USA). Fragments were visualized under UV light and photographed with a digital camera to enable scoring of haplotypes (similar to that described by Conod *et al*. 2002). All haplotypes were scored independently by two researchers and crosschecked for congruence prior to statistical analyses.

4.2.3 Microsatellite DNA amplification

We examined variation at ten blacklip microsatellite loci using two multiplex PCR reactions. These loci (Hrub10.G02, 10.E02, 12.G07, 4.A11, 1.D04, 4.E06, 16.G01, 8.A09, 9.F11, 2.G01; referred to as Locus 1…10, respectively) were obtained from Baranski *et al*. (2006). Each 25 µl multiplex per individual was performed in an Eppendorf Mastercycler® (as above). Amplifications consisted of 1 µl of 10 mM dNTP's (Promega), 2.5 µl of 25 mM $MgCl_2$ (Applied Biosystems), 2 µl of 10× AmpliTaq Gold Buffer (Applied Biosystems), 1.2 – 1.4 µM of both forward and reverse primers (forward primers were fluorescently labeled; Applied Biosystems), 0.25 µl of AmpliTaq Gold (Applied Biosystems) and 10 – 15 ng of template DNA, adjusted to a final volume of 25 µl with ddH_2O.

The PCR cycling conditions were an initial denaturation at 93°C for 10 min, 40 cycles of 93°C for 30 s, 55°C for 1 min 30 s, and 72°C for 2 min. A final extension cycle of 72°C for 10 min was followed by an indefinite 4°C hold. One µl of the amplified products were diluted in a mix of HiDi Formamide (Applied Biosystems) and ddH_2O and denatured at 94°C for 2 min. Samples were run on an ABIPrism® 3100 Genetic Analyser against an internal GeneScan™-500 LIZ Size Standard (Applied Biosystems). GeneMapper™ version 3.7 (Applied Biosystems) software was used to set the parameters and bin ranges that enabled routine genotyping. For each collection, samples were scored as they were run; as with the mtDNA RFLP haplotypes, genotypes were independently scored by two researchers. Genotypes were checked again after all samples had been run for all loci.

4.2.4 Statistical analysis

4.2.4.1 *Within collection diversity*

For mtDNA, the most common haplotype from each restriction digest was identified by the letter A. Variable restriction patterns, per enzyme digest, were subsequently designated alphabetically. The composite haplotypes for each individual consisted of five letters. In the analysis, the only individuals used were those for which data from all five restriction enzymes were available.

Standard RFLP coding (based on the presence/absence of restriction sites) was used. Composite haplotype data and restriction site information was then analysed in ARLEQUIN (Excoffier *et al*. 2006) to calculate unbiased haplotype diversity (*h*; Nei 1987) and nucleotide diversity (π; Tajima 1983; Nei 1987). Haplotype diversity potentially ranges from zero (all individuals share a common haplotype) to one (all individuals have different haplotypes).

For the microsatellite analyses, allele frequencies, number of alleles ($N_{alleles}$), observed (H_o) and expected (H_e) heterozygosities for each collection and locus were calculated in FSTAT (Goudet 2001). The rarefaction approach in FSTAT was used to calculate 'allelic richness' (A); this enables comparisons among collections of differing sample sizes. Deviations from Hardy-Weinberg Equilibrium (HWE) at each locus and for each collection were calculated in ARLEQUIN using a Markov chain approach. Micro-checker version 2.2.1 (van Oosterhout *et al*. 2003, 2004) assessed the potential for large allele dropout, scoring errors due to stuttering and the potential for null alleles by comparing observed and expected homozygote genotype frequencies and associated bin sizes. Linkage disequilibrium among loci was assessed using Fisher's exact tests in GENEPOP version 3.3 (Raymond and Rousset 1995). Simulation tests for historic changes in allele frequency distributions were performed in BOTTLENECK version 1.2 (Piry *et al*. 1999; populations that experience recent declines in effective population sizes often exhibit a reduction in allele number and gene diversity, with loci not at mutation-drift equilibrium).

4.2.4.2 *Among collection diversity*

Analysis of molecular variance (AMOVA), based on analogues of Weir and Cockerham (1984) F parameters, was used to investigate differentiation among collections and State regions in ARLEQUIN (undertaken separately for the two marker types). The analogue of F_{ST}, Φ_{ST}, was obtained as the estimated variance component resulting from differences among collections divided by the estimated total variance. Collection differentiation, based on multilocus F_{ST} statistics (Wright 1951; Weir and Cockerham 1984), was calculated and examined across all loci and pairwise comparisons, in ARLEQUIN. Spatial variation in mtDNA composite haplotype frequencies was assessed using standard Monte-Carlo chi-square approaches in the program CHIRXC (Zaykin and Pudovkin 1993), with 10,000 randomisations of the data being used to estimate P values. The significance levels for multiple tests were adjusted following a sequential Bonferroni approach (Rice 1989).

4.3 Results

4.3.1 Within collection diversity

Amongst the 303 blacklip individuals, a high level of haplotype diversity was observed in the *ND3/COIII* region (Table 4.2). Twenty-five different composite haplotypes were observed although the majority of animals displayed one of four haplotypes (AAAAA, BBBCA, AAAAB and AAABA). The blacklip collections showed an average haplotype diversity of 0.753 (SE ± 0.017) and nucleotide diversity of 0.137 (SE ± 0.003). Within collection

haplotype diversity was high, ranging from 0.711 to 0.837, and nucleotide diversity was less than 0.150 in all collections. There was no significant haplotype differentiation among the collections (χ^2 = 12.304, df = 6, P > 0.05), and the four most common haplotypes were observed in all collections.

Table 4.2: RFLP analysis of the *ND3/COIII* mtDNA fragment based on five restriction enzymes (*DdeI, DpnII, HaeIII, MspI* and *RsaI*) showing the distribution of 25 haplotypes among the seven blacklip collections. Comprehensive details for each site are provided in Table 4.1. Total RFLP success and both haplotype (*h*) and nucleotide (π) diversity are also shown.

Haplotype		Collection							Total
		CN	RR	AR	No2	RB	MP	GB	
1	AAAAA	21	18	16	21	21	13	17	127
2	BBBCA	8	5	16	13	12	10	10	74
3	AAAAB	3	3	5	7	5	3	5	31
4	AAABA	2	6	4	3	4	4	2	25
5	BBCCA	3	1		1		2	1	8
6	ABBCA	1	2	1	1		1	1	7
7	BABCA	1	2						3
8	AABAA						1		1
9	CCACA			1	1	3			5
10	AADBA		1						1
11	ABGCA					2	1		3
12	CBACA	1	2						3
13	AAAAC	1						1	2
14	ABAAA						2		2
15	ADAAA						1		1
16	BBACA						1	1	2
17	ACACA						1		1
18	AABCA					1			1
19	ABACA		1						1
20	ABCCA			1					1
21	BBBCD	1							1
22	BBBCE		1						1
23	BDABA						1		1
24	DAAAA	1							1
25	DBFCA	1							1
	Total	44	42	44	47	48	41	38	303
	RFLP	92%	88%	92%	98%	100%	85%	79%	
	h	0.741	0.786	0.729	0.711	0.738	0.837	0.727	
	π	0.135	0.131	0.144	0.130	0.144	0.149	0.127	

For the microsatellite loci, between 272 and 301 individuals were genotyped, depending on the locus (Dr Sharon Appleyard, CSIRO, unpublished data). While ten loci were screened, a large number of individuals did not amplify at Locus 4 (from Master Mix 1). Subsequently, this locus was omitted from further analyses. Tests for linkage disequilibrium (following Bonferroni correction) indicated no significant comparisons in all collection pairs. The loci were considered independent, as no two markers were associated in all collections.

All loci displayed moderate to high levels of polymorphism. The average number of alleles per locus ranged from 13 (Locus 10) to 35 (Locus 9; Table 4.3) and allelic richness varied considerably among the loci (11.01 – 26.94 depending on the locus). Loci 1 (0.962) and 2 (0.498) displayed the highest and lowest H_o values across the seven collections, respectively.

There was very low-level evidence of private alleles (*i.e.* alleles observed in a single collection), but of the 345 alleles observed over the nine loci, only 35 were private and each was present at a frequency of less than 0.005. Average H_e across the nine loci per collection was at least 90%. On a per locus scale, in all instances, H_e was very high ranging from 0.869 to 0.975 although ~50% of genotypic tests across the nine loci in the seven collections did not conform to HWE (following Bonferroni correction; Table 4.3). In most instances, this was due to a lack of heterozygotes (*i.e.* excess homozygotes). Results from Micro-checker indicated that most of the loci within each collection that did not conform to HWE were probably characterised by null alleles. Stuttering and large allele dropout were, however, not evident. As most loci demonstrated the likely presence of null alleles, the collection variability statistics were not re-analysed, as these deviations are unlikely to affect the overall comparisons given the alleles were scored across all collections in the same manner.

The tests outlined in BOTTLENECK showed no significant departure from allele frequencies expected under mutation-drift equilibrium. All other collections and loci conformed to expectations, with equal probability that a locus showed a diversity excess or deficit. Consequently, there was no evidence to suggest reductions in the effective population sizes of these blacklip collections**.**

4.3.2 Among collection diversity

An overall exact test of sample differentiation based on mtDNA haplotype frequencies across the seven collections was not significant ($P > 0.05$). Similarly, all pairwise comparisons among the collections in this fishery were not significant (data not shown). There were also no significant mtDNA F_{ST} comparisons observed among the seven collections. Indeed all F_{ST} values were very low and often negative (Table 4.4).

Table 4.3: Summary statistics for microsatellite loci (L) screened in blacklip collections. Mean sample size per locus (N), number of alleles ($N_{alleles}$), allelic richness (A), heterozygosity observed (H_o), and heterozygosity expected under equilibrium conditions (H_e) are shown. Significant H_o estimates following Bonferroni correction are shown in bold. Comprehensive details for each site are provided in Table 4.1.

Collection	Statistic	L 1	L 2	L 3	L 5	L 6	L 7	L 8	L 9	L 10
CN	N	44	43	42	42	45	45	45	40	45
	$N_{alleles}$	32	22	31	25	22	18	25	35	15
	A	24.58	16.59	23.20	21.40	18.40	13.90	19.76	27.25	12.12
	H_o	0.977	**0.465**	**0.738**	**0.786**	0.956	0.800	0.933	0.675	**0.644**
	H_e	0.967	0.917	0.946	0.963	0.940	0.851	0.948	0.979	0.889
RR	N	39	36	38	39	42	40	42	39	42
	$N_{alleles}$	33	19	28	23	26	23	22	37	13
	A	26.12	15.78	20.98	19.23	20.45	18.19	18.43	28.96	10.88
	H_o	1.000	**0.417**	0.842	0.718	0.929	0.875	0.881	0.769	**0.643**
	H_e	0.971	0.905	0.914	0.951	0.950	0.916	0.945	0.979	0.875
AR	N	41	38	40	39	40	41	41	40	40
	$N_{alleles}$	32	22	27	28	25	18	26	32	12
	A	24.90	17.34	19.49	23.10	19.73	15.16	21.21	24.85	9.95
	H_o	0.927	**0.553**	**0.650**	**0.538**	0.850	0.829	**0.732**	**0.650**	**0.625**
	H_e	0.967	0.920	0.901	0.970	0.946	0.902	0.954	0.965	0.843
No2	N	41	37	35	39	43	43	43	40	43
	$N_{alleles}$	29	20	23	27	23	18	25	38	14
	A	23.41	17.18	18.67	22.03	18.64	14.21	20.18	28.86	10.74
	H_o	0.878	**0.514**	**0.543**	**0.718**	0.884	0.791	0.907	**0.725**	**0.535**
	H_e	0.964	0.927	0.896	0.960	0.941	0.883	0.947	0.979	0.855
RB	N	43	42	39	43	44	44	44	42	44
	$N_{alleles}$	31	21	27	27	22	17	26	36	12
	A	23.26	17.03	20.55	21.36	18.09	14.03	20.66	26.87	10.01
	H_o	1.000	**0.452**	**0.718**	**0.698**	0.932	0.841	0.977	0.643	0.636
	H_e	0.961	0.939	0.926	0.953	0.946	0.883	0.949	0.975	0.860
MP	N	43	42	41	43	46	46	46	46	46
	$N_{alleles}$	33	27	39	27	23	17	26	36	14
	A	25.00	20.13	27.82	21.62	18.27	13.34	20.18	26.71	11.22
	H_o	0.953	**0.714**	0.878	**0.791**	**0.826**	0.761	0.935	**0.609**	**0.587**
	H_e	0.966	0.943	0.958	0.950	0.943	0.849	0.951	0.977	0.879
GB	N	44	43	37	39	44	44	43	36	43
	$N_{alleles}$	28	19	20	27	25	18	23	30	14
	A	22.35	15.72	16.36	21.68	19.81	14.17	17.71	25.07	12.15
	H_o	1.000	**0.372**	**0.595**	**0.667**	0.909	0.841	0.884	**0.611**	**0.535**
	H_e	0.959	0.926	0.905	0.959	0.946	0.868	0.937	0.971	0.880
Average	N	42	40	39	41	43	43	43	40	43
	$N_{alleles}$	31	21	28	26	24	18	25	35	13
	A	24.23	17.11	21.01	21.49	19.06	14.71	19.73	26.94	11.01
	H_o	0.962	0.498	0.709	0.702	0.898	0.820	0.893	0.667	0.600
	H_e	0.965	0.925	0.921	0.958	0.946	0.879	0.947	0.975	0.869

Table 4.4: Pairwise F_{ST} values among the seven blacklip collections based on composite mtDNA-RFLP haplotypes (below the diagonal) and multilocus microsatellite loci (above the diagonal). Values are given to three decimal places; negative values are equal to zero. Bolded values are significant after Bonferroni correction. Comprehensive details for each site are provided in Table 4.1.

	CN	RR	AR	No2	RB	MP	GB
CN	-----	0.001	0.004	0.001	0.007	0.003	0.003
RR	-0.008	-----	0.007	0.003	0.005	0.004	0.006
AR	-0.008	0.011	-----	0.000	0.000	0.002	0.004
No2	-0.017	-0.010	-0.009	-----	0.002	0.001	0.002
RB	-0.011	-0.012	-0.004	-0.016	-----	0.001	0.002
MP	-0.013	0.000	-0.019	-0.013	-0.009	-----	-0.002
GB	-0.022	-0.009	-0.012	-0.023	-0.014	-0.016	-----

Likewise, there were no significant allele frequency differences observed at the microsatellite loci across the seven collections (exact test, $P = 1.000$). F_{ST} comparisons among the seven collections were all small and not significant (Table 4.4).

Non-hierarchical AMOVA analyses within the collections demonstrated very small Φ_{ST} results for both mtDNA and microsatellite data. All of the mtDNA variance and <0.3% of the microsatellite variance was attributed to among collection differences (Table 4.5). Hence, there was no molecular evidence to suggest sub-structuring of blacklip collections within the SZ, on the basis of the samples screed in this study.

Table 4.5: Blacklip non-hierarchical AMOVA based on mtDNA haplotypes and microsatellite genotypes. *P* values are provided in parentheses.

Source of variation	mtDNA variance	% Variation	F_{ST} mtDNA	Microsatellite variance	% Variation	F_{ST} microsatellite
Among collections	-0.030	-1.10	-0.011 (0.489)	0.009	0.26	0.003 (0.095)
Within collections	2.749	101.10		3.552	99.74	

4.4 Discussion

The focus of this Chapter was to investigate the spatial stock structure of blacklip across the SZ. Both mtDNA and microsatellite variation revealed little genetic differentiation among the collections. We therefore could not reject the null hypothesis of genetic homogeneity for blacklip within this region. We observed high levels of mitochondrial and nuclear genetic diversity in all collections. Average mtDNA haplotype diversity in the current study ($h = 0.753$) was very similar to that obtained by Conod *et al*. (2002) for four Tasmanian

blacklip collections screened previously (h = 0.708), and that observed by Li *et al*. (2006) from a small pilot study on blacklip from several additional South Australian sites (h = 0.804). Observed heterozygosity levels for our nine microsatellite loci were generally high, although the levels were not consistent across all loci. Similar levels of variation, albeit based on different microsatellite loci, have previously been reported for blacklip (Huang *et al*. 2000; Conod *et al*. 2002; Evans *et al*. 2004a; Li *et al*. 2006). The collections from this study do not appear to have been bottlenecked or founded from small numbers of individuals. This, combined with the high levels of genetic variation observed at both nuclear and mitochondrial loci, indicates that these blacklip collections are 'genetically healthy' and should be resilient to population disturbance and/or impact by fishing pressures.

We detected many heterozygote deficiencies in the microsatellites. The deviations are, therefore, probably not the result of inbreeding (see also Evans *et al*. 2004a) but more likely caused by other factors such as null alleles, which can cause heterozygote deficiencies (Callen *et al*. 1993; Estoup *et al*. 1995). Null alleles may result from mutations in primer regions (*i.e*. base changes) or from preferential PCR amplification (small alleles preferentially amplifying over larger alleles; O'Connell and Wright 1997). As Micro-checker did not highlight any loci that were characterised by large allele dropout, it is more likely that our loci are characterised by base changes in the primer binding sites yielding null alleles. Null alleles have been observed in many other shellfish including Pacific oysters (Launey and Hedgecock 2001; Appleyard and Ward 2006), mussels (Del Rio-Protilla and Beaumont 2001; Astanei *et al*. 2005) and indeed abalone (Brown and Murray 1992; Smith and Conroy 1992; Gonzalez *et al*. 2000; Conod *et al*. 2002; Withler *et al*. 2003; Evans *et al*. 2004a,b; Baranski *et al*. 2006; Li *et al*. 2006). Since undertaking this study, we have reassessed our microsatellite loci for their utility in molecular pedigree suites and their ability to assign parentage from cultured abalone. The reassessment was based on observed levels of heterozygosity, probable null alleles, polymorphism content, exclusion ability and Mendelian inheritance studies in both blacklip and greenlip abalone (*H. laevigata*) wild and cultured collections. We now use six of the nine loci outlined in this study, with an additional four loci from Baranski *et al*. (2006) optimised for use in two new sets of microsatellite master mixes.

The low and non-significant F_{ST} values observed among the SZ collections indicate that processes are acting to maintain genetic homogeneity across these geographically close areas. After fertilisation, blacklip eggs are negatively buoyant, but after hatching the larvae migrate to the surface for an active swimming phase (Shepherd and Brown 1993). Larvae can exist in the upper water column for up to 10 days (although this is influenced by water temperatures) and hydrodynamic conditions determine dispersal rates (Shepherd and Brown 1993; Hamm

and Burton 2000 and references within), until they settle on suitable habitat (McShane *et al*. 1988). Due to the sedentary nature of the adults, it is likely that larval dispersal is maintaining gene flow.

Unlike the allozyme study of Brown (1991), we did not observe spatial heterogeneity among the SZ collections, despite geographical distances of between 2 and 80 km. We also did not detect the same level of genetic subdivision reported by Huang *et al*. (2000) in blacklip populations based on different microsatellites (Φ_{ST} = 0.067, P < 0.001) and RAPD loci Φ_{ST} = 0.074, P < 0.001). However, our results are consistent with other previously reported studies for blacklip populations in Australia (Conod *et al*. 2002; Evans *et al*. 2004a; Li *et al*. 2006). Both our marker types suggest a panmictic model for stock structure of these blacklip collections within South Australian waters. Collections within this area fall well into the '500 km neighbourhood size' estimated by Brown (1991).

The genetic evidence from this research indicates that blacklip populations could possibly be managed as one unit within the SZ, as the panmictic model suggested from our data demonstrates some level of recruitment of individuals among collection sites. Currently, management of most abalone fisheries conform to this model and are managed on a broad-scale (100's – 1000's km). However, this is at odds with more recent abalone population theory that suggests abalone form discrete self-sustaining populations that are highly variable in their life-history characteristics (Chapters 2 and 3; Shepherd and Hearn 1983; McShane *et al*. 1988; Worthington *et al*. 1995; Worthington and Andrew 1997, 1998; Tarbath 2003; Tarbath *et al*. 2003; Morgan and Shepherd 2006). Notably, broad-scale management does not account for differences in life history among populations, and can leave some populations vulnerable to overfishing. Importantly, application of a 'morphometric marker' to commercial shell samples (Chapter 6) has identified numerous potential 'management units' (*i.e.* independent stocks, each with unique life-history characteristics, and that should be separately managed) for the SZ.

The discrepancy between the scale of spatial variation detected by genetic and morphological markers in blacklip may result from only a few migrant larvae per generation maintaining genetic homogeneity among putative populations (Slatkin 1985; Miller and Shanks 2004). Additionally, it is highly likely that localised environmental influences play an important role in developing morphologically discriminated populations and variances in the expression of morphological traits, through genetic x environment interactions (G x E effects). Although these morphological characteristics may be environmentally induced (Swain and Foote 1999; Swain *et al*. 2005), the highly localised populations formed by abalone, which have limited

adult movement and larval dispersal, are likely to exist at similar scales to this environmental variation. Further, environmental influences do not prevent gene flow among blacklip populations, assuming that gametes are still compatible and have the opportunity to mix.

While we were unable to reject the null hypothesis of genetic homogeneity for blacklip from the SZ, there are several caveats around this finding. The failure to disprove the null hypothesis does not mean that genetic stock structuring does not exist; only that we did not detect it in the current study. Thus, while blacklip may be truly panmictic, it may be that our inability to reject the null hypothesis is related to the power of the genetic markers employed (Graves and McDowell 2003) – despite two different molecular markers being screened, the relatively small sample sizes examined (particularly for the hyper-variable microsatellite loci), the period of isolation of the stocks from which the collections were taken relative to the time periods that may be required for significant genetic differences to accumulate, or the lack of suitability of the spatial scales over which we were analysing genetic connectivity (see Temby *et al*. 2007).

4.5 Conclusions

Our findings show that the blacklip sampled here displayed relative genetic homogeneity across the SZ. We further demonstrated the concordance between the mtDNA and microsatellite markers; both indicated genetic homogeneity.

When compared with the data presented previously (Chapters 2 and 3), the genetic data suggest a broader-scale approach for blacklip management. This is in strong contrast to recent, increasing calls for recognising the spatial variability among abalone populations, and managing these populations according to their specific life-history characteristics. Consequently, in combination, our data suggest a holistic approach that encompasses genetics, morphology and biology, is required for assessment and management of abalone populations.

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CHAPTER 5. Identification and Evaluation of Approaches for Effective fine-scale Compliance.

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5.1 Introduction

The aim of a fisheries compliance program in a commercial, quota-managed fishery is to ensure that individual fishers only access their individual quota entitlements, so the integrity of the fishery is maintained and illegal activity detected. These programs are designed to promote voluntary compliance with legislation and, in the event this is not achieved, provide an effective deterrent by monitoring, detecting and prosecuting any illegal activity as well as ensuring compliance with other regulations in the fishery.

Most abalone fisheries around the world are managed over large spatial scales (100 – 1000s km). This is despite the disaggregate structure of abalone stocks, the considerable spatial variation in biological parameters and the likely limited dispersal of abalone larvae all suggesting that the spatial scales appropriate to improve the probability of maintaining sustainable abalone populations are smaller than those currently employed.

Reducing the spatial scale at which abalone fisheries are managed (*e.g.* implementation of numerous, separately-managed fishing areas (termed 'management units') within current fishing Zones) presents new fisheries compliance challenges. This is because the compliance program needs to be sufficiently flexible to allow abalone to be harvested from multiple areas with different regulations (*e.g.* size limits) on the same fishing day, whilst remaining both cost effective and efficient. Such a program must address risks across the entire catching process, from the harvesting of abalone off the reef, through to the 'weighing off of the catch' at the processor. Thus, under fine-spatial-scale management, the challenge for fisheries compliance managers is to track the taking of abalone from multiple fishing areas with different minimum legal lengths, to ensure fishing matches the harvest strategies.

In this Chapter we (1) highlight the principles underpinning compliance programs in quota-managed fisheries, (2) provide details of the fine-scale compliance approaches trialled, and (3) evaluate the merits, and identify the limitations of each approach.

5.2 Fisheries compliance programs

Fisheries compliance programs are developed using a risk assessment that takes into consideration risks associated with the commercial sector, the non-commercial sector, fish processors and any other associated risks, such as illegal fishing. The risks for the commercial sector are prioritised according to their impact upon the sustainability of the fishery. In South Australia (SA), this is done during the development of an annual State-wide Master Operational Compliance Plan. In the development of fisheries compliance programs, several principles are taken into consideration. They include:

- Cost effectiveness and efficiency;
- Coverage across all high level risks associated with quota evasion;
- Emerging risks;
- Flexibility in the delivery of services;
- A mix of covert and overt strategies; and
- Application of new technology and innovation.

Major risks associated with abalone fisheries include quota evasion and the taking of undersize abalone. Under the concept of increased spatial management, potential risks relate to the taking of different size fish from separately managed areas on the same fishing day.

5.3 Development of compliance options and trials

On 1 April 2005, a broad spectrum of abalone fishery stakeholders met in Mt Gambier, SA, to discuss current abalone fishery compliance arrangements and to 'brainstorm' compliance options and requirements that would need to be considered in light of a reduction in the spatial scale of management. The list of potential compliance approaches included:

- The current compliance program;
- Memoranda of understanding;
- A 'prior-to-fishing' report;
- A 'prior-to-landing' report;

- A ‘prior report’ on moving between separately-managed areas;
- Sealing bins with tags prior to moving between separately-managed areas;
- Completion of ‘catch disposal record’ within 50 m of landing;
- Consignment of catch to fish processor for weighing;
- Vessel monitoring system (VMS);
- Using a data logger to count and measure catch in separately-managed areas; and
- Using the ‘morphometric marker’ to distinguish between ‘stunted’ and undersize abalone.

As most current fisheries compliance programs comprise a mixture of these tools, to ensure cover across the entire catching process, they were amalgamated into four potential compliance programs, the details of which are provided in Table 5.1. The four options were:

1. Current compliance program (*i.e.* a control; Option 1)
2. Prior reporting (Option 2; see also Figure 5.1)
3. VMS and prior reporting (Option 3; see also Figures 5.2 and 5.3)
4. Data logger (Option 4; see also Figure 5.4)

Table 5.1: Summary of the range of compliance tools considered in relation to the four compliance options tested.

Compliance tool	Compliance option			
	1	2	3	4
VMS turned on prior to leaving home			■	
‘Prior-to-fishing’ report prior to leaving home			■	
‘Prior-to-fishing’ report at launching site	■	■		■
Data logger turned on at launching site				■
Count and measure all blacklip abalone within each separately-managed fishing area				■
Blacklip and greenlip abalone stored separately	■	■	■	■
Abalone placed into bins sealed with sequentially numbered tags	■	■	■	■
‘Prior report’ on moving between separately-managed fishing areas[1]		■	■	
Complete catch disposal record before moving between separately-managed fishing areas		■	■	■
Complete catch disposal record before landing				■
‘Prior-to-landing’ report[2]		■	■	
Abalone landed whole (in the shell)	■	■	■	■
CDR completed within 50 m of the shore after landing	■	■	■	
Consignment of the catch to fish processor for weighing	■	■	■	■

1 Details provided include the number of bins of abalone harvested, and their tag numbers.
2 Details provided include the last area fished, number of bins of abalone harvested, and their tag numbers.

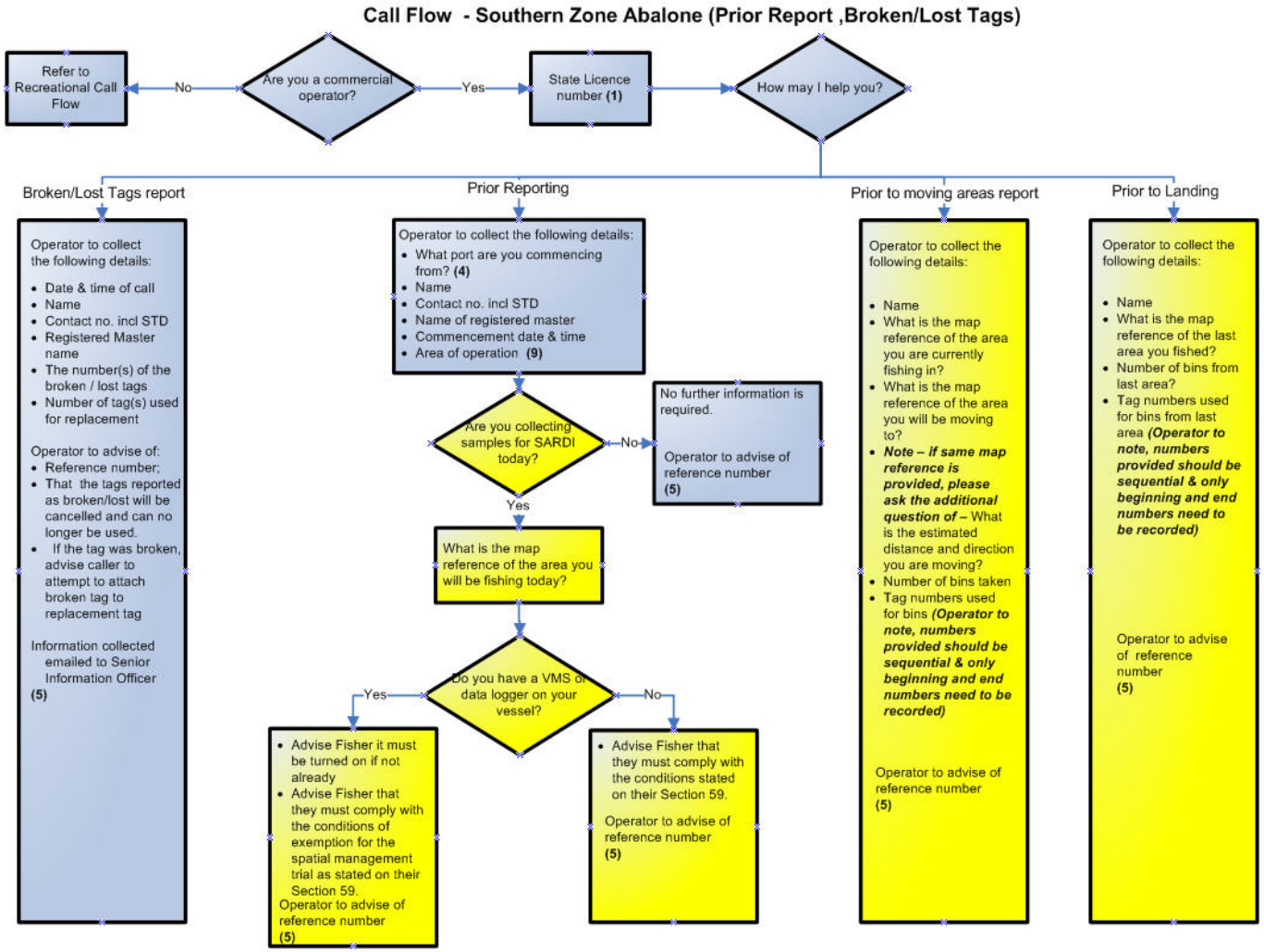

Figure 5.1: Schematic illustrating the prior reporting process used during the compliance trials.

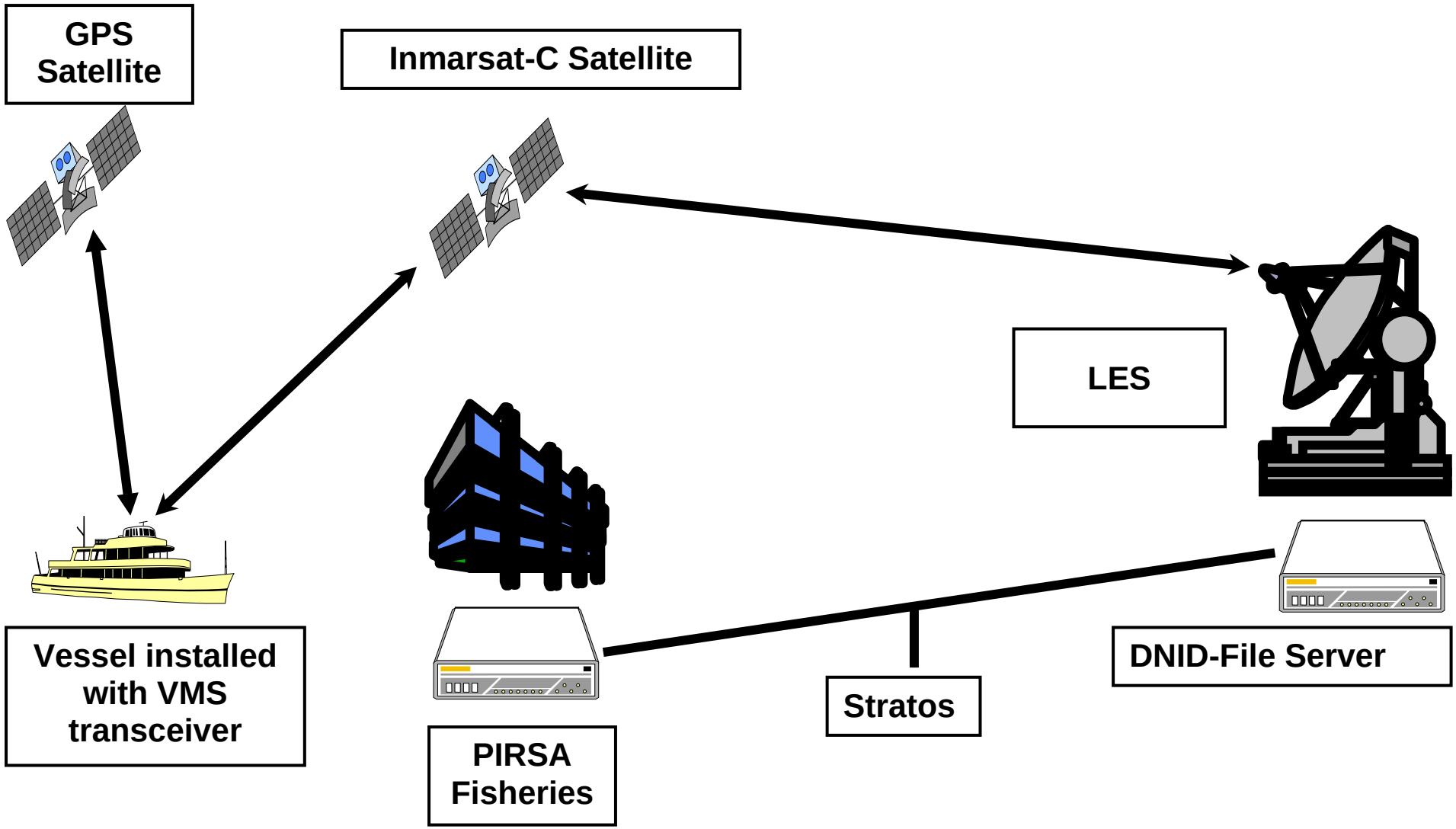

Figure 5.2: Schematic illustrating the process by which data from the VMS unit is transmitted to PIRSA Fisheries. LES indicates land earth station.

Figure 5.3: Mini-C VMS unit (left) and its installation on a SZ abalone fishing vessel (right). Unit is available from Electrotech Australia and costs ~$3500. Polling attracts an additional charge.

Figure 5.4: GPS and shell measuring data logger. Unit is available from Scielex (Hobart, Tasmania) and costs ~$5,000. It records the GPS position, heading and speed of the vessel every 10 seconds, and each shell measurement.

5.4 Evaluation of the compliance options

In the current compliance program, Fisheries Officers check and test the adherence to licence conditions, both on land and at sea. This combination of at-sea checks and shore-based surveillance activities are necessary to ensure compliance across the entire catching process, from harvesting of abalone off the reef, through to 'weighing off of the catch' at the processor. The use of sealed bins and the completion of a catch disposal record within 50 m of the point of landing (by which the fisher commits to a number of sequentially-tagged bins) substantially increase the efficiency and cost-effectiveness of the compliance program. However, a significant drawback of the current system is the lack of flexibility for fishers to harvest blacklip abalone (*Haliotis rubra*; hereafter referred to as blacklip) from two separately-managed areas (including different minimum legal size limits) on the same fishing day. This is because, outside of the 'one area, one day' restriction, the current system does not provide a mechanism for determining the area from which the catch was harvested.

This lack of flexibility would be exacerbated should the scale of management, and thus the scale of harvest, be reduced. Therefore, additional compliance tools needed to be considered, building upon the existing compliance program, to ensure compliance integrity in a fishery managed through multiple 'management units' (see Chapter 6), each with a potentially unique minimum legal length. The three alternative compliance approaches trialled were selected and developed to address this issue. These aimed to provide approaches for ensuring effective fine-scale compliance to support fishing in multiple managed areas (including consideration of different minimum legal size limits) on the same fishing day – *i.e.* a substantial increase in flexibility.

Using the current compliance program as a control, we have undertaken a preliminary evaluation of three alternate/complementary compliance approaches (VMS and prior reporting, prior reporting only and data logger) for provision of effective compliance were an abalone fishery to be managed at a finer spatial scale. This evaluation was based primarily on feedback and discussions during the second compliance workshop, held in Mt Gambier on 1 February 2007. The workshop followed the limited, directed sampling of sub-legal-sized blacklip from across the fishery (see Chapter 6) that required fishers to harvest individuals of different sizes and from different areas on the same day.

The 'prior-reporting' option involved the use of detailed reporting before fishing, upon moving among separately-managed areas and before landing. This option received the least amount of support from the fishers that trialled it, primarily because of difficulty with telephone reception in some locations, the need to handle telephones with wet hands or in wet

conditions and the impact on available fishing time. This option also necessitates at-sea and/or on-landing checks. However, the detailed information provided in the reports would again facilitate efficient compliance checks, but to a lesser degree than the VMS.

Our trial of VMS was the first in an Australian abalone fishery, and the first time that VMS has been fitted to small trailer boats in any South Australian fishery. One of the key concerns was its viability given the limited, on-board power supply typical of small trailer boats used by abalone divers. To overcome this, fishers were only required to have the unit operational from 'home' to 'home', rather than continuously as is the case in other fisheries (*e.g*. South Australian Northern Zone rock lobster fishery). There were no problems with power supply during the course of the trial. Further, the fishers that trialled the VMS appreciated it's ease of use. One drawback of VMS is that, whilst providing a real-time vessel track, it provides limited information on the location of fishing, and no information on the size of abalone being harvested (Figure 5.5). Consequently, testing of VMS was linked to an expanded prior-reporting system. Whilst the integrity of this approach is highly dependent on at-sea and/or on-landing checks, the real-time information provided by the VMS facilitates efficient use of Fisheries Officer field time, among other resources.

Use of a data logger with the ability to measure and count blacklip and with an inbuilt GPS provides the opportunity for a large amount of information on the fishing activity to be acquired at the conclusion of the trip. In our trial, all blacklip were required to be measured within the area from which they were captured, and prior to moving to another fishing area. The strength of this approach is that these data (spatially-resolved catch, by number and length) are invaluable for research and fishery management (Figure 5.6). However, the fishers' trialling this equipment provided mixed reviews, and identified several drawbacks. These included the difficulty (and length of time) in processing all the catch through the data logger prior to moving between areas, the size of the unit, and the units' reliability. Furthermore, the data relies upon the fisher placing all blacklip through the logger prior to moving to another fishing area. This leaves the risk that abalone from one fishing area could be "passed off" as being taken from another fishing area. This is particularly relevant if the subsequent area had a different size limit. Consequently, integrity of this option would be enhanced with elevated prior reporting (Option 2) that could be used to crosscheck against the data logger information and, as with VMS, facilitate efficient use of Fisheries Officer field time in conducting at-sea checks.

Testing these alternate compliance options also provided the opportunity to test the utility of the 'morphometric marker' (see Chapter 1) as a compliance tool – ostensibly for classifying

blacklip into one of three categories ('stunted', 'non-stunted' and 'intermediate'; see Chapter 6). There was a strong correlation between the shell measurements obtained by both Fisheries Officers and research scientists; consequently, there was also a high degree of similarity in the classification of individual blacklip into the three categories (Figure 5.7).

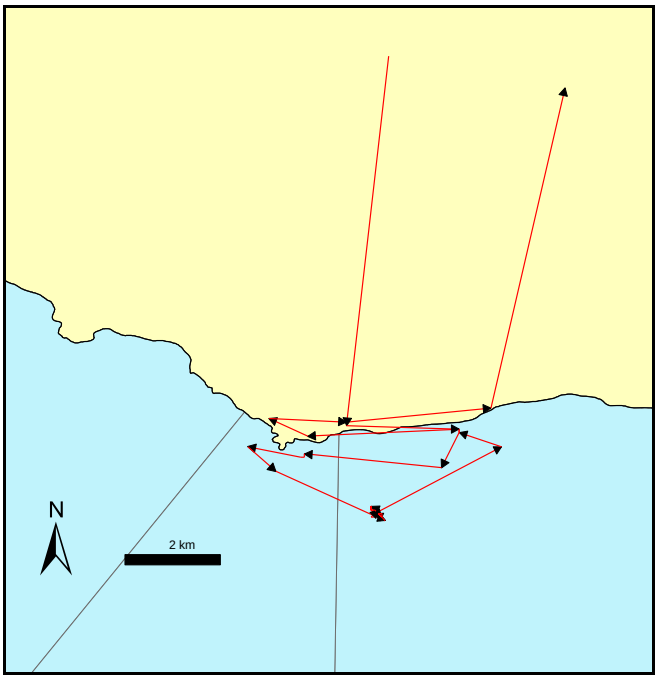

Figure 5.5: Map (exact location not provided to retain confidentiality), showing a typical VMS track obtained during the compliance trials.

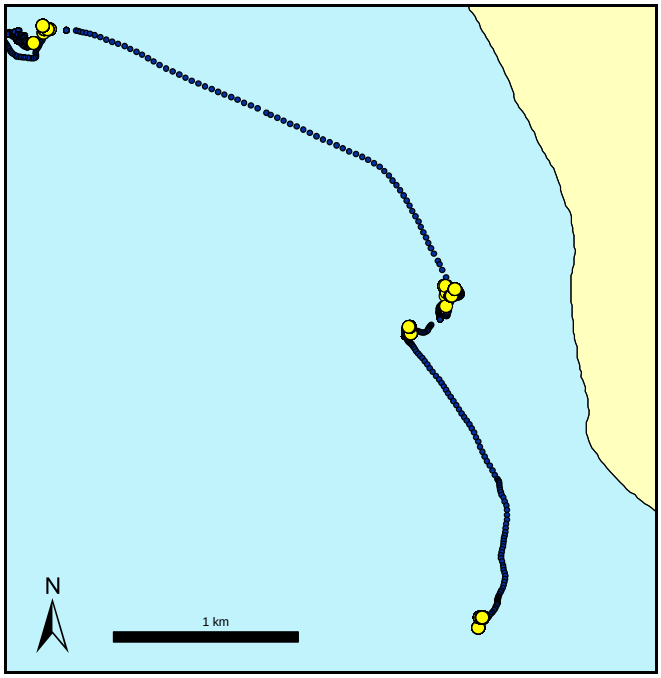

Figure 5.6: Map (exact location not provided to retain confidentiality), showing a typical track (blue symbols) and locations where blacklip were measured (yellow symbols) obtained from the GPS logger during the compliance trials.

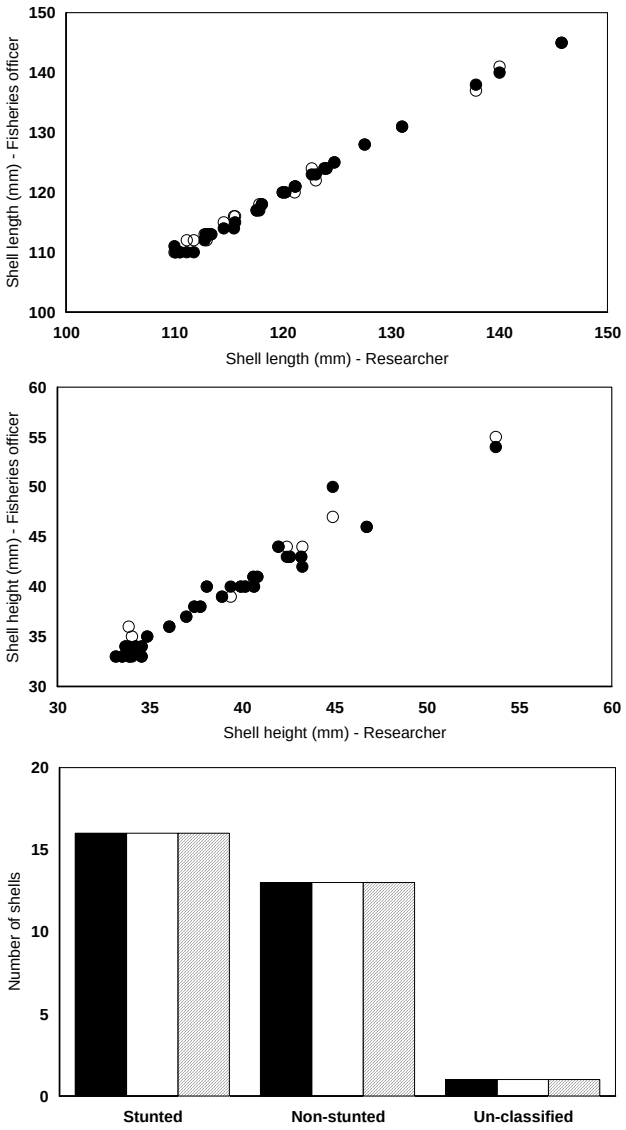

Figure 5.7: Relationships between shell length (top) and shell height (middle) measured by two Fisheries Officers and one Researcher, and number of blacklip shells classified into each of the three categories (bottom) by the two Fisheries Officers (shaded and clear bars) and one Researcher (cross-hatch shading).

5.5 Conclusions

Any future compliance program designed to deal with the challenges of abalone fishery management at fine spatial scales will need to draw upon a number of existing compliance tools, and will likely be supplemented by the approaches trialled here. Development of a viable compliance program required to address new risks associated with changing the spatial paradigm under which these fisheries are managed, should be undertaken through consultation among all stakeholders. This consultative process is likely to require more formal risk assessment, additional field trials of compliance approaches and legislative review.

CHAPTER 6. Application of the 'Morphometric Marker' to Develop Management Units

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6.1 Introduction

Many marine species form numerous populations across their geographic range (Taylor and Hellberg 2003; Cowen *et al.* 2006) that are effectively isolated from conspecifics by reproduction and migration (Berryman 2002; Swearer *et al.* 2002). These populations exist across a range of spatial scales, are rarely uniformly distributed or homogeneous (Wilen 2004), and frequently differ in their life-history parameters (Begg and Waldman 1999; Sponaugle *et al.* 2002; Bergenius *et al.* 2005). Differences in population parameters, such as reproduction, recruitment, survival and rates of growth, outweigh the effects of immigration and emigration, thereby strongly influencing their productivity (Begg and Waldman 1999; Holland 2003). Consequently, these populations (or stocks) respond independently to the effects of fishing (Jennings *et al.* 2001; Holland 2003).

The importance of considering demographic differences among populations to manage against over fishing and localised depletion has long been recognised (Begg *et al.* 1999), and has led to the concept of identifying 'management units' (MUs). These MUs can be defined as demographically independent populations that should be managed and monitored separately (Taylor and Dizon 1999; Martien and Taylor 2003; Palsbøll *et al.* 2007). Fundamental to the successful development of MUs is the ability to discriminate among component populations and, subsequently, to manage each of these on the basis of their biological parameters and associated productivity (Taylor and Dizon 1999; Martien and Taylor 2003; Bergenius *et al.* 2005; Defeo and Castilla 2005; Hammer and Zimmermann 2005).

The recognition of fine-scale stock structure and consequent need for the development of MUs has perhaps been most common for a range of sedentary marine invertebrates, including abalone (Prince, 2005; Naylor *et al.*, 2006), sea urchins (Prince and Hilborn 2003; Perry *et al.* 2002) and scallops (Smith and Rago 2004). Typically, these species have limited larval dispersal and form individual populations, across multiple spatial scales, which often vary greatly in their life-history parameters (McShane *et al.* 1988b; Orensanz and Jamieson 1995; Withler *et al.* 2003; Orensanz *et al.* 2005; Temby *et al.* 2007). However, a lack of appropriate, spatially-resolved data describing population structure has hindered the development of MUs (Leiva and Castilla 2001; Castilla and Defeo 2005; Prince 2005) leaving management regimes operating over large spatial scales (Wilen 2004).

In the majority of cases, management areas are linked to 'non-biological' jurisdictions, typically defined by political and regulatory boundaries (Prince 2005). Failure to manage these fisheries at appropriate spatial scales has resulted in many of these species becoming serially depleted, with stock collapses occurring in some extreme cases (Tegner *et al.* 1996; Perry *et al.* 2002; Orensanz *et al.* 2004). However, it is this same complex spatial structure, and associated, biological variability, that makes developing MUs for these fisheries so challenging. This is because of the extreme difficulties and high cost of acquiring information on the boundaries and biological characteristics of a large number of component populations that occur across a range of spatial scales (Prince 2005).

Abalone (Genus *Haliotis*) are typical of these sedentary species, in that they comprise numerous discrete populations across their geographical extent (Prince 2005; Morgan and Shepherd 2006). These populations are highly variable in their life-history characteristics (Shepherd and Hearn 1983; McShane *et al.* 1988b; Worthington *et al.* 1995; Worthington and Andrew 1997) with many containing 'stunted' abalone that have a slower growth rate and/or a smaller maximum size compared to abalone in adjacent populations (Shepherd 1988; Nash 1992; Wells and Mulvay 1995). As with most sedentary marine invertebrates, the current broad-scale (100 – 1000 km of coastline; McShane *et al.* 1994) management of abalone fisheries fails to account for this fine-scale, population structure. This leaves fast-growing, 'non-stunted' populations prone to over fishing and slow-growing, 'stunted' populations under utilised (Strathmann *et al.* 2002; Prince 2005). Identification of appropriate MUs, which reflect abalone population structure, could overcome this problem.

The most common method that has been employed to identify the population structure for abalone has been the analysis of genetic divergence among hypothesised populations (Hamm and Burton 2000; Zuniga *et al.* 2000; Conod *et al.* 2002; Withler *et al.* 2003; Chambers *et al.*

2006). However, these studies have typically shown differences at scales that are larger than would be expected given their larval dispersal capabilities (McShane *et al*. 1988a; Guzmán del Próo *et al.* 2000; Chambers *et al.* 2006; Stephens *et al*. 2006; Temby *et al.* 2007), which can lead to the definition of a few large MUs that are not appropriate to effectively manage local populations (Martien and Taylor 2003). The inferences made from genetic studies on population structure are probably a result of just a few migrants per generation (<10) being required to maintain genetic homogeneity among populations (Slatkin 1985). This number is demographically trivial because recruitment events that act to sustain populations typically consist of orders of magnitude more individuals (Miller and Shanks 2004).

An alternative approach is identification of separate populations based on spatial variability in morphology (Cadrin 2005). This method, which relies on the relationship between morphology and the growth and maturation rates of individuals (Cadrin 2000), is ideally suited to species that have easily-measurable, hard-body parts that reflect their ontogenetic history. Discrimination among populations can be achieved by identifying spatially distributed samples with similar morphology (Cadrin 2005; Cadrin and Silva 2005). The substantial spatial variation in abalone morphology (Chapters 2 and 3; Breen and Adkins 1982; McShane *et al.* 1994; Worthington *et al.* 1995; Saunders *et al.* 2008) suggests that this may be an effective method for identifying appropriate MUs. This approach has the added potential benefit of estimating the specific life-history characteristics of these populations because of the strong links between morphology and biology (Cadrin 2005).

Notably, this concept is central to the qualitative assessment underpinning an initiative in the Western Zone of the Victorian abalone fishery, in which fishing effort is focused towards the harvest of abalone with domed and fouled shells (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). One limitation of this approach is the current absence of calibration between shell shape or appearance and key biological parameters. Chapter 2 and Saunders *et al.* (2008) provide a more formal method through development of a quantitative 'morphometric marker'. They demonstrated that this marker, which is based on the ratio of shell length to shell height (SL/SH ratio), was able to differentiate between 'stunted' and 'non-stunted' abalone populations in the Southern Zone of the South Australian abalone fishery (SZ). That marker was subsequently shown to be strongly linked to growth rate, size-at-maturity and fecundity (Chapter 3; Saunders and Mayfield in press). Thus, this 'morphometric marker' is potentially a powerful tool for identifying and distinguishing among abalone populations, and for inferring important life-history characteristics.

The objective of this Chapter was to identify potential MUs in the SZ by determining the broad-scale, spatial distribution of 'stunted' and 'non-stunted' populations of blacklip abalone (*H. rubra*; hereafter referred to as blacklip) in the fishery, through categorising commercial shell samples, on the basis of the SL/SH ratio (Chapter 2; Saunders *et al*. 2008). Potential MUs, containing separate blacklip populations, were identified and their key biological parameters estimated using the relationships between the SL/SH ratio and blacklip biology (Chapter 3; Saunders and Mayfield in press). Data from fine-scale, systematic sampling by commercial fishers in one of the principal SZ fishing areas were used to confirm the spatial patterns observed in the SL/SH ratio from the broadly-distributed commercial catch samples. The disparity between these data and current management arrangements are highlighted, and principals for an initial framework for aiding development of a MU-based approach are discussed.

6.2 Methods

6.2.1 Study site

This study was conducted in the SZ, which includes all coastal waters of South Australia east of Meridian 139°E, with the exception of the Coorong and waters inside the Murray River mouth (Figure 6.1). The fishery is well described (see Section 1.4), and only a brief description is provided below.

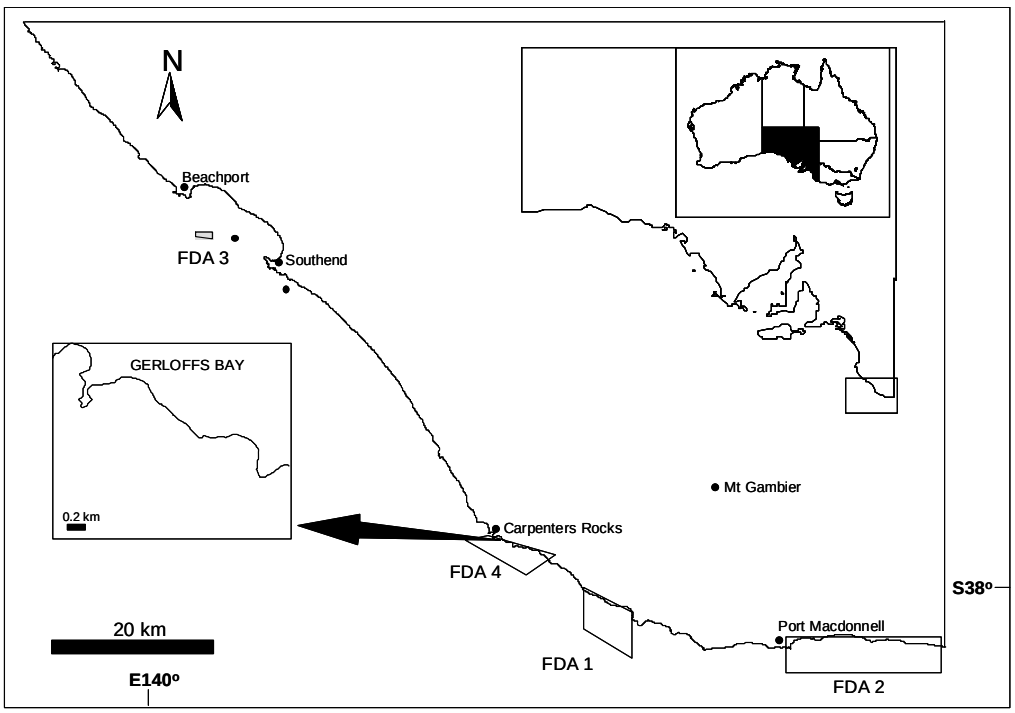

Figure 6.1: Map of the SZ showing location of FDAs and Gerloffs Bay (insert).

The fishery operates under South Australian legislation, including a formal management plan. The fishery is managed through a regime of input (*e.g.* limited entry) and output (*e.g.* minimum legal length (MLL), quotas) controls. The fishing season extends from 1 September to 31 August. Most (98%) of the total allowable commercial catch (TACC) is comprised of blacklip. In 2006/07 the blacklip TACC was 144 t shell weight. A small amount of greenlip abalone was also harvested (TACC: 6 t shell weight). The TACC for blacklip has generally been stable in recent years and levels of recreation and illegal harvest are considered negligable. The SZ includes four 'fish-down' areas (FDAs) where 'stunted' blacklip are thought to occur (FDA 1: Nene Valley; FDA 2: East of Port MacDonnell: FDA 3: Ringwood Reef; and FDA 4: Gerloffs Bay; Figure 6.1). These are managed separately with a MLL of 110 mm shell length (SL), 15 mm smaller than that in the 'non-fish-down' areas (non-FDAs). The TACCs in the non-FDAs and FDAs in 2006/07 were 99 and 45 t, respectively.

6.2.2 Broad-scale, spatial distribution of 'stunted' and 'non-stunted' blacklip

Data on the broad-scale, spatial distribution of blacklip populations were obtained from 104 commercial samples, each consisting of at least 50 abalone shells provided by commercial fishers across the spatial extent of the fishery. Permits were issued to fishers that allowed harvest of sub-legal-sized abalone (>110 mm SL) from pre-defined fishing areas (based on local commercial fisher knowledge) so that samples could be obtained from populations in the non-FDAs that fail to attain the regulated MLL (*i.e.* 125 mm SL) applicable in these areas. Metadata provided by the commercial fishers included latitude, longitude and depth of the sample location. The SL and shell height (SH) of each shell in all samples was measured, whereafter the mean (± 1 SE) of the ratio between SL and SH (*i.e.* the 'morphometric marker'; Chapter 2; Saunders *et al.* 2008) was calculated for each sample.

A SL/SH ratio value of 3.25 was found to distinguish between 'stunted' and 'non-stunted' blacklip populations (Chapter 2; Saunders *et al.* 2008). Consequently, this value was used to classify samples into one of three categories. Samples with mean ratios >1 SE smaller than 3.25 were classified as 'stunted', while those samples with mean ratios >1 SE larger than 3.25 were classified as 'non-stunted'. The small number of samples (~10%) where the mean ratio was within 1 SE of 3.25 were classified as 'intermediate'. Pearson's correlation analyses were used to determine whether these categories were related to latitude or longitude.

The locations of each categorised sample were mapped using ArcMap version 9.2. Relationships between sample category and both the current fishing areas and FDAs were evaluated qualitatively. Clusters of samples categorised as 'stunted' and 'non-stunted' were identified, and used as the basis for indicating the size and location of potential MUs.

6.2.3 Fine-scale, spatial distribution of 'stunted' and 'non-stunted' blacklip

To evaluate whether the density of data from the broad-scale commercial samples were sufficient to identify potential MUs, fine-scale systematic commercial samples were collected by commercial fishers in Gerloffs Bay. This area was selected as it was known to contain both 'stunted' and 'non-stunted' blacklip populations, and it is one of the principal fishing areas in the SZ, contributing ~50% of the FDA TACC. Systematic sampling was achieved by identifying the outer boundary of the fishing grounds in Gerloffs Bay and subdividing the fishing area into blocks 200 m in length and width (*cf.* Figure 6.6; Groeneveld and Cockcroft 1997; Mayfield *et al.* in press).

The commercial fishers were assigned a series of blocks to sample and were provided with the GPS positions of the corner and centre points of each block. In addition, 10 blocks located across the principal fishing ground within Gerloffs Bay were repeat-sampled by four different commercial fishers. The samples from each block comprised 20-80 abalone that were all larger than 110 mm SL. Morphometric data were collected from each shell and each sample then classified into one of three categories ('stunted', 'non-stunted' or 'intermediate'), as described above.

Preliminary analysis of these data showed that many of the blocks classified as 'stunted' and several that were classified as 'intermediate' contained numerous large blacklip that were inconsistent with the mean and maximum SL of blacklip from remaining samples that were classified as 'stunted'. This inconsistency was a result of an over-representation of older abalone with higher shells in areas that have had little historic fishing activity (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). To identify these samples, analysis of variance (ANOVA) was carried out on the length of the blacklip shells for each block. Plots of residuals against group means revealed that these data satisfied the assumptions of normality and homogeneity of variance (Quinn and Keough 2002). Blocks were treated as a fixed factor.

A Tukey's HSD test was then conducted to reveal where these differences lay. The results of the ANOVA revealed significant differences in the SL amongst blocks ($F_{57,\ 3776} = 19.5$, $P < 0.001$). Those blocks categorised as 'stunted' or 'intermediate' by the SL/SH ratio with a significantly higher average SL compared to those with typically 'stunted' blacklip were subsequently re-classified as 'non-stunted' (n = 5; Figure 6.2). In addition, blocks categorised as 'intermediate' with a similar average SL to those with typically 'stunted' blacklip were re-classified as 'stunted' (n = 2; Figure 6.2).

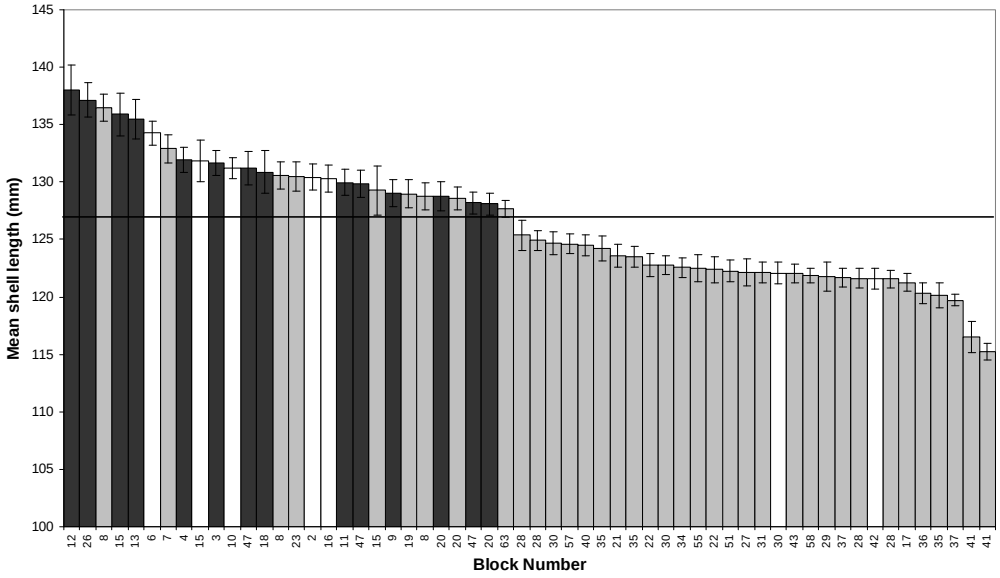

Figure 6.2: Mean SL for each of the systematic samples from Gerloffs Bay. Black, grey and white bars show samples classified into the 'non-stunted', 'stunted' and 'intermediate' categories, respectively. The mean SL of samples above the horizontal line were significantly higher than those below. Error bars indicate 1 ± SE.

The locations of each categorised sample were mapped as described above. Relationships between sample category and the broad-scale data were evaluated qualitatively. Clusters of samples categorised as 'stunted' and 'non-stunted' were identified, and used as the basis for indicating the size and location of two potential MUs within Gerloffs Bay.

6.2.4 Estimates of biological parameters for potential MUs

Estimates of the key biological parameters for ten potential MUs (8 identified from the broad- and 2 identified from the fine-scale spatial distribution of 'stunted' and 'non-stunted' blacklip) were determined by the linear relationships between the SL/SH ratio and growth residuals and L_{50} (Chapter 3; Saunders and Mayfield in press). These were:

$$G_r = -16.99R + 25.30$$

and

$$L_{50} = 26.18R - 12.51,$$

where G_r is the growth residual, R is the mean SL/SH ratio and L_{50} is the SL at 50% maturity. Using these relationships, the value of L_{50} for each potential MU was calculated from the mean estimate of this parameter from the commercial samples within that area. Similarly, the

growth residuals were then calculated for these samples to predict the rate of growth at L_{50} within each potential MU. This was achieved by using the average growth relationship for all sites sampled in Saunders and Mayfield (in press) to determine the growth rate at L_{50}. The growth rate at L_{50} for each potential MU was then calculated by adding (or subtracting) the residual value predicted by the SL/SH ratio of the samples in that area. These relationships were used to estimate increases in SL from L_{50} after 2 and 4 years (after Tarbath 2003).

6.3 Results

6.3.1 Broad-scale, spatial distribution of 'stunted' and 'non-stunted' blacklip

Using the SL/SH ratio, 58 samples were categorised as 'non-stunted', 33 as 'stunted' and 13 as 'intermediate' (Figure 6.3). There were no significant correlations between the SL/SH ratio and either latitude (r = 0.164, df = 103, P > 0.05; Figure 6.4a) or longitude (r = 0.158, df =103, P > 0.05; Figure 6.4b). This was reflected by the mixture of samples categorised as 'stunted', 'non-stunted' or 'intermediate' along the SZ coastline when each sample was plotted simultaneously against both latitude and longitude (Figure 6.4c).

The broad-scale samples were unevenly distributed along the coastline (Figure 6.5a). Notably, there were several fishing areas from which either none, or very few (<3) samples were obtained. In most cases, commercial catches from these areas were small. There was limited consistency in sample category within the current fishing/management areas, including most of the FDAs (Figure 6.5a,b). Nevertheless, there were eight locations in the SZ across which the spatially-resolved samples were similarly categorised. These locations with a consistent spatial pattern comprised the basis for identifying the size and location of potential MUs that contain separate blacklip populations. Potential MUs with 'stunted' blacklip included Ringwood Reef, Red Rock Bay, Gerloffs Bay South and Acis Reef. Those potential MUs with 'non-stunted' blacklip were Salmon Hole, Gerloffs Bay North, Middle Point and Cape Northumberland (Figure 6.5b).

6.3.2 Fine-scale, spatial distribution of 'stunted' and 'non-stunted' blacklip

In Gerloffs Bay, samples from 30 blocks were categorised as 'stunted' while 28 blocks were categorised as 'non-stunted'. There were 20 blocks within which no blacklip were observed (Figure 6.6). All multiple samples, collected from within the same block, were similarly categorised. These fine-scale data suggested that there were two potential MUs (one 'stunted' and one 'non-stunted') in Gerloffs Bay. The locations of these MUs were consistent with those identified by the broad-scale commercial samples collected from this area (Figure 6.6).

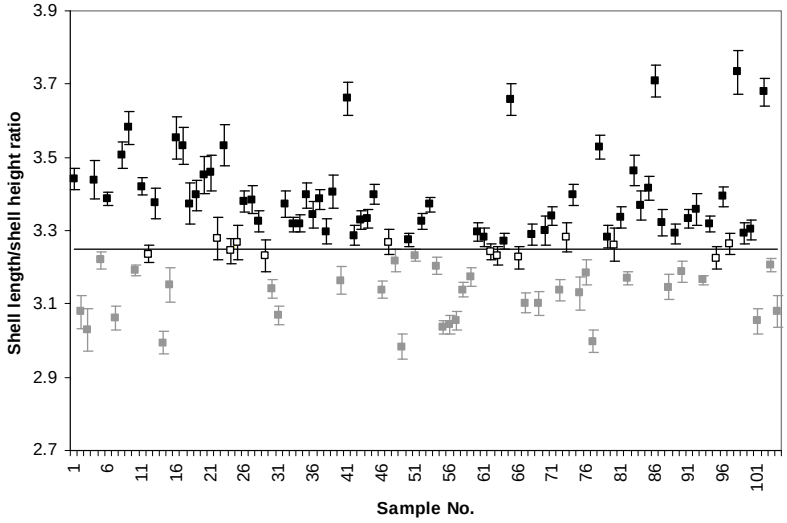

Figure 6.3: Mean SL/SH ratio for each commercial abalone shell sample classified into the 'non-stunted'(black squares), 'stunted' (grey squares) and 'intermediate' (white squares) categories, respectively in the SZ. Horizontal black line indicates a SL/SH ratio value of 3.25 that separates the 'non-stunted' and 'stunted' (grey squares) categories. Error bars indicate 1 ± SE.

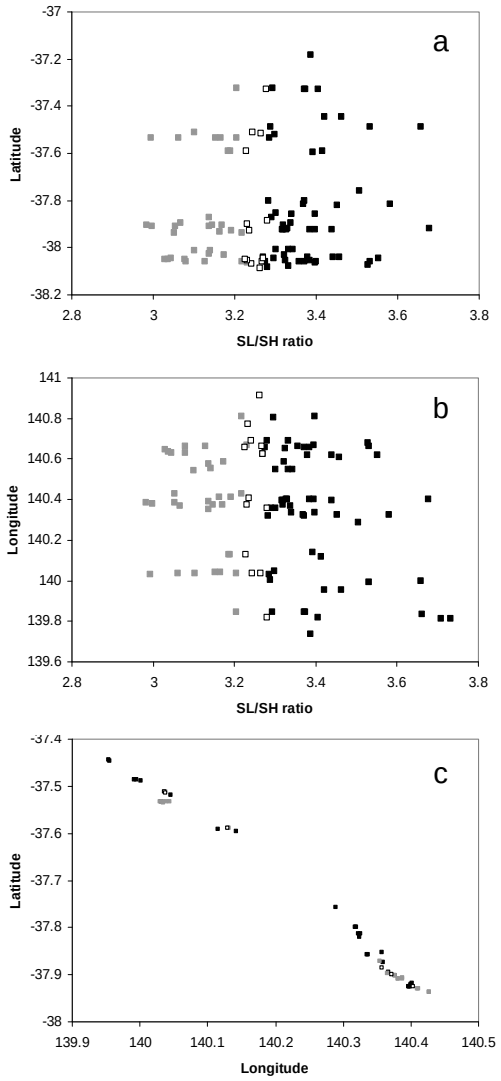

Figure 6.4: Relationships between the SL/SH ratio obtained from the commercial abalone shell samples and latitude (a), longitude (b) and the interaction of latitude and longitude (c). 'Non-stunted', 'stunted' and 'intermediate' samples represented by black, grey and white squares, respectively.

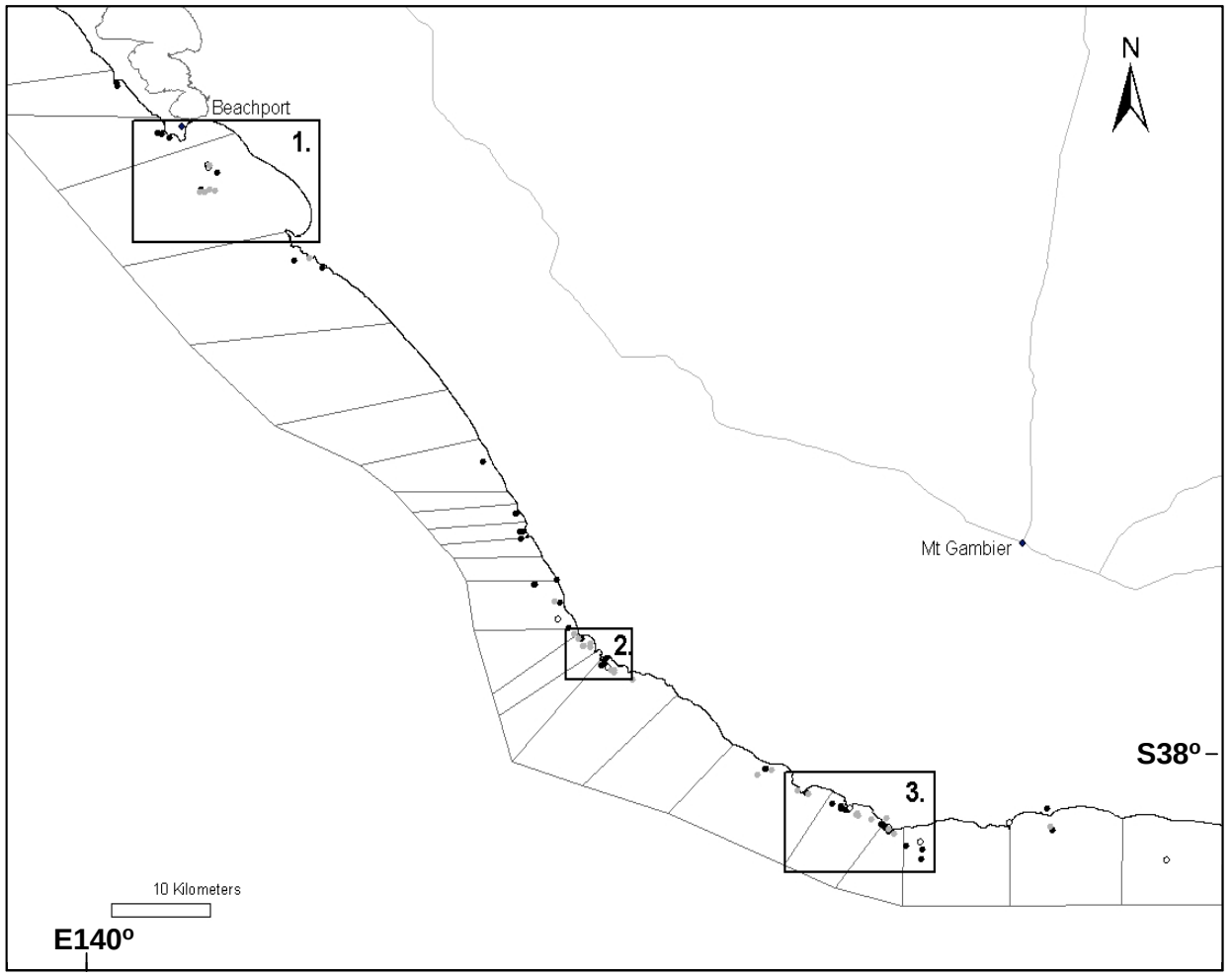

Figure 6.5a: Map showing distribution of commercial shell samples classified into the 'non-stunted' (black dots), 'stunted' (grey dots) and 'intermediate' (white dots) categories along the SZ coastline. Rectangles indicate sections of coastline that are enlarged in Figure 6.5b. Grey shading indicates FDAs and divisions show boundaries of the current fishing areas.

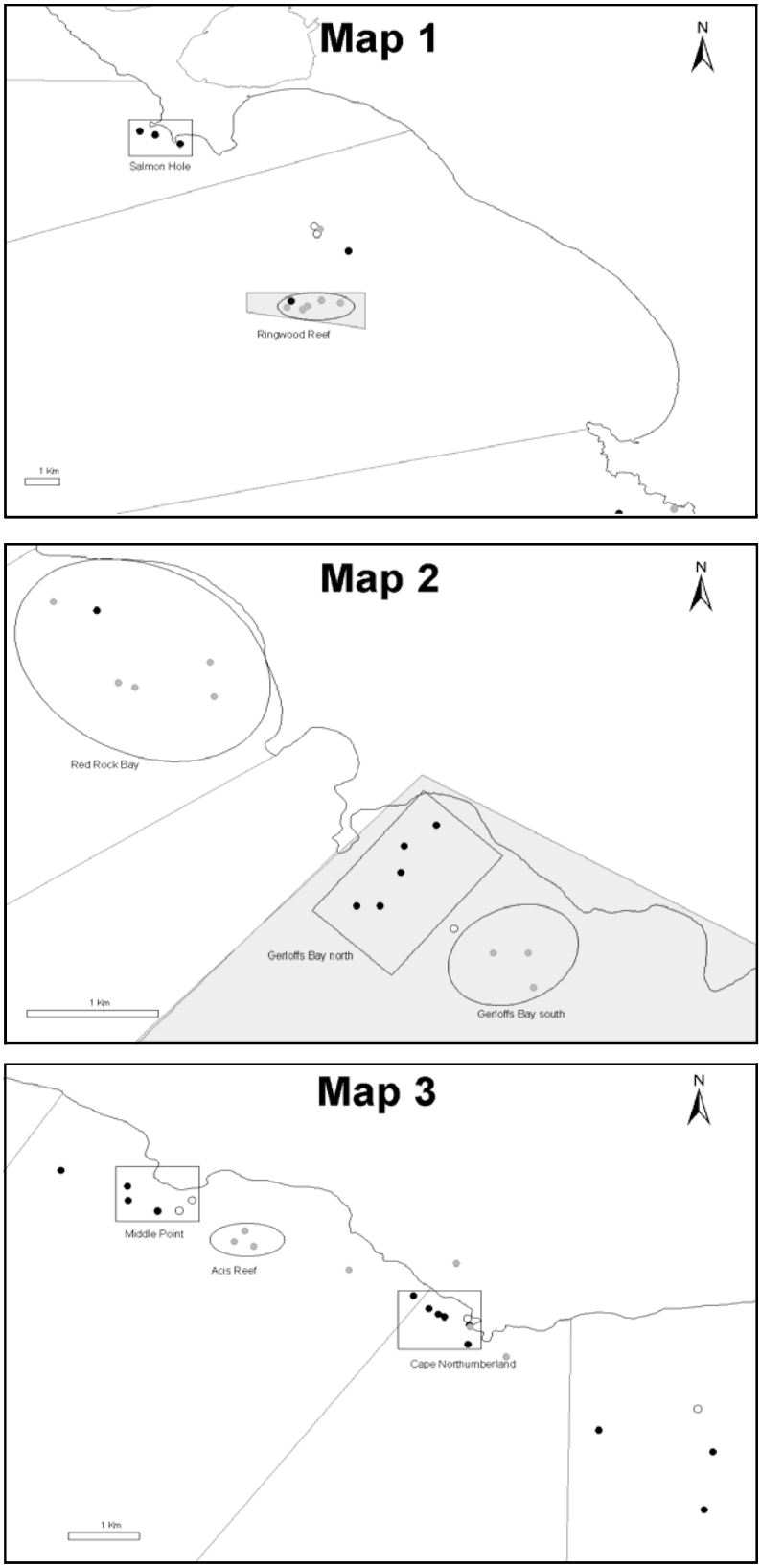

Figure 6.5b: Maps showing enlarged sections of the SZ coastline along which rectangles and ellipses indicate potential MUs at Salmon Hole and Ringwood Reef (Map 1), Red Rock Bay, Gerloffs Bay North and Gerloffs Bay South (Map 2) and Middle Point, Acis Reef and Cape Northumberland (Map 3). Grey shading indicates FDAs and divisions show boundaries of the current fishing areas.

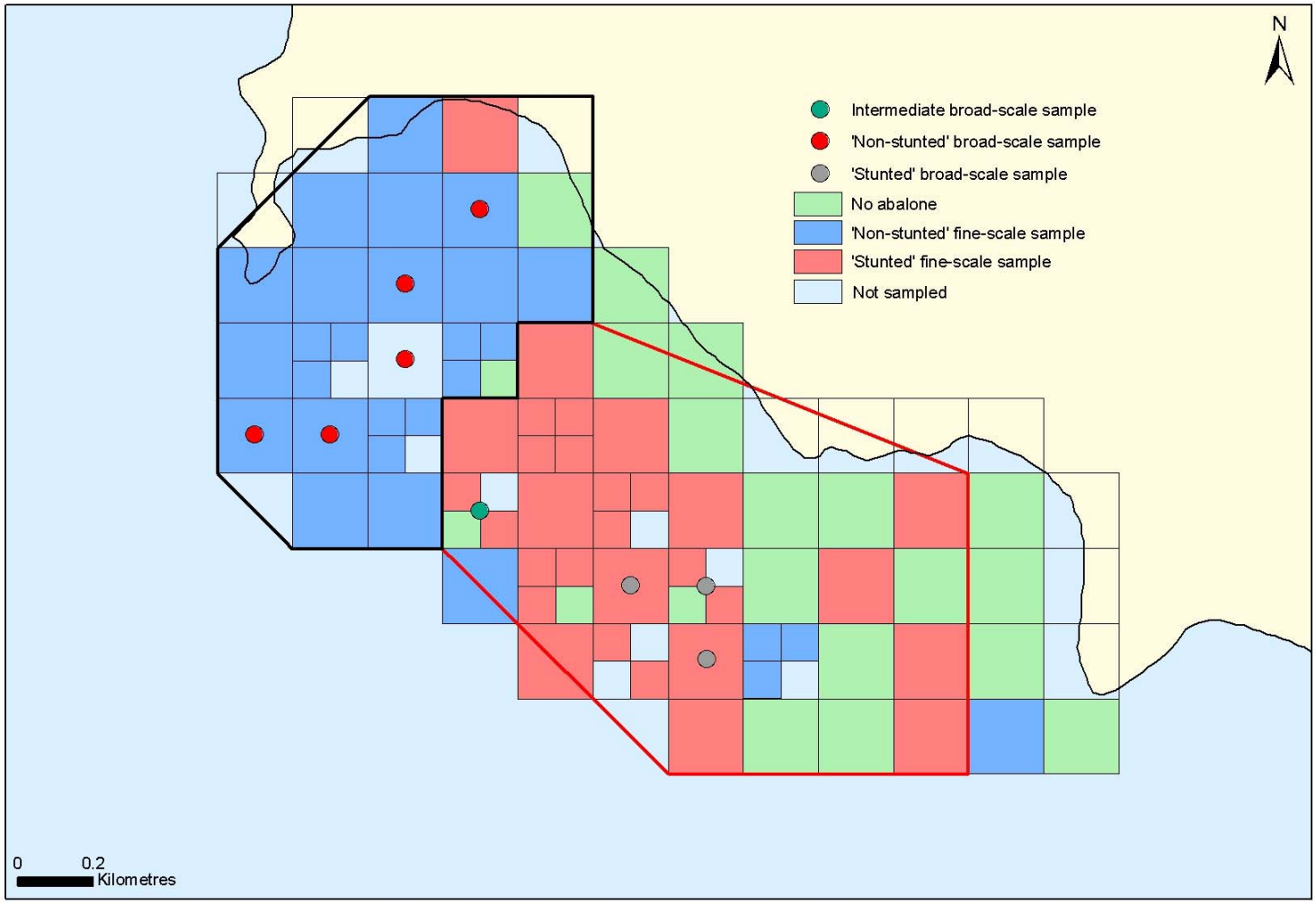

Figure 6.6: Map showing the distribution of commercial shell samples classified into the 'non-stunted' (blue shading) and 'stunted' (red shading) categories in Gerloffs Bay. Blocks that were repeat-sampled have four subdivisions. Locations and categories of broad-scale samples obtained from this area are also shown ('non-stunted': red dots; 'stunted': grey dots; and 'intermediate': green dots). The black and red boundary lines outline the potential 'non-stunted' and 'stunted' management units in this area, respectively.

6.3.3 Estimates of biological parameters for potential MUs

Within the 'stunted' potential MUs, estimates of L_{50} ranged between 68 (AR) and 71 mm SL (RB). It was predicted that blacklip from these two populations would grow to between 88 and 92 mm SL and to between 102 and 107 mm SL, respectively, after two and four years growth. In contrast, for the 'non-stunted' potential MUs, estimates of L_{50} ranged between 76 (CN) and 84 mm SL (SH). It was predicted that blacklip at Cape Northumberland would grow to 99 and 116 mm SL, with those from Salmon Hole from 110 to 127 mm SL after two and four years of growth, respectively (Figure 6.7). The estimates of L_{50} and SL after two and four years for blacklip in the 'stunted' and 'non-stunted' potential MUs in Gerloffs Bay were consistent for the samples collected at both the broad and fine spatial scales (Figure 6.7).

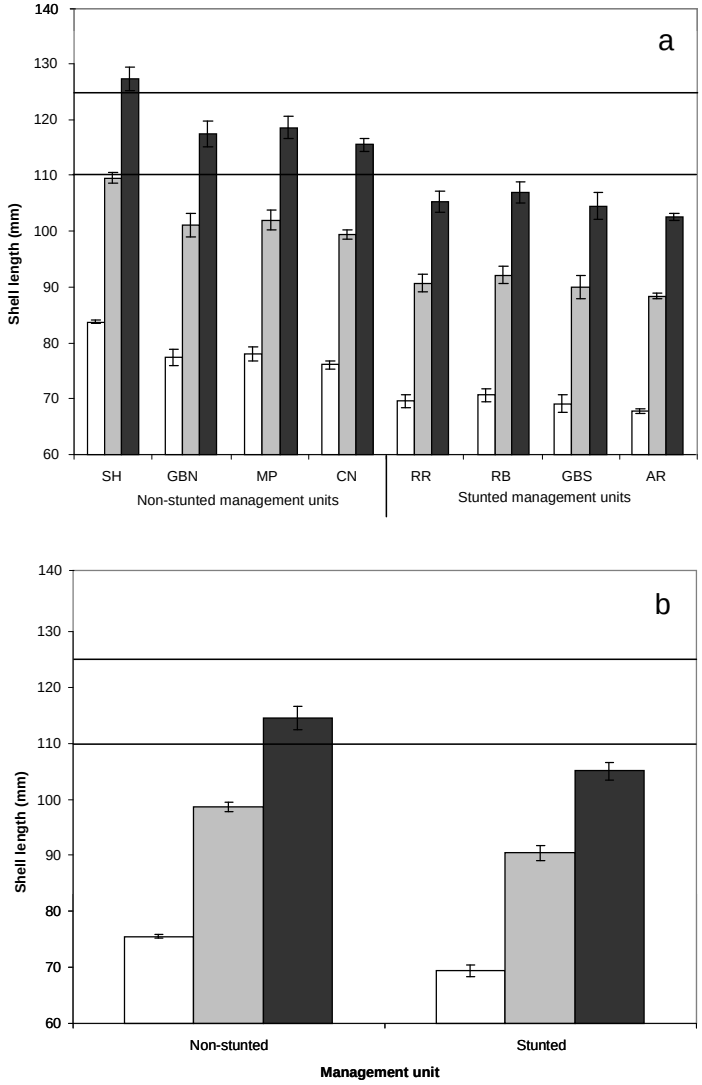

Figure 6.7: Estimates of L_{50} (white bars), L_{50} + 2 years growth (grey bars) and L_{50} + 4 years growth (black bars) calculated from the SL/SH ratio for the potential MUs identified by the broad-scale commercial samples (a) and systematic, fine-scale samples in Gerloffs Bay (b). Horizontal black lines indicate the current MLLs in the SZ and error bars show ± 1 SE. Locations of each potential MU are provided in Figure 6.5.

6.4 Discussion

Successful application of MU principles is predicated on the ability to discriminate among component stocks and, subsequently, to manage each of them on the basis of their biological parameters and associated productivity (Taylor and Dizon 1999; Martien and Taylor 2003; Bergenius *et al.* 2005; Defeo and Castilla 2005; Hammer and Zimmermann 2005). In this study, we were able to identify potential MUs as a result of the significant spatial variability observed in the SL/SH ratio from commercial shell samples obtained across the SZ coastline. Notably, the location, distribution and spatial extent of the potential MUs were largely inconsistent with that of the current fishing/management areas, or the FDAs. Importantly, the location of 'stunted' and 'non-stunted' MUs (Gerloffs Bay) were consistent across the broad- and fine-scale datasets, although the fine-scale samples were more informative for identifying a potential boundary between the two. It is likely that the potential MUs that were identified represent separate blacklip populations as these occur at fine spatial scales (10's to 100's of metres; Temby *et al.* 2007) reflecting limited larval dispersal (Prince *et al.* 1988). In addition to identifying the size and location of potential MUs, relationships between the SL/SH ratio and key biological parameters for blacklip permitted estimation of the biological characteristics for blacklip within these areas. These data would likely remain unavailable if traditional biological sampling were required to obtain them. Thus, our approach allows practical determination of MUs, along with their life-history characteristics, at relevant spatial scales.

There was no significant correlation between latitude or longitude and the SL/SH ratio, suggesting that the environmental factors that are probably causing this variability are acting at finer spatial scales (Swain *et al.* 2005). Relatively consistent spatial patterns in the SL/SH ratio only occurred at the scale of one of the current fishing areas (Red Rock Bay) and one FDA (Ringwood Reef). While these and the other areas with spatial consistency in the SL/SH ratio could constitute potential MUs, the size and locations of these require further validation through the collection of fine-scale, systematic, commercial catch samples.

This fine-scale information was obtained from Gerloffs Bay as the patterns observed from the broad-scale sampling suggested the presence of two potential MUs (one 'stunted' and one 'non-stunted') in this area. Importantly, the systematic sampling in Gerloffs Bay showed that these potential MUs exist in the same area as that identified by the broad-scale samples. These results suggest that the density of original commercial samples (nine in total) collected in this area was sufficient to identify these potential MUs and, consequently, that similar sampling intensities elsewhere in the SZ should be equally informative. However, the systematic sampling allowed more accurate delineation between these areas. While these

potential MUs still contain a limited mix of 'stunted' and 'non-stunted' blacklip, the proposed boundary follows a shallow reef that acts as a natural boundary between these two populations which can easily be identified from the surface. The small pockets of blacklip that are different to the primary category of the MU are unlikely to contribute greatly to the population in that area given their low abundance and patchy distribution (Thor Saunders, SARDI, unpublished data).

Stock identification is an integral component of modern fisheries science and underpins effective fisheries management (Jennings *et al*. 2001). This is because management is best achieved at spatial scales that reflect the actual population structure of the species (Taylor and Dizon 1999; Martien and Taylor 2003; Bergenius *et al.* 2005). Yet, despite their importance, stock definitions are rarely re-considered in fisheries management (Begg *et al*. 1999). Importantly, use of the SL/SH ratio to describe potential MUs provides a simple, cost-effective tool to re-visit the stock structure, and re-consider the management arrangements for blacklip in the SZ, so that they better reflect the population structure of this species (Begg and Waldman 1999). Our data suggest that only one current fishing area and one FDA constitute potential MUs while the creation of at least six additional MUs is warranted within the current management areas. These include Salmon Hole, Gerloffs Bay North, Middle Point and Cape Northumberland that contain 'non-stunted' blacklip, and Ringwood Reef, Red Rock Bay, Gerloffs Bay South and Acis Reef that contain 'stunted' blacklip. Further sampling from the commercial catch, which is relatively easy and inexpensive, is likely to suggest more MUs in the future.

Identifying and then discriminating between these MUs comprises the first step in applying MU principals. Subsequently, the biological characteristics of the potential MUs identified were estimated, to provide initial information on size limits to support their appropriate management. Size limits are commonly used in abalone, and other fisheries, as a tool to ensure adequate reproductive capacity among populations and reduce the likelihood of recruitment overfishing (Shepherd *et al.* 1995). In the Tasmanian abalone fishery, size limits are designed to provide abalone with two spawning seasons between L_{50} and the MLL (Nash 1992; Tarbath 2003). Applying this model to the SZ suggests size limits for the 'stunted' MUs identified could range from 88 to 92 mm SL, whilst those for the 'non-stunted' MUs would need to be substantially larger, varying between 99 and 110 mm SL. These estimates of MLL are substantially smaller than the current size limits in the fishery (110 mm SL for 'stunted' and 125 mm SL for 'non-stunted' blacklip). As the current size limits seldom constrain catch rates (CPUE), an alternative approach to setting size limits in the potential MUs would be to retain the current values. This would substantially increase potential levels

of egg production as blacklip in both 'stunted' and 'non-stunted' MUs would generally be provided with >4 spawning seasons after attaining L_{50}, under these arrangements. This more conservative approach is probably justified because there is no empirical evidence to support the Tasmanian model (L_{50} + 2 years).

More formal approaches need to incorporate the inferred biological parameters, with other data, in egg-production models (Nash 1992; Shepherd *et al.* 1995; Mayfield *et al.* 2007). Undertaking these analyses is important in light of previous assessments on *H. roei*, that show very low levels of retained egg production even if the MLL provides two spawning seasons post L_{50} (Preece *et al*. 2004). These analyses should also be supported through application of an integrated, length-structured stock assessment model (Breen *et al.* 2003; Gorfine *et al.* 2005; Mayfield *et al.* 2007) tailored for each MU. Stock assessment and simulation models incorporating spatial complexity are becoming more common (Meester *et al.* 2001; Holland 2003; Fu and Fanning 2004). While implementation of such models may be hampered by low levels of both data and data diversity available for individual MUs (Chen *et al.* 2003), where sufficient data are available the models may perform better than when applied at broader scales because the need to aggregate data across component populations is removed (Punt 2003; Naylor *et al.* 2006). This approach will aid establishment of catch and effort limits within MUs, which are important in a fishery with intensive spatial management (Hewitt *et al.* 2004; Dr Jeremy Prince, Biospherics Pty Ltd, personal communication).

The regional- or zonal-scale application of the 'morphometric marker' to identify potential MUs and predict the life-history parameters of abalone within these, provides additional challenges for management of sedentary marine invertebrate fisheries. These arise from the need to combine a wealth of data (and other fishery-related information) into a revised management framework under a new paradigm that explicitly requires reductions in the spatial scale of management (Meester *et al.* 2001; Prince and Hilborn 2003; Wilen 2004; Castilla and Defeo 2005; Prince 2005; Naylor *et al.* 2006). Adoption of fine-scale management necessitates consideration of the limitations of the data available, as well as the requirements for effective (and efficient) management and compliance arrangements both within, and across, any MUs identified. For example, our data from Gerloffs Bay suggest the need for two MUs within this small area, each <2 km^2 in size. Should MUs be warranted at this spatial scale throughout the SZ, the potential number of MUs exceeds 100 – with each of these potentially demonstrating unique life-history characteristics and, therefore, requiring separate assessment (*e.g.* fishery-independent surveys, catch and effort monitoring, commercial catch sampling and integration of data in a length-structured model) and management (*e.g.* quotas and size limits). This number of MUs is substantially greater than

the number (~30) of reef codes assessed and managed annually in the Western Zone of the Victorian abalone fishery (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). It would also greatly exceed the number of MUs that could realistically be assessed and managed by a Government Agency without the associated costs becoming prohibitive (Prince 2005).

Thus, the challenge for all stakeholders – scientists, fishers and fisheries managers – will be to respond through developing new, spatially-explicit management policies (Wilen 2004) and seeking recent/novel methods for data collection, synthesis and analysis to provide an integrated and sound basis for the rational management of these resources (Eekhout *et al.* 1992). In most cases, this is likely to require a pragmatic approach (Koljonen 2001), with management becoming adapted to the biological reality (Hammer and Zimmerman 2005), working within the constraints imposed by the practical limitations associated with assessment, management and compliance, and the associated increased costs that may offset perceived benefits (Criddle *et al.* 2001). We contend that a framework underpinning successful implementation of MUs for species with spatially-complex population structure require a holistic approach. Notably, at a workshop we hosted in the SZ in 2007, stakeholders in the fishery identified seven key steps necessary to move from a sub-regional to MU-based spatial scale in this fishery. These were (1) clear, relevant and realistic management objectives; (2) transparency through effective and ongoing stake-holder engagement and consultation; (3) robust, reliable and accurate measures for discriminating among, and estimating the biological parameters of, component stocks; (4) practical selection, clear definition and appropriate scales for MUs; (5) clear management (and compliance) arrangements; (6) robust reporting systems; and (7) reliable, cost-effective data underpinning defensible assessments, that encompasses the use of suitable performance measures. These steps were similar to those previously identified by (Perry *et al.* 1999) and several have already been considered in other fisheries. This includes industry-based surveys for the provision of stock-assessment data (Prince and Hilborn 2003), implementation of a territorial user rights system (Castilla and Fernandez 1998; Criddle *et al*. 2001; Leiva and Castilla 2001; Defeo and Castilla 2005; Orensanz *et al.* 2005) and the extension of VMS to the electronic monitoring of both vessels and gear that would permit the spatial distribution of harvesting to be regulated (Wilen 2004). Whatever the approach, successful implementation is likely to depend heavily on extensive collaboration (Perry *et al.* 2002; Haapasaari *et al.* 2007; van Densen and McCay 2007) and increasing responsibility and accountability of all stakeholders (Hilborn 2002; Parma *et al.* 2006).

6.5 Conclusions

This Chapter linked morphology and biology, to provide a mechanism to simply, practically and cost-effectively overcome the crucial first step of being able to discriminate among, and estimate the biological parameters of, component populations. Without this knowledge, MUs cannot be appropriately developed or managed. The tool we have developed can be applied at any spatial scale to address the observed mix of variability and lack of predictability of the size and location of abalone populations. When used within a suitable management framework, it can provide the necessary information to enable practical reductions in the scale of abalone fishery management, which has previously been hampered by the inability to gather detailed demographic data at appropriate spatial scales. This approach is not limited to abalone. Rather, it is applicable to many sedentary invertebrate species for which fine-scale, population structures exist.

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CHAPTER 7. Application of a Length-Structured, Stock Assessment Model to two Potential Management Units.

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7.1 Introduction

The National Abalone Model (FRDC 1999/116; Gorfine *et al*. 2005) has been used to aid assessment of the blacklip abalone (*Haliotis rubra*; hereafter referred to as blacklip) fisheries in the Southern (Mayfield *et al*. 2004, 2005c), Central (Mayfield *et al*. 2005a, 2006) and Western (Mayfield *et al*. 2005b; Chick *et al*. 2006) Zones of the South Australian abalone fishery since 2004. Over time, substantial changes have been made to improve application of the model (Mayfield *et al*. 2006; Chick *et al*. 2006). These have included a range of sensitivity tests, examining the appropriateness of the priors (and associated distributions) including use of both 'exploratory' (*i.e.* diffuse) and 'driving' (*i.e.* informative) prior distributions, employing an increasingly rigorous suite of diagnostic tools for assessing model performance (*e.g.* temporal patterns in recruitment deviations) and re-evaluation of the data used to fit the model. Other, more minor changes, including a re-evaluation of the data used within the model were also implemented. Despite these improvements, it is important to note that the model has only recently been developed, is still being refined and only limited sensitivity testing has been completed. It is also evident that the data (1) defining some model parameters, (2) being used to estimate informative priors and, (3) used to fit the model require ongoing revision to ensure they appropriately represent the blacklip populations being modelled. Hence, outputs from the model may not yet be representative of the status of the modelled stocks, and may change substantially through future model and data refinement.

In this Chapter, we describe the application of a Fortran 90 implementation of the National Abalone Model to assessment of the blacklip stocks in two of the possible 'management units' (MUs) identified in Chapter 6. This is the first time that such an integrated, length-structured, stock assessment and risk analysis model has been used to assess the status of blacklip stocks below a zonal spatial scale in the South Australian abalone fishery. The two areas selected were Ringwood Reef and Middle Point. These possible MUs contain 'stunted' and 'non-stunted' blacklip, respectively. The assessment used Bayesian techniques to estimate (1) model parameters; (2) determine current stock status relative to that in 1967 (*i.e*. B_0); and (3) determine the uncertainty of those estimates.

7.2 Methods

7.2.1 Model overview

A detailed description of the model can be found in Gorfine *et al*. (2005). The formulae and parameter priors underpinning the model are provided in Section 7.7. Briefly, the model considers the population divided into small (2-mm) length classes with the number of blacklip in each length class calculated through time. The numbers of blacklip in each length class are calculated by applying growth, fishing mortality, natural mortality and recruitment to each length class each year. Biomass estimates are derived from a length-weight relationship. These calculations provide estimates of model-based catch rates and length-frequency distributions that are compared to the available data (*i.e.* observations). Unlike the AbModeller implementation of the National Abalone Model, the Fortran 90 implementation does not require a Maximum Likelihood estimation phase. Instead a Markov chain-Monte Carlo (MCMC) algorithm is used directly to obtain Bayesian posteriors for the model parameters. Normal proposal distributions for the Metropolis algorithm employed in the MCMC procedure are initially assigned standard deviations corresponding to <3% of the width of the parameter bounds for the parameter in question. If the resulting MCMC acceptance rate lies outside the preferred range of 30 – 40%, the proposal distributions are adjusted accordingly until the desired acceptance rate is obtained.

7.2.2 Base-case model for Ringwood Reef

A variety of data are required to fit the base-case model for Ringwood Reef to the observed data. This includes the catch and fishing selectivity from the commercial sector of the fishery, fishery-independent estimates of abundance and populations length-frequency distribution, and a range of biological information.

7.2.2.1 *Commercial, recreational and illegal catches*

Estimates of annual commercial catch for the period 1968 – 2005 were obtained from research logbooks completed for each fishing day and submitted to SARDI Aquatic Sciences (Figure 7.1; see also Mayfield *et al*. 2007). Ringwood Reef comprises only a portion of mapcode 36B and catch records prior to 1997/98 provide no information on whether catch extracted from or effort expended in this mapcode occurred at Ringwood Reef or elsewhere. Thus, estimates of the historical catch were obtained by determining the proportion of the total catch for mapcode 36B harvested from Ringwood Reef (1997/98 to 2002/03), and applying a simple back-calculation. Estimates of fishing effort at Ringwood Reef were similarly derived. Recreational and illegal catches were assumed to be zero in all years, as they are likely to have been negligible.

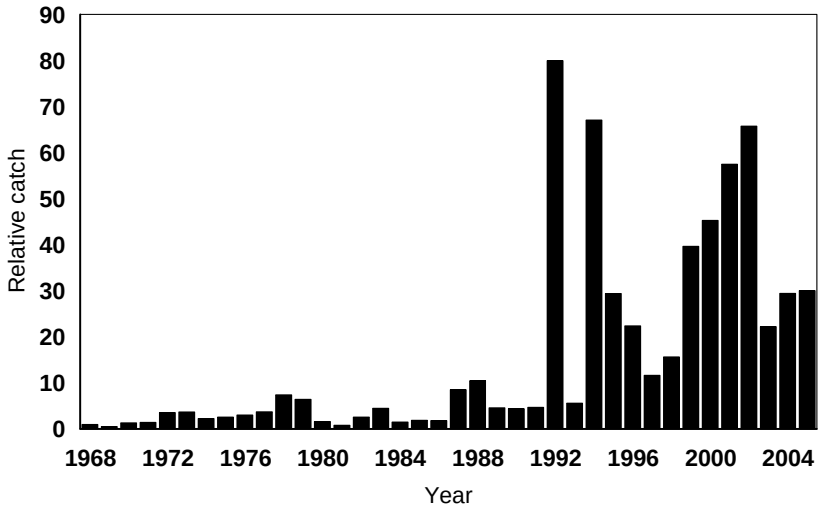

Figure 7.1: Estimated catch of blacklip, relative to that in 1968, harvested from Ringwood Reef between 1968 and 2005.

7.2.2.2 *Length-frequency distribution of the commercial catch and fishing selectivity*

Data on the length-frequency distribution of the commercial catch were available from 2000 to 2005. For blacklip above the minimum legal length (MLL), the fraction of available blacklip at a given length that are actually caught (relative to the fraction caught at lengths where this fraction is maximal) is termed the fishing selectivity curve. The fishing selectivity curve from 1968 to 2005 was estimated from the abovementioned commercial shell samples (n = 2 158). The modal length for each annual commercial length-frequency dataset was obtained and an average taken over all years. The average modal length was used as the upper (100% selectivity) endpoint of a linear selectivity ogive, with the lower endpoint being set at the MLL with 5% selectivity. For Ringwood Reef, these endpoints were 127 and 110 mm shell length (SL), respectively.

7.2.2.3 *Survey estimates of abundance and length-frequency distribution of the population*

Survey estimates of abundance and the length-frequency distribution of the population were obtained from fishery-independent surveys, based on the leaded-line method (McGarvey 2006; McGarvey *et al*. in press), undertaken at Ringwood Reef from 2002 to 2005. Both datasets were truncated so that only blacklip larger than 70 mm SL were included.

7.2.2.4 *Biological data*

Growth was assumed to be constant over time and the same for both sexes. It was incorporated in the model as a transition matrix, where blacklip from each 2-mm length class at the start of each season grow into a range of larger (2-mm) length classes during each season (Figure 7.2). The growth transition matrix was determined from tag-recapture data for blacklip at Ringwood Reef using a probabilistic Gompertz model (see Bardos 2005).

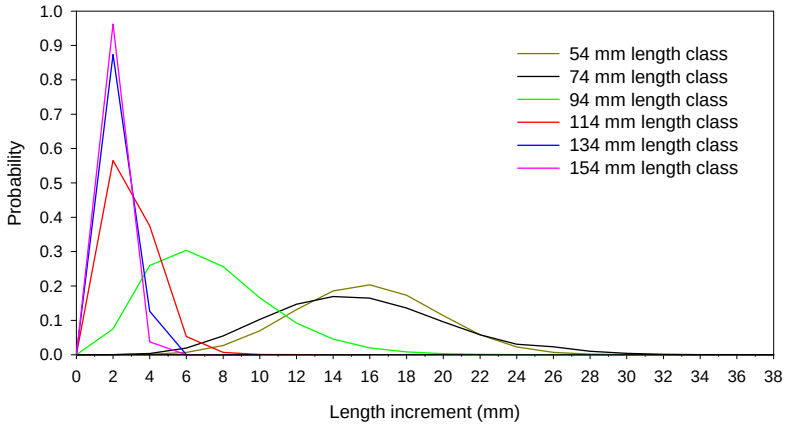

Figure 7.2: Probability of annual length increments for blacklip in the 54, 74, 94, 114, 134 and 154 mm length classes at Ringwood Reef.

The proportion of sexually mature individuals within each length class was determined from data obtained from Ringwood Reef. Visual assessment of the relationship between SL and maturity enabled crude estimates of L_{50} and the maturity ogive width (ϕ). For Ringwood Reef, these values were 75 and 15 mm SL, respectively. The allometric relationship between SL and whole weight was obtained from Gorfine *et al*. (2005).

7.2.2.5 *Fishing penalty*

A fishing penalty term was added to the log-likelihood, to prevent the model from drifting toward solutions having implausibly high biomass and thus improbably small catch as a fraction of exploitable biomass. This was implemented by assuming that the largest catch in the time series for Ringwood Reef must represent a substantial fraction of the (selected) exploitable biomass for that year. The fishing penalty term was of the form $L = \min(aF^n, 1)$,

so that log(L) = min (log a + n log F, 0). The parameters a and n are adjustable. For Ringwood Reef, their values were 50 and 50, respectively.

7.2.2.6 *Markov chain-Monte Carlo simulation (MCMC)*

Uncertainty in the mature and exploitable biomass estimates during each year (1968 – 2005) and estimates and posterior distributions for the model-estimated parameters (initial recruitment (R_{init}), steepness of the Beverton-Holt stock-recruit relationship (h), and the emergence ogive (L_{50} and ϕ)) were evaluated using an MCMC procedure, employing the Metropolis algorithm to generate 1 million MCMC iterations. The first 100 000 iterations were discarded and the remaining iterations were then systematically sampled at a rate of 10% (*i.e.* 90 000 iterations were retained). Annual recruitment deviations (parameters that allow for annual fluctuations in recruitment for each of the 38 years; R_{devs}) were not estimated (*i.e.* R_{dev} = 0 in all years) as the fitted deviations displayed persistent trends, rather than sporadic isolated fluctuations, during preliminary model runs. This probably reflects the model compensating for the slow growth data at Ringwood Reef that are inconsistent with the length-frequency distributions of both the commercial catch and fishery-independent surveys at this site.

7.2.2.7 *Model outputs*

Outputs from the model included (1) fits to each year of fishery-independent abundance and length-frequency data; (2) estimates and posterior distributions of the 42 parameters; and (3) trajectories of mature and exploitable biomass for each year, relative to B_0.

7.2.3 Base-case model for Middle Point

A variety of data are required to fit the base-case model for Middle Point to the observed data. This includes the catch and fishing selectivity from the commercial sector of the fishery, fishery-independent estimates of abundance and populations length-frequency distribution, and a range of biological information.

7.2.3.1 *Commercial, recreational and illegal catches*

Estimates of annual commercial catch for the period 1968 – 2005 were obtained from research logbooks completed for each fishing day and submitted to SARDI Aquatic Sciences (Figure 7.3). Middle Point comprises only a portion of mapcode 39G and catch records provide no information on whether catch extracted from or effort expended in this mapcode occurred at Middle Point or elsewhere. To overcome this, estimates of the proportion of the catch harvested from Middle Point were obtained from each of the six current divers in the

fishery, and the historical catch determined by applying a simple back-calculation. Estimates of fishing effort at Middle Point were similarly derived. Recreational and illegal catches were assumed to be zero in all years, as they are likely to have been negligible.

7.2.3.2 *Length-frequency distribution of the commercial catch and fishing selectivity*

Data on the length-frequency distribution of the commercial catch were available from 2001, 2002, 2003 and 2005. The fishing selectivity curve from 1968 to 2005 was estimated from these commercial shell samples (n = 1 888). The modal length for each annual commercial length-frequency dataset was obtained and an average taken over all years. The average modal length was used as the upper (100% selectivity) endpoint of a linear selectivity ogive, with the lower endpoint being set at the MLL with 5% selectivity. For Middle Point, these endpoints were 133.5 and 125 mm SL, respectively.

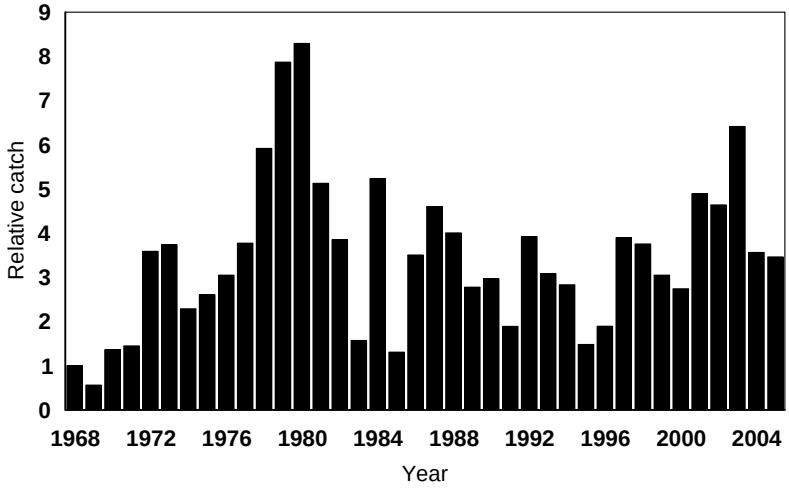

Figure 7.3: Estimated catch of blacklip, relative to that in 1968, harvested from Middle Point between 1968 and 2005.

7.2.3.3 *Survey estimates of abundance and length-frequency distribution of the population*

Survey estimates of abundance (2002 to 2005) and the length-frequency distribution of the population (2003 to 2005) were obtained from fishery-independent surveys, based on the leaded-line method (McGarvey 2006; McGarvey *et al*. in press), undertaken at Middle Point. Both datasets were truncated so that only blacklip larger than 70 mm SL were included.

7.2.3.4 *Biological data*

Growth was assumed to be constant over time and the same for both sexes. It was incorporated in the model as a transition matrix, where blacklip from each 2-mm length class at the start of each season grow into a range of larger (2-mm) length classes during each

season (Figure 7.4). The growth transition matrix was determined from tag-recapture data for blacklip at Middle Point using a probabilistic Gompertz model (see Bardos 2005).

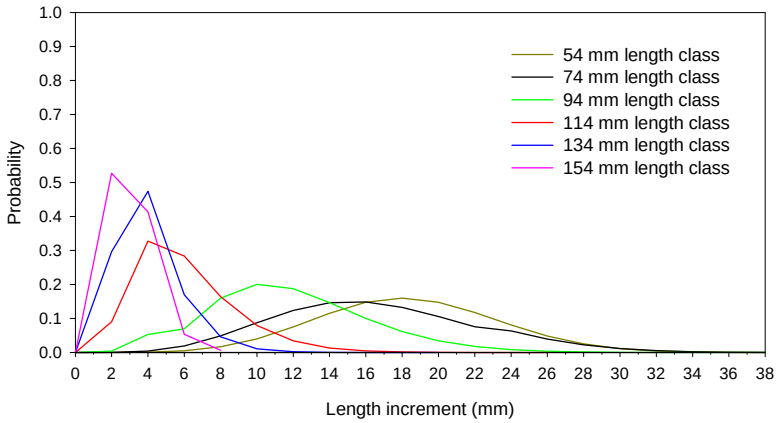

Figure 7.4: Probability of annual length increments for blacklip in the 54, 74, 94, 114, 134 and 154 mm length classes at Middle Point.

The proportion of sexually mature individuals within each length class was determined from data obtained from Middle Point. Visual assessment of the relationship between SL and maturity enabled crude estimates of L_{50} and ϕ. For Middle Point, these values were 79 and 14 mm SL, respectively. The allometric relationship between SL and whole weight was obtained from Gorfine *et al*. (2005).

7.2.3.5 *Fishing penalty*

A fishing penalty term was added to the log-likelihood, to prevent the model from drifting toward solutions having implausibly high biomass and thus improbably small catch as a fraction of exploitable biomass. This was implemented by assuming that the largest catch in the time series for Middle Point must represent a substantial fraction of the (selected) exploitable biomass for that year. The fishing penalty term was of the form $L = \min(aF^n, 1)$, so that $\log(L) = \min(\log a + n \log F, 0)$. For Middle Point, the values of a and n were 50 and 5, respectively.

7.2.3.6 *Markov chain-Monte Carlo simulation (MCMC)*

Uncertainty in the mature and exploitable biomass estimates during each year (1968 – 2005) and estimates and posterior distributions for the model-estimated parameters (R_{init}, h, L_{50}, ϕ and annual recruitment deviations (parameters that allow for annual fluctuations in recruitment for each of the 38 years; R_{devs})) were evaluated using an MCMC procedure, employing the Metropolis algorithm to generate 1 million MCMC iterations. The first

100 000 iterations were discarded and the remaining iterations were then systematically sampled at a rate of 10% (*i.e.* 90 000 iterations were retained).

7.2.3.7 *Model outputs*

Outputs from the model included (1) fits to each year of fishery-independent abundance and length-frequency data; (2) estimates and posterior distributions of the 42 parameters; and (3) trajectories of mature and exploitable biomass for each year, relative to B_0.

7.3 Results

There were large differences in the catch histories and fisheries biology of blacklip at Ringwood Reef and Middle Point. These differences were reflected in the parameters and biomass trajectories estimated through the modelling process.

7.3.1 Ringwood Reef

7.3.1.1 *Base-case model fits to observed data*

The model outputs poorly fitted the proportions-at-length obtained from the fishery-independent surveys (Figure 7.5). This was particularly the case for blacklip larger than 124 mm SL. In contrast, model outputs more closely fitted the fishery-independent estimates of abundance (Figure 7.6), with this latter fit being of similar quality to those in other abalone models (*e.g.* Worthington *et al*. 2001; Breen *et al*. 2003; Mayfield *et al*. 2005a,b,c; Chick *et al*. 2006).

7.3.1.2 *Parameter estimates*

Mean estimates of R_{init}, h, L_{50} and ϕ were 1.1 x 10^6, 0.55, 109 and 47, respectively. The base-case model provided information useful for estimation of R_{init} and h, but was less informative for estimating L_{50} and ϕ, for which the estimated posterior means were close to the upper bounds of the respective priors.

7.3.1.3 *Temporal patterns in mature and exploitable biomass*

Base-case model outputs suggest that, as a consequence of the low levels of catch, mature and exploitable biomass declined minimally during the first 25 years of the fishery (1968 – 1992; Figure 7.7). Both declined rapidly between 1993 and 2003, during which they were 86.5% and 74.0%, relative to B_0, respectively. Model estimates of mature and exploitable biomass increased marginally in 2004 and 2005.

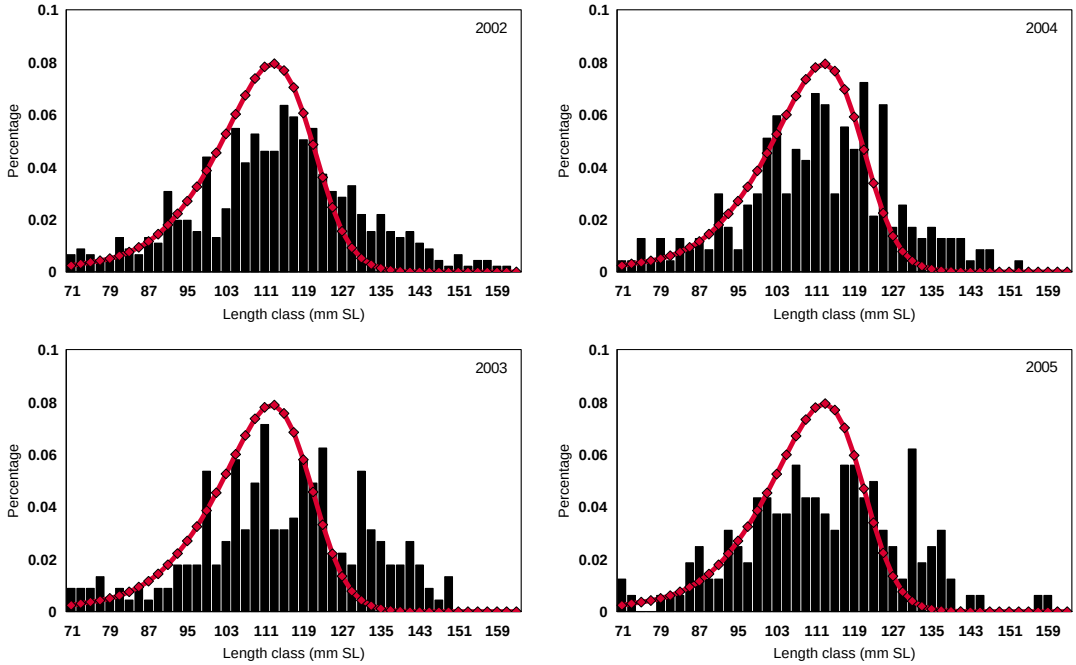

Figure 7.5: Model fit (red lines) to the proportion-at-length observed (black bars) during fishery-independent, blacklip surveys at Ringwood Reef from 2002 to 2005.

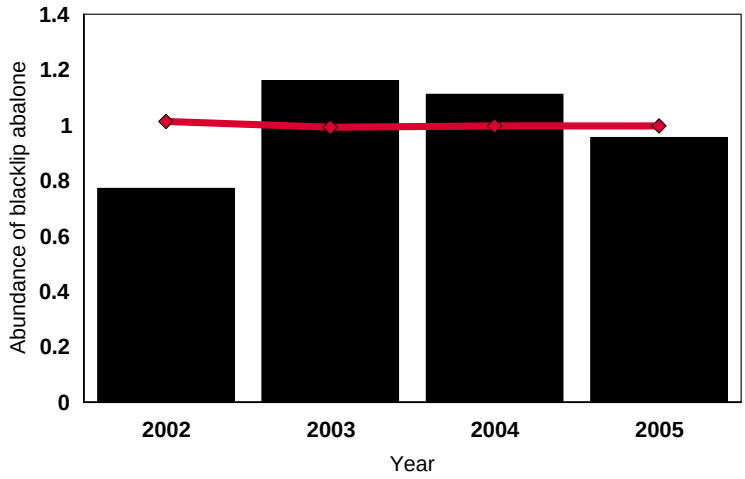

Figure 7.6: Model fit (red line) to fishery-independent estimates of blacklip abundance at Ringwood Reef from 2002 to 2005.

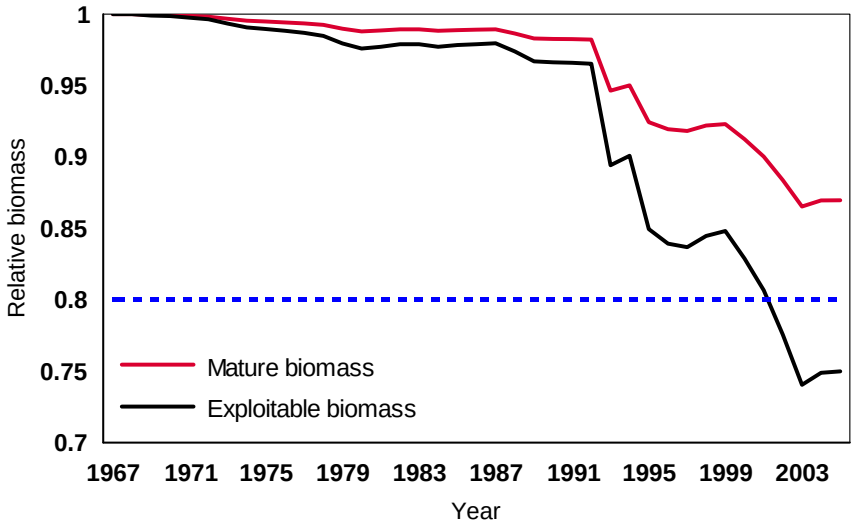

Figure 7.7: Trajectories of mature (red line) and exploitable (black line) biomass, relative to B_0, simulated from the base-case model at the posterior means of the estimated parameters, for Ringwood Reef from 1967 to 2005. The horizontal blue line is for reference only and indicates 80% of B_0.

7.3.2 Middle Point

7.3.2.1 *Base-case model fits to observed data*

The model outputs closely fitted the proportions-at-length (Figure 7.8) and estimates of abundance (Figure 7.9) obtained from the fishery-independent surveys. These fits are of similar quality to those in other abalone models (*e.g.* Worthington *et al*. 2001; Breen *et al*. 2003; Mayfield *et al*. 2005a,b,c; Chick *et al*. 2006). Perhaps the most significant lack of fit related to the inability of the model to fit apparent annual changes in the proportions at length (*e.g.* 2004 and 2005). While this is also a common feature of other abalone fishery models, it is less clear how such annual changes are caused (*e.g.* changes in sampling and/or selectivity).

7.3.2.2 *Parameter estimates*

Mean estimates of R_{init}, h, L_{50} and ϕ were 1.4 x 10^5, 0.59, 109 and 35, respectively. The base-case model provided information useful for estimation of R_{init}, h, and ϕ, but was less informative for estimating L_{50}, for which the estimated mean of the posterior was high, and close to the upper bound imposed on it by the prior.

The base-case model was also informative in determining the R_{devs}. This was evident in the temporal patterns in recruitment among years (Figure 7.10). These outputs suggest that recruitment was low in 2000, 2001 and 2002.

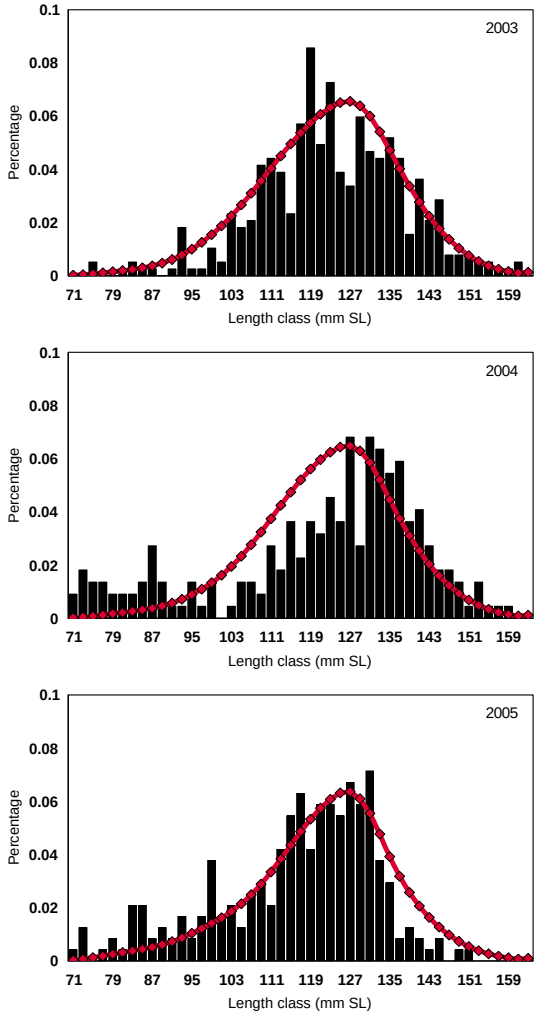

Figure 7.8: Model fit (red lines) to the proportion-at-length observed (black bars) during fishery-independent, blacklip surveys at Middle Point from 2003 to 2005.

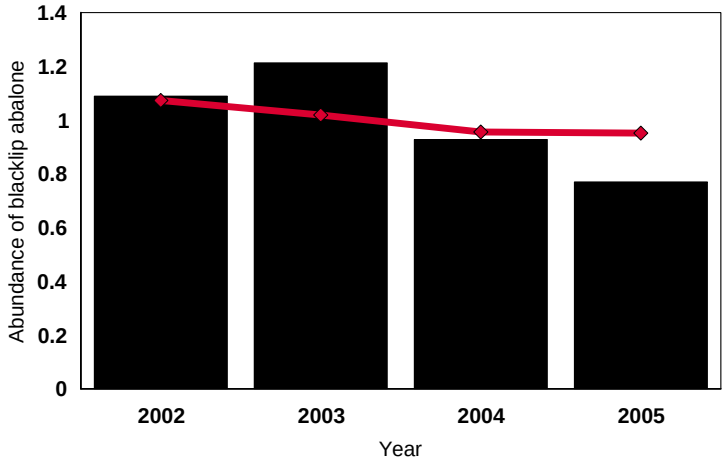

Figure 7.9: Model fit (red line) to fishery-independent estimates of blacklip abundance at Middle Point from 2002 to 2005.

7.3.2.3 *Temporal patterns in mature and exploitable biomass*

Base-case model outputs suggest that mature and exploitable biomass declined rapidly during the first 18 years of the fishery (1968 – 1983; Figure 7.11). Both increased between 1984 and 1997, whereafter estimates of mature and exploitable biomass declined steadily, reaching 59.4% and 42.2%, relative to B_0, during 2005, respectively.

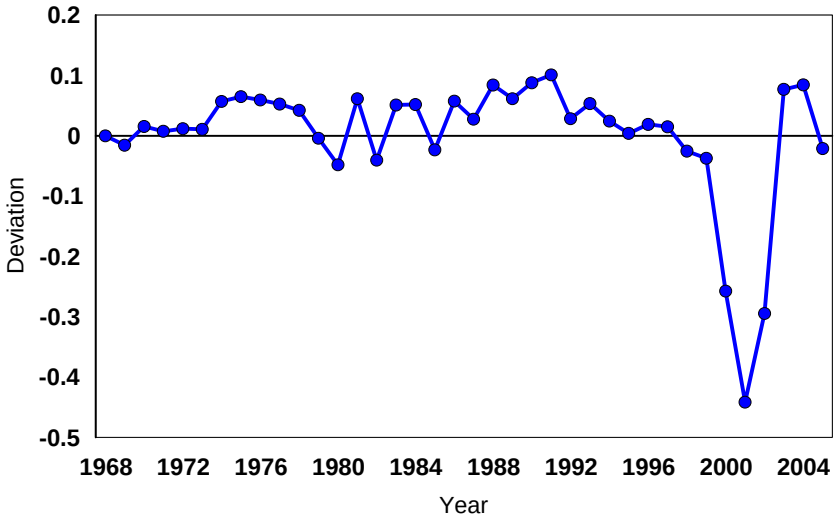

Figure 7.10: Estimated R_{devs} between 1968 and 2005.

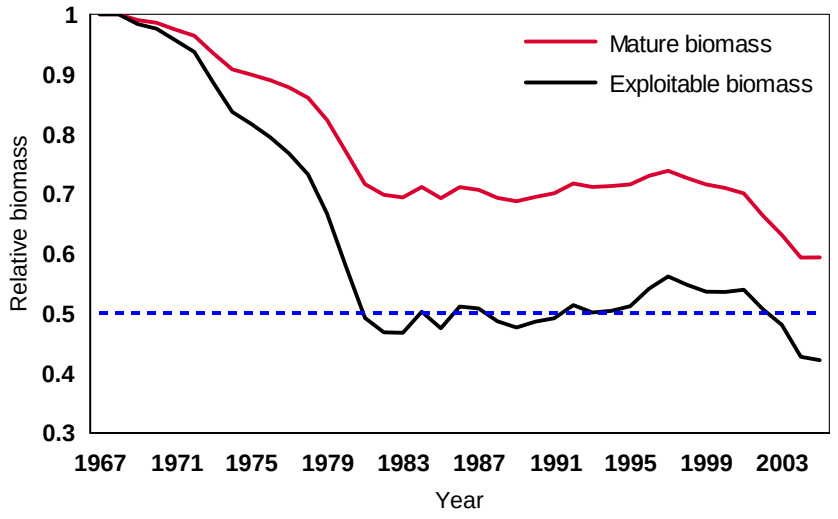

Figure 7.11: Trajectories of mature (red line) and exploitable (black line) biomass, relative to B_0, simulated from the base-case model at the posterior means of the estimated parameters, for Middle Point from 1967 to 2005. The horizontal blue line is for reference only and indicates 50% of B_0.

7.4 Discussion

In concert with the application of the National Abalone Model (FRDC 1999/116; Gorfine *et al*. 2005) at a reef-code scale to aid current assessment of the Victorian Western Zone abalone fishery (FRDC 2007/066 – *Rapid response to abalone virus depletion in western Victoria: information acquisition and reefcode assessment models*), our assessment of the blacklip stocks at Ringwood Reef and Middle Point clearly demonstrate the utility of this model to be applied at fine spatial scales, where appropriate data exist. This builds on previous blacklip stock assessments, based on this model, in the Southern (Mayfield *et al*. 2004, 2005c), Central (Mayfield *et al*. 2005a, 2006) and Western (Mayfield *et al*. 2005b; Chick *et al*. 2006) Zones of the South Australian abalone fishery, and in the Victorian fishery (Dr Harry Gorfine, PIRVic, personal communication), that were undertaken at much larger spatial scales (by Zone in SA and by region (=sub-zone) in Victoria).

The integrated, length-based, stock assessment model used combines multiple data sets from a variety of sources. Nevertheless, the outputs are limited by the spatial extent and quality of the input data and have considerable levels of associated uncertainty. For example, data used to fit the models were only available from 2002, despite the models providing estimates from 1968. Thus, the level of precision in the outputs is limited by the short time series of the data being fitted. Reliability of the outputs is also strongly influenced by: (1) growth rate, especially the degree to which the growth parameters reflect the magnitude and variability of growth in the Zone; and (2) the degree to which the biological data reflect blacklip populations in the two areas.

Notably, estimates of growth rates for Ringwood Reef appear overly pessimistic. The growth matrix estimated by the 'Estimatrix' program, based on a probabilistic Gompertz model (Bardos 2005), appears to fit the tag-recapture data very well. However, the growth data for Ringwood Reef are inconsistent, for blacklip larger than 124 mm SL, with commercial and fishery-independent length-frequency data from this area. These data show substantial numbers of blacklip >124 mm SL, whereas the tag-recapture data have just 13 blacklip >124 mm SL, of which 12 showed zero growth. Consequently, the growth matrix based on the Ringwood Reef tag-recapture data indicates large blacklip growing minimally. Thus, current model outputs for Ringwood Reef are likely to underestimate the productivity of the stock while overestimating the level of depletion. A range of modelling approaches could be adopted to alleviate this problem. These include allowing the model to fit growth internally (*i.e.* exploiting the commercial length-frequency data) or modifying the treatment of the Ringwood Reef tag-ecapture data prior to fitting it. Examples of the latter approach would be excluding data for blacklip >124 mm SL, or combining tag-recapture data from Ringwood

Reef with data from other highly productive reefs, adjusted to match the Ringwood Reef data for blacklip <124mm SL. In contrast, no analogous difficulties were encountered for Middle Point.

Furthermore, current use of the model is low. Consequently, the model is still being refined and, to date, only limited sensitivity testing has been completed. As refinement of the model, and the data used in future years could possibly change the model outputs considerably, current outputs from the model may not be representative of the status of the stock. Nevertheless, these current outputs provide an indication of trends in biomass (*i.e.* dynamical response of biomass trends to changes in fishing pressure), rather than the absolute estimates of biomass (*i.e.* their magnitude). This is because the qualitative nature of the biomass trajectories was more robust to variations in model assumptions, whereas the magnitude of the estimated biomass varied substantially.

For both areas, there was reasonable agreement between model outputs and the available data. These fits are of similar quality to those in other abalone models (*e.g.* Worthington *et al*. 2001; Breen *et al*. 2003; Mayfield *et al*. 2005a,b,c; Chick *et al*. 2006). The strength of this relationship was greatest for Middle Point, for which the model outputs closely fitted both the proportions-at-length and estimates of abundance obtained from the fishery-independent surveys. In common with other abalone fishery models, the model had difficulty fitting apparent annual changes in the proportions-at-length (*e.g.* 2004 and 2005). Estimates of recruitment deviations appear to be realistic in that these R_{devs} displayed sporadic, isolated fluctuations in the absence of fitting data (*i.e.* prior to 2002), rather than persistent trends. Further, there was a strong relationship between catch history and both the mature and exploitable biomass trajectories, in that they both respond sensibly to fishing pressure and are biologically realistic. Nevertheless, some parameter estimates (*e.g.* L_{50}) were close to the bounds imposed on them. This may have arisen through the model compensating for an incorrect fixed assumption (e.g. mortality, growth or selectivity), thus providing biologically plausible biomass trajectories in the absence of the "correct" combination of fixed and estimated model parameters. Overall, the base-case model outputs suggest that mature and exploitable biomass declined rapidly during the first 18 years of the fishery (1968 – 1983), but that both increased between 1984 and 1997, whereafter estimates of mature and exploitable biomass declined steadily. They were estimated to have reached 59.4% and 42.2%, relative to B_0, during 2005, respectively.

For Ringwood Reef, although model outputs closely fitted the fishery-independent estimates of abundance, the outputs poorly fitted the proportions-at-length obtained from these surveys.

This was particularly the case for blacklip larger than 124 mm SL. In attempting to fit the fishery-independent, length-frequency data, the model appears to have compensated for inadequate growth rates by estimating unrealistic R_{devs}. These R_{devs} displayed persistent trends in the absence of fitting data (*i.e.* prior to 2002), rather than sporadic, isolated fluctuations. Thus there was a poor relationship between catch history and the mature biomass trajectory, such that the latter was biologically unrealistic. To overcome this problem for the purposes of the current analysis, the R_{devs} were set at zero. While this led to biologically sensible and reasonable trajectories of mature and exploitable biomass, the inadequate growth rates still ensured that the model fit to the proportions-at-length obtained from the fishery-independent surveys remained poor. Consequently, for Ringwood Reef, a re-assessment of the growth data would be required for any future assessments of this nature. Overall, the base-case model outputs for Ringwood Reef suggest that, as a consequence of the low levels of catch, mature and exploitable biomass declined minimally during the first 25 years of the fishery (1968 – 1992), but that both declined rapidly between 1993 and 2003, during which they were 86.5% and 74.0%, relative to B_0, respectively. Model estimates of mature and exploitable biomass increased marginally in 2004 and 2005.

For convenience, we have reported estimates of current mature and legal biomass (termed B_{2005} or $B_{current}$) relative to that in 1967 (termed B_0). While there is uncertainty in determining the current biomass levels, the value of B_0 is typically even more poorly estimated by fisheries models, because 'initial biomass' generally occurred well before the commencement of any sampling (Hilborn 2002). There is strong evidence for this – simulations by Punt (2003) have shown that despite having a model that is a correct representation of the population with standard inputs (*e.g.* M) known without error, estimates of B_0 are heavily biased and uncertain. Consequently, any future modelling in the SZ need to consider the manner in which current biomass levels, relative to historical levels, are reported.

In New South Wales, model outputs are presented as $B_{current}/B_{1994}$ because, as a consequence of the annual fishery-independent surveys undertaken since 1994, $B_{current}/B_{1994}$ is considered better defined than $B_{current}/B_0$ (Worthington *et al*. 2001). Similarly, for the Victorian blacklip fishery, current biomass is presented relative to that in 2000 ($B_{current}/B_{2000}$) because, in the absence of information on the minimum level of egg production required to ensure a sustainable fishery, it was considered undesirable for the mature biomass to decline to less than B_{2000} (Anon 2002). If these approaches were followed for blacklip at Ringwood Reef and Middle Point, appropriate historical reference points could include B_{1989} (the year in which the TACC was implemented) or B_{2002} (the first year for which data on the length-frequency distribution of the commercial catch are available).

Finally, more exhaustive investigation of the fitting of the National Abalone Model to both Ringwood Reef and Middle Point would involve extending the current assessment in several ways. These include: (1) fitting mortality; (2) fitting growth; (3) fitting selectivity; (4) fitting to the commercial length-frequency data; (5) establishing the relationship between blacklip abundance and CPUE and then fitting to the commercial CPUE data; (6) obtaining data on the size of emergence; and (7) undertaking a range of sensitivity tests. Among others, such sensitivity tests need to incorporate evaluation of the sensitivity of the base-case model outputs to *h* (steepness of the Beverton-Holt recruitment relationship), fixed versus size-specific mortality, fitting to alternative data sets, the magnitude of the observation errors and growth rates.

7.5 Conclusions

Our assessment of the blacklip stocks at Ringwood Reef and Middle Point clearly demonstrate the utility of the National Abalone Model to be applied at fine spatial scales, where appropriate data exist. This builds on previous blacklip stock assessments in all three Zones of the South Australian abalone fishery, and in the Victorian fishery, that were undertaken at much larger spatial scales. This conclusion is also similar to that reached by a concurrent FRDC project (FRDC 2007/066). For both areas, there was reasonable agreement between model outputs and the available data. The strength of this relationship was greatest for Middle Point, but the fits were of similar quality to those in other abalone models. Future modelling needs to consider (1) the manner in which current biomass levels, relative to historical levels, are reported; (2) more exhaustive investigation of the fitting of the National Abalone Model to both Ringwood Reef and Middle Point; and (3) undertaking a range of sensitivity tests.

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7.7 Appendix: Detailed description of the length-based stock assessment model

This description is based on details provided in Gorfine *et al*. (2005).

7.7.1 Model structure and formulae

The model was developed in AD Model Builder (Otter Research Ltd). It is length based. The lower size limit is 52 mm SL. There are 66, 2 mm SL length classes. Sexes are not distinguished. The model runs on an annual time step. Catches from commercial, recreational and illegal fishers were used in the model, each with their own fishing selectivity.

The model operates by estimating the numbers of abalone in each length class at the start of each season by applying growth, natural mortality, fishing mortality and recruitment to each length class each year. This process is numerically represented by:

$$N^{c}_{t,l,m} = \alpha_{t,l,m\text{-}1}\Big(\sum_{l'\le l} N^{c}_{t,l',m\text{-}1}\, e^{-M^{c}_{l'}}\Big[1-\sum_{i} F^{i}_{t,m\text{-}1}\, S^{i}_{t,l',m\text{-}1}\Big]X^{c}_{l,l',m\text{-}1} + \sum_{l'\le l} N^{\tilde{c}}_{t,l',m\text{-}1}\, e^{-M^{\tilde{c}}_{l'}}\, X^{\tilde{c}}_{l,l',m\text{-}1}\Big)$$

$$N^{\tilde{c}}_{t,l,m} = (1-\alpha_{t,l,m\text{-}1})\Big(\sum_{l'\le l} N^{c}_{t,l',m\text{-}1}\, e^{-M^{c}_{l'}}\Big[1-\sum_{i} F^{i}_{t,m\text{-}1}\, S^{i}_{t,l',m\text{-}1}\Big]X^{c}_{l,l',m\text{-}1} + \sum_{l'\le l} N^{\tilde{c}}_{t,l',m\text{-}1}\, e^{-M^{\tilde{c}}_{l'}}\, X^{\tilde{c}}_{l,l',m\text{-}1}\Big) + R_{t,l,m\text{-}1}$$

where $N^{c}_{t,l,m}$ is the number of abalone in size-class *l* in non-cryptic habitat at the start of season *i* of year *i*

$N^{\tilde{c}}_{t,l,m}$ is the number of abalone in size-class *l* in cryptic habitat at the start of season *m* of year *t*

$\alpha_{t,l,m\text{-}1}$ is the probability that an animal in size-class *l* is in the non-cryptic habitat at the end of season *m-1* of year *t*

$M^{c/\tilde{c}}_{l}$ is the instantaneous rate of natural mortality on animals in size-class *l* in the non-cryptic / cryptic habitat

$X^{c/\tilde{c}}_{l,l',m\text{-}1}$ is the probability that an animal in the non-cryptic / cryptic habitat and size-class *l'* grows into size-class *l* at the end of season *m-1* (the size-transition matrix)

$F^{i}_{t,m\text{-}1}$ is the fully-selected exploitation rate by sector *i* (commercial, recreational, and illegal) during season *m-1* of year *t*

$S^{i}_{t,l,m\text{-}1}$ is the selectivity of sector *i* on animals in size-class *l* during season *m-1* of year *t*

$R_{t,l,m\text{-}1}$ is the recruitment to size-class *l* at the end of season *m-1* of year *t*

7.7.1.1 Exploitation rate

The fully-selected exploitation rate for each sector, $F^{i}_{t,m}$, is defined as the ratio of the catch to the exploitable biomass:

$$F^i_{t,m} = \frac{C^i_{t,m}}{B^{e,i}_{t,m}} = \frac{C^i_{t,m}}{\sum_l w_l \, S^i_{t,l,m} \, N^c_{t,l,m} \, e^{-M^c_l \Delta t}}$$

where $C^i_{t,m}$ is the catch by sector *i* at the end of season *m* of year *t*

$B^{e,i}_{t,m}$ is the exploitable biomass corresponding to sector *i* during season *m* of year *t*,

w_l is the mean weight of an animal in length-class *l*

Δt is one year

7.7.1.2 Growth

Growth parameters are specified by a growth matrix derived from tag-recapture data from Ringwood Reef and Middle Point generated using Estimatrix (after Bardos 2005).

7.7.1.3 Length-weight relationship

Weight, as a function of length, is given by:

$$w_l = a \, \bar{l}^{\,b}$$

where $\bar{l}$ is the maximum shell length.

a , b are the parameters of the weight-length relationship.

7.7.1.4 Fishing selectivity

Fishing selectivity, as a function of length-class is given by the proportion selected:

$$S^i_{t,l,m} = \begin{cases} 0, l < l_{\min,i} \\ p^i_{t,m} + (1 - p^i_{t,m})(l - l_{\min}) / (l_{\max} - l_{\min}), l_{\min,i} > l > l_{\max,i} \\ 1, l \geq l_{\max,i} \end{cases}$$

where $l^i_{50,t}$ is the length of 50% selectivity for sector *i* during season *m* and year *t*

$l_{min,i}$ is the minimum length fished for sector i during season *m* and year *t*

$l_{max,i}$ is the first length fully fished for sector i during season *m* and year *t*

$p^i_{t,m}$ is the proportion of animals selected for sector *i* at $l_{min,t}$ during season *m* and year *t*

7.7.1.5 Transition from cryptic to non-cryptic habitat

Emergence, as a function of length class, is given by:

$$\alpha_{t,l,m} = (1 + \exp(-\ell n19(\bar{l} - l_{50,t,m}) / \phi_{t,m}))^{-1}$$

where $\alpha_{t,l,m}$ is the probability of an animal in size-class *l* being in non-cryptic habitat at the end of season *m* of year *t*

$\phi_{t,m}$ is the width of the emergence ogive during season *m* of year *t*

$l_{50,t,m}$ is the size-at-50%- emergence during season *m* of year *t*

7.7.1.6 Maturity

Maturity, as a function of length class is described by an ogive where 50% of individuals at Ringwood Reef and Middle Point were mature at 75 and 79 mm SL, and the ogive width was 15 and 14 mm SL, respectively.

7.7.1.7 Recruitment

The recruitment by size-class, year and season is given by:

$$R_{t,l,m} = \omega_{l,m} \sum_{t' \le t} \theta_{(t-t')} \frac{(B^S_{t'} / B^S_{-\infty})\, e^{\mathrm{R}_{\mathrm{dev}}(t)}}{\tilde{\alpha} + \tilde{\beta}(B^S_{t'} / B^S_{-\infty})}$$

where $\omega_{l,m}$ is the fraction of the recruitment that occurs to size-class l during season m

$\theta_{(t-t')}$ is the weighting from spawning in year t' to recruitment in year t; $\sum_{t' \le t} \theta_{(t-t')} = 1$

$\tilde{\alpha}$, $\tilde{\beta}$ are the parameters of the stock-recruitment relationship (defined in terms of the "steepness" of the relationship, h, and the virgin recruitment, $R_{-\infty}$)

$$\tilde{\alpha} = \frac{(1-h)}{4hR_{-\infty}} \quad and \quad \tilde{\beta} = \frac{(5h-1)}{4hR_{-\infty}}$$

h is the steepness of the stock-recruitment relation so that

$$hR = \frac{0.2}{\alpha + 0.2\beta} \text{ and } R = \frac{1}{\alpha + \beta}$$

B^S_t is the mature biomass corresponding to the recruitment during year t:

$$B^S_t = \sum_l w_l\, f_l\, (N^c_{t',l,m(S)} + N^{\tilde{c}}_{t',l,m(S)})$$

f_l is the fraction of animals in size-class l that are mature

w_l is the weight at length l

$m(S)$ denotes the season of spawning

$\mathrm{R}_{\mathrm{dev}}(t)$ is the 'recruitment deviation' for year t

7.7.2 Likelihood (estimation) functions

7.7.2.1 Fishery-independent proportion-at-length

The robust likelihood function of Fournier *et al*. (1998) is used:

$$\log L = -0.5 \sum_t \sum_l \log[2\pi(\xi_{l,t} + 0.1/I)] - \sum_t I \log(\tau_t) + \sum_t \sum_l \log[\exp\{-\frac{(\rho^{obs}_{l,t} - \rho^{pred}_{l,t})^2}{2(\xi_{l,t} + 0.1/I)\tau_t^2}\} + 0.01]$$

where $\rho^{obs}_{l,t}$ is the observed proportion of animals in length class l and year t

$\rho^{pred}_{l,t}$ is the predicted proportion of animals in length class l and year t

$$\xi_{l,t} = (1 - \rho_{l,t}^{obs})\rho_{l,t}^{obs}$$

$$\tau_t^2 = 1/\min(S_t, N_{eff})$$

S_t is the sample size for the length frequency data for year *t*

N_{eff} is the effective sample size

I is the number of length classes in the sample

7.7.2.2 Fishery-independent abundance

$$-\ln L = \sum_t [\ln \sigma_i + \frac{1}{2\sigma_i^2}(\ln A_t - \ln(\hat{q}\sum_l (S_l^i N_{l,t}))^\gamma)^2]$$

where Nl,t is the estimated number ,

A_t is the observed cpue,

S_l^i is the selectivity of the fishing on animals in the commercial sector i

σ_i is the standard error from the data and

$$\hat{q} = \exp[\frac{1}{n}\sum_y (\ln A_t - \ln(\sum_l (S_l^r N_{l,t}))^\gamma)]$$

7.7.3 Priors, parameter values and parameter estimates

Parameter	Description	**(Prior)** / Fixed value	Parameter bounds	Parameter estimates
R_{init}	Initial Recruitment (millions)	**U(0.05, 5)**	-	Ringwood Reef: 1.1 Middle Point: 0.14
h	Steepness of the Beverton Holt recruitment relationship	**N(0.6, 0.2)**	0.21 – 1.0	Ringwood Reef: 0.55 Middle Point: 0.59
M	Natural mortality	0.15	-	
R_{dev}	Recruitment deviations	**N(0, 0.7)**	-0.7 – 0.7	
a	Coefficient of the relationship between weight and length	0.0001	-	
b	Power of the relationship between weight and length	3.08	-	
l_{min}	Minimum size harvested (commercial)	Ringwood Reef: 110 Middle Point: 125	-	
p	% of minimum size retained (commercial)	5%	-	
l_{max}	Size at which 100% are retained (commercial)	Ringwood Reef: 127 Middle Point: 133.5	-	
L_{50}	Size-at-50%- emergence	**U(60, 110)**	-	Ringwood Reef: 109 Middle Point: 109
ϕ	Width of the emergence ogive	**U(10, 50)**	-	Ringwood Reef: 47 Middle Point: 35

CHAPTER 8. General Discussion

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There is an increasing body of evidence that sedentary marine invertebrate species demonstrate complex, fine-scale population structures across their distribution (Castilla and Defeo 2005; Orensanz *et al.* 2005; Prince 2005), with this reflected in variability in the morphology and key biological parameters of the component populations (McShane *et al.* 1988; Orensanz and Jamieson 1995; Castilla *et al.* 2000; Withler *et al.* 2003). These patterns have most commonly been observed among abalone species that tend to form discrete populations that vary in their life-history parameters within their geographical range (McShane *et al.* 1988; Worthington *et al.* 1995; Tarbath 2003; Prince 2005; Morgan and Shepherd 2006). Current broad-scale management, that does not account for variability among component populations (or stocks) in managing these fisheries, places populations with fast-growing individuals at risk of being over-exploited, while leaving slow-growing components under utilised (Strathmann *et al.* 2002; Prince 2005). Increased recognition of their complex spatial structure has led to renewed calls for the scales of abalone fishery management to be more closely aligned with those of the component populations (Nash 1992; Prince 2005; Naylor *et al.* 2006; Temby *et al.* 2007). However, it is precisely that same complex spatial structure, and associated variability, that makes achieving fine-scale management of these fisheries so challenging. This is because collecting information on the boundaries and biology of numerous populations by traditional methods is difficult and prohibitively expensive (Nash 1992; Prince 2005; Naylor *et al.* 2006).

One of the earliest examples of a reduction in the spatial scale of abalone fishery management was the introduction of separately-managed, 'fish-down' areas (FDAs) in the Southern Zone of the South Australian fishery (SZ) in 1994 (see section 1.4). The biological and morphological variability of blacklip abalone (*Haliotis rubra*; hereafter referred to as blacklip) was recognised in the management of this Zone, in that the FDAs were designed to encompass components of the fishery within which blacklip were considered to be 'stunted'

(Tyrer 1995; Mayfield *et al.* 2007). Quotas obtained from these areas are harvested at a reduced minimum legal length (MLL). More recently, in 2002, the Western Abalone Divers Association Inc. (WADA), the industry association representing divers and licence holders in the Western Zone of the Victorian abalone fishery, began assessing and managing their fishery at a reef-code scale. They achieve this using a harvest policy framework underpinned by a "rapid assessment" of abalone population "health", visually determined from the shape and appearance of abalone shells from the commercial catch (Dr Jeremy Prince, Biospherics Pty Ltd, personal communication). Evolution of the process over time has led to increasingly complex, spatial management of the resource, including reef-specific catch limits and MLL.

Alongside the WADA initiative, FRDC project No. 2005/024 (*Abalone industry development: local assessment and management by industry*) and FRDC project No. 2007/066 (*Rapid response to abalone virus depletion in western Victoria: information acquisition and reefcode assessment models*), this project is among the first to provide a mechanism to more closely align the scale of assessment and management with the scale of the morphological and biological variability across the component populations. This current project focussed on developing a simple, practical and cost-effective tool to aid optimisation of abalone fishery management and was conducted in two distinct phases. The first phase of the project was centred on determining the spatial variation in blacklip (1) morphology, including development of a 'morphometric marker' for distinguishing among populations (Chapter 2; Saunders *et al.* 2008); (2) biology (Chapter 3; Saunders and Mayfield in press); and (3) genetic structure (Chapter 4; Appleyard *et al*. in review) across the SZ. The second phase was directed towards (1) application of the 'morphometric marker' to determine the distribution of 'stunted' and 'non-stunted' blacklip in the SZ (Chapter 6; Saunders *et al*. in review); (2) evaluating a range of options to facilitate effective, finer-scale compliance (Chapter 5); (3) outlining an initial framework for the practical and realistic development, and subsequent management, of potential 'management units' (MUs; Chapter 6); and (4) examining the relevance of applying current length-based stock assessment models to assessment of component populations (Chapter 7).

Broad-scale sampling occurred at eight sites, comprising four sites with 'stunted' blacklip, and four sites with 'non-stunted' blacklip. Data on the fine-scale variation in the morphological and biological parameters were obtained from a series of sub-sites located within 1 km of each of two primary sites (one 'stunted' and one 'non-stunted'). The data we obtained included a series of shell measurements (*e.g.* shell length (SL), shell height (SH), shell width, shell weight and shell volume), rates of growth, size-at-maturity, fecundity and genetic structure. These data confirm previous findings that blacklip show highly variable

morphology and biology among populations (Breen and Adkins 1982; McShane *et al.* 1988; Shepherd *et al.* 1991; McShane *et al.* 1994; McShane and Naylor 1995; Campbell *et al.* 2003; Naylor *et al.* 2006), and that these divisions are difficult to detect with current molecular techniques (Chapter 4; Guzmán del Próo *et al.* 2000; Hamm and Burton 2000; Chambers *et al.* 2006).

We demonstrated that a 'morphometric marker', based on the ratio between SL and SH (termed the SL/SH ratio), was robust in discriminating among 'stunted' and 'non-stunted' blacklip populations (Chapter 2; Saunders *et al.* 2008). Perhaps more importantly, we identified strong correlations between this 'morphometric marker' and several key life-history parameters (Chapter 3; Saunders and Mayfield in press). Thus, this 'morphometric marker' is a powerful tool for identifying and distinguishing among abalone populations (or stocks) and for estimating some of their important life-history characteristics. Consequently, this marker is fundamental to the practical determination (*e.g.* size and location) of management units (MUs) along with their life-history characteristics, at relevant spatial scales. In the absence of this tool, cost-effective application of the principals underpinning MUs (Begg *et al.* 1999; Begg and Waldman 1999; Jennings *et al.* 2001), and thus practical identification and management of individual abalone stocks, is unlikely to be achieved.

Collectively, the data and information presented in this report – especially the 'morphometric marker' and the strong links between this marker and blacklip life-history characteristics – provide at least an initial opportunity to reconsider the spatial scales of blacklip management in the SZ, thereby tailoring management towards spatial scales that reflect the actual population structure of the species (Taylor and Dizon 1999; Martien and Taylor 2003; Bergenius *et al.* 2005). Such a process is rare because, despite stock identification being an integral component of modern fisheries science and underpining effective fisheries management (Jennings *et al*. 2001), stock definitions are seldom re-considered in the management of fisheries (Begg *et al*. 1999; Begg and Waldman 1999). Information on the broad-scale distribution of 'stunted' and 'non-stunted' blacklip in the SZ was obtained by applying the 'morphometric marker' to over 100 commercial shell samples distributed throughout the fishery (Chapter 6; Saunders *et al.* in review). There was no significant correlation between latitude or longitude and the SL/SH ratio, and only limited consistency in the SL/SH ratio among samples from within the current fishing areas. Notably, these were only evident in one current fishing area (Red Rock Bay) and one 'fish-down' area (FDA; Ringwood Reef). Nevertheless, there were several locations in the SZ across which samples had similar SL/SH ratios and, thus, were similarly categorised. Identification of these areas comprises the basis for determining the size and location of potential MUs that contain

separate blacklip populations. We also evaluated whether the density of data from the broad-scale commercial samples were sufficient to identify potential MUs by obtaining fine-scale, systematic commercial samples from Gerloffs Bay. These fine-scale data suggested that there were two MUs (one 'stunted' and one 'non-stunted') in Gerloffs Bay and their locations were consistent with those identified from the broad-scale commercial samples. This suggests the density of the original commercial samples (nine in total) collected in this area was sufficient to identify these potential MUs, and, consequently, that similar sampling intensities elsewhere in the SZ should be equally informative. However, the systematic sampling allowed more accurate delineation between these areas (Chapter 6; Saunders *et al*. in review).

Regional- or zonal-scale application of a tool such as the 'morphometric marker' for identifying potential MUs and predicting life-history parameters provides additional challenges. These arise from the need to combine a wealth of data (and other fishery-related information) into a revised management framework under a new paradigm that explicitly requires reductions in the spatial scale of management (Meester *et al.* 2001; Wilen 2004; Castilla and Defeo 2005; Prince 2005; Naylor *et al.* 2006). Adoption of this approach necessitates consideration of the limitations of the data available, as well as the requirements for effective (and efficient) management and compliance arrangements both within, and across, any MUs identified.

Data and information from all Chapters, along with that contributed by stakeholders in a series of workshops, were combined in the development of an initial framework for the practical and realistic development, and subsequent management, of potential MUs. We argue that a framework underpinning successful implementation of MUs for species, like abalone, with spatially-complex population structures requires a holistic approach. Seven key steps necessary to move from a sub-regional to MU-based spatial scale in this fishery have been identified. These were (1) clear, relevant and realistic management objectives; (2) transparency through effective and ongoing stake-holder engagement and consultation; (3) robust, reliable and accurate measures for discriminating among, and estimating the biological parameters of, component stocks; (4) practical selection, clear definition and appropriate scales for MUs; (5) clear management (and compliance) arrangements; (6) robust reporting systems; and (7) reliable, cost-effective data underpinning defendable assessments, that encompasses the use of suitable performance measures.

In an abalone fishery where fine-spatial-scale management is employed, the challenge for fisheries compliance managers is to track the taking of abalone from multiple, spatially-defined fishing areas with variable MMLs, to ensure fishing matches the harvest strategies.

We evaluated four alternative approaches, including the use of VMS and a GPS data logger, for ensuring effective, fine-scale compliance associated with a reduction in the spatial scale of management (Chapter 5). As each approach we tested delivered benefits, but also limitations, future compliance programs designed to deal with a decrease in the spatial scale at which an abalone fishery is managed, will need to draw upon a number of existing compliance tools, supplemented by the approaches trialled here. This will require a consultative process among all stakeholders that should include formal risk assessments, additional field trials of compliance approaches and legislative review.

Assessing blacklip stocks at fine spatial scales also provides additional challenges to current abalone stock assessment models. However, the preliminary application of a Fortran 90 implementation of the National Abalone Model (Gorfine *et al.* 2005) to two potential MUs, Ringwood Reef and Middle Point, identified in Chapter 6, clearly demonstrated the suitability of this model to fine-scale stock assessment (Chapter 7). Although relationships between model outputs and the available data were stronger for Middle Point, for both areas the model fits were of similar quality to those obtained elsewhere (*e.g.* Worthington *et al*. 2001; Breen *et al*. 2003; Mayfield *et al*. 2005a,b,c; Chick *et al*. 2006). Despite this close alignment, refinement of the model and data in future years may substantially change the outputs. Consequently, current outputs provide an indication of trends in biomass, rather than the absolute estimates of biomass.

If, as our data suggest, there is a need for large numbers of MUs – with each of these demonstrating potentially unique life-history characteristics and, therefore, requiring separate assessment (*e.g.* fishery-independent surveys, catch and effort monitoring, commercial catch sampling and integration of data in a length-structured model) and management (*e.g.* quotas and size limits) – this may greatly exceed the number that could realistically be assessed and managed by a Government Agency without the associated costs becoming prohibitive (Prince 2005). Thus, the challenge for all stakeholders – scientists, fishers and fisheries managers – will be to respond through developing new, spatially-explicit management policies (Wilen 2004) and seeking recent/novel methods for data collection, synthesis and analysis to provide an integrated and sound basis for the rational management of these living resources (Eekhout *et al.* 1992). In most cases, this is likely to require a pragmatic approach (Koljonen 2001), with management becoming adapted to the biological reality (Hammer and Zimmerman 2005), working within the constraints imposed by the practical limitations associated with assessment, management and compliance, and potential, associated increased costs that may offset perceived benefits (Criddle *et al.* 2001). Whatever the approach, successful implementation is likely to depend heavily on extensive collaboration (Perry *et al.* 2002;

Haapasaari *et al.* 2007; van Densen and McCay 2007) and increasing responsibility and accountability of all stakeholders (Hilborn 2002; Parma *et al.* 2006).

Despite these challenges for moving towards fine-scale management in abalone fisheries, we have demonstrated a link between morphology and biology that provides a mechanism to simply, practically and cost-effectively overcome the crucial first step of being able to discriminate among, and estimate the biological parameters of, component stocks. Without this knowledge, MUs cannot be appropriately developed or managed. The tool we have developed can be applied at any spatial scale. When used within a suitable management framework, it can provide the necessary information to enable practical reductions in the scale of abalone fishery management, which has previously been hampered by the inability to gather detailed demographic data at appropriate spatial scales. Further, our approach is not limited to abalone. Rather, it is applicable to many sedentary invertebrate species that exhibit fine-scale, population structure.

This report deliberately makes no recommendations about changing management arrangements in the SZ. Rather, it provides a tool for stakeholders in the fishery to use, in conjunction with Primary Industries and Resources South Australia, Abalone Management South Australia Inc. and the South Australian Research and Development Institute, in re-considering and, where appropriate, amending current arrangements for the fishery. This reflects the strong, interactive, collaborative ('co-management') approach to managing this valuable resource currently enjoyed in this fishery.

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CONCLUSION

In concert with the initiative by the Western Abalone Divers Association Inc. and two concurrent Fisheries Research and Development Corporation projects (2005/024 and 2007/066), this project is among the first to provide a mechanism to facilitate a reduction in the spatial scale of abalone fishery assessment and management. The project (1) developed a simple, practical and cost-effective tool to discriminate among, and estimate key life-history parameters of, blacklip abalone (*Haliotis rubra*; hereafter referred to as blacklip) stocks; (2) identified potential 'management units' (MUs) and their associated life-history characteristics; and (3) outlined an initial framework, including consideration of population genetics, fisheries compliance and stock-assessment modelling, for MU implementation.

A principal output of this project was the identification of a 'morphometric marker', based on the ratio between shell length and shell height, which could both discriminate among blacklip stocks and predict their biological characteristics. This tool can be used as a basis for identifying and managing MUs for blacklip at relevant ecological scales, that are difficult to detect with genetic approaches. Importantly, it can be applied at any spatial scale, thereby overcoming the observed mix of variability and lack of predictability of the size and location of blacklip populations. When used within a suitable management framework, it can provide the necessary information to enable practical reductions in the scale of blacklip fishery management, which have previously been hampered by the inability to gather detailed demographic data at appropriate spatial scales. This approach will aid optimisation of blacklip fishery management because individual stocks can now be identified and then separately managed on the basis of their individual life-history characteristics. This provides the opportunity for better resource use and, consequently, a reduction in the risk of fishery collapse.

BENEFITS AND ADOPTION

This project has substantially enhanced our understanding of blacklip abalone population structure, and the associated fine-scale variability in key life-history parameters. Identification of a simple 'morphometric marker' will enable stakeholders in the Southern Zone abalone fishery to identify, and then appropriately manage, management units at relevant spatial scales. This provides them with the opportunity for better, and more efficient resource use and, consequently, a reduction in the risk of fishery collapse. This approach could be adopted elsewhere in South Australia, and in other States, with a small amount of corroborative data

collection and analysis. These flow of benefits is well matched with that identified in the original project proposal.

FURTHER DEVELOPMENT

Shells from commercial samples from throughout the Southern Zone could be measured (shell length and shell height) and each sample classified into one of three categories ('stunted', 'non-stunted' and 'intermediate') on the basis of the 'morphometric marker' developed here. These data can be used to identify the size and location of potential management units, that should be confirmed through subsequent, fine-scale, systematic sampling in relevant locations. In combination, these data provide a tool for stakeholders in the fishery to use, in conjunction with Primary Industries and Resources South Australia, Abalone Management South Australia Inc. and the South Australian Research and Development Institute, in re-considering and, where appropriate, amending current arrangements for the fishery. Application of this approach to other blacklip abalone fisheries, could be considered. This will require low levels of sample and data collection to confirm the broad-scale applicability of the 'morphometric marker' to separate 'stunted' and 'non-stunted' blacklip abalone populations outside the Southern Zone.

Two manuscripts from this work have been published:
Saunders, T.M., Mayfield, S. and Hogg, A. 2008. A simple, cost-effective, morphometric marker for characterising abalone populations at multiple spatial scales. *Marine and Freshwater Research*, 59: 32-40.

Saunders, T.M. and Mayfield, S. In press. Predicting biological variation using a simple 'morphometric marker' in a sedentary marine invertebrate (*Haliotis rubra*). *Marine Ecology Progress Series*.

One manuscript has been submitted for publication:

Saunders, T.M., Mayfield, S. and Hogg, A. In review. Using a simple 'morphometric marker' to identify spatial units for abalone fishery management. *ICES Journal of Marine Science*.

Other manuscripts are being prepared for publication, principally one based on Chapter 4.

PLANNED OUTCOMES

There were several planned outcomes for this project that were identified in the original project proposal. These were:

1. An evaluation of the utility of a 'morphometric marker' to differentiate between abalone populations in the Southern Zone;
2. An assessment of approaches that may provide for effective management and compliance at fine spatial scales;
3. An examination of the spatial variation of the fisheries biology, morphology and genetic structure of blacklip abalone populations in the Southern Zone;
4. Model outputs from modelling blacklip abalone populations in the Southern Zone at scales appropriate to the variation observed; and
5. Establishment of a framework that will assist in the development of appropriate spatial scale 'management units', using all the data from (1), (2) and (3) above.

Each of these was achieved. While the principal output was the identification of a 'morphometric marker', based on the ratio between shell length and shell height, which could both discriminate among blacklip stocks and predict their biological characteristics, resultant outcomes (*e.g.* changes in assessment and management arising from application or implementation of the outputs) have been more slowly forthcoming. Ongoing discussions among PIRSA, SARDI, AIASA and AMSA are aimed at reconsidering and, where appropriate, amending the spatial-management system in the SZ. Nevertheless, the tool developed here is proving a key component of this process. This is because it can be applied at any spatial scale and, when used within a suitable management framework, it can provide the necessary information to enable practical reductions in the scale of blacklip fishery management, which have previously been hampered by the inability to gather detailed demographic data at appropriate spatial scales.

APPENDIX 1: INTELLECTUAL PROPERTY

There are no intellectual property issues associated with this project.

APPENDIX 2: STAFF

Sharon Appleyard	CSIRO	Research Officer
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Nick Elliott	CSIRO	Co-Investigator
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