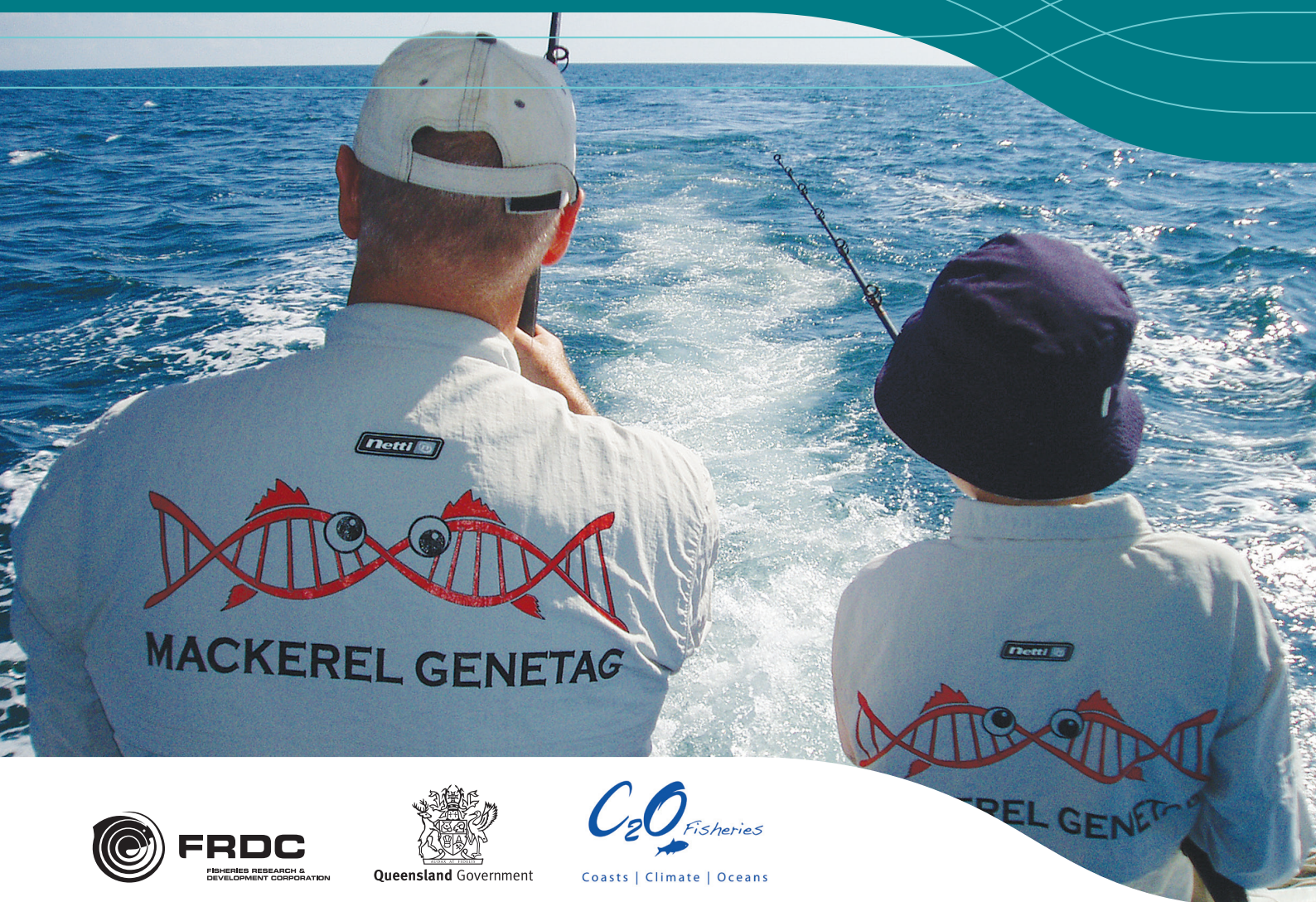CSIRO

Scoping current and future genetic tools, their limitations and their applications for wild fisheries management

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Project details

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Objectives

The overarching goal of this project was to prepare a document that summarises past, present and emerging ways in which research using genetic technology can assist the Australian fishing industry to maintain productive and sustainable harvests. The project achieved the following specific objectives:

1. Documented existing and prospective biotechnologies and genetic analysis tools that are relevant to wild fisheries management, and their availability and application at a national and international level;
2. Documented the FRDC's past and current investment in biotechnology and genetic tools used in wild fisheries management research;
3. Documented the different biotechnology and genetic tools that are being used in wild fisheries management research in Australia, and the nature and location of key research groups;
4. Described what management question each tool has been used for (e.g. stock structure, biomass estimation, product provenance, disease monitoring);
5. Identified those tools and approaches (existing and future) most likely to deliver significant advances in fisheries management;
6. Identified the potential for collaborations which could improve the focus and impact of work in this area.

Outcomes achieved to date

1. Raised the profile of genetics in fisheries with stakeholders from Australia and overseas through personal contact with the review team and a workshop.

2. Provided funding and management agencies with a review that provides:

   a. An appraisal of ways that genetic technology can be deployed in Australian fisheries, including a stand-alone, plain language summary of each theme.

   b. A prioritised list of the most important issues facing fisheries management in Australia.

   c. A 'look-up' table to allow managers and scientists to understand which form of genetic technology is useful and why, and to allow geneticists to understand the fisheries management context for their research.

   d. Ways to address the highest priority gap (communication) that is blocking the uptake and implementation of genetics in Australian fisheries.

3. Invited to organise a mini-symposium "Fisheries Genetics – What Managers Really Want?" at the ASFB/OCS conference in Adelaide in July 2012.

4. The review and consultation process has resulted in FRDC being:

   a. Better informed about current and future applications of genetics tools to fisheries management; and

   b. In a better position to develop an investment strategy in the area of applying genetics to wild fisheries management.

Non-technical summary

Significant changes have occurred in the fields of fisheries management and genetics since the partnership began 50 years ago. FRDC commissioned this review of attributes of the partnership to gather information about genetic technologies and the role that it is playing in the management process for achieving sustainable harvesting of wild fisheries (now and in the future). The review will support their role as a major funder of research in this area to optimise both the benefit and uptake of research outcomes for fisheries management in Australia.

This report consists of two major parts; a comprehensive review of genetic literature, and analysis and evaluation of consultation with stakeholders. The consultation involved both Australian and international stakeholders, including geneticists, fisheries scientists, fisheries managers (management and policy) and fishing industry representatives. The aim was to canvas perceptions about genetics and how it informs current and future fisheries management issues. Consultation was carried out in two parts: 1) an interview process using structured questionnaires, and 2) a workshop that discussed genetic technologies and interview results and identified potential solutions to knowledge gaps and blockages.

The literature review summarises the features of genetic technologies that are relevant to fisheries management. There are eleven genetic themes, each of which encapsulates a genetic sub-discipline focused on a specific type of biological question relevant to fisheries management. The themes are addressed in the same way - How does it work? How is it relevant? How is it used? What are its technical challenges? What are the barriers to its uptake in fisheries management? What is its future? The review highlights the diversity of biological information that can be derived from genetics, including several unique

contributions. The review includes the types of collaborative teams that are needed across genetic themes, and is followed by a snapshot of expertise in genetic research across Australia.

During the interview phase of the project, 88 stakeholders were interviewed, including 63 from Australia. Interview questions addressed awareness and knowledge of genetic methods and applications; perceptions about the usefulness of genetics in fisheries; adequacy of communication between geneticists and stakeholders; and future issues in genetics and management. The key findings were that most stakeholders were generally positive about genetics for fisheries management, but apart from the use of genetics to define fish stocks, the level of understanding of genetics was generally low. Improved communication was commonly recommended as a way to improve understanding. There were divergent views about whose responsibility it was to improve communication, but the consensus was that the responsibility should lie with both scientists (including geneticists) and managers, potentially through formal arrangements. Fisheries management issues identified during the interviews were collated into eleven themes, independent of the role of genetics. Interviewees were recontacted and asked to rank the eleven management themes in terms of importance to resource sustainability. The highest ranked theme was *Management frameworks*, followed by themes with a biological basis such as: *Fishery status and dynamics*, *Population ecology/life history/stock structure*, *Impact of fishing*, and *Climate change and adaptation*.

The report also describes linkages between the management and genetic themes. Genetics provides useful outcomes for seven of the eleven management themes, generally those that have a biological basis. This section provides examples of how genetic technologies can address particular management themes. It documents and evaluates the linkages by scoring the relative cost, readiness, utility and maturity of genetic technologies to address management themes. The links between management and genetic themes are summarised in a 'look-up' table that allows managers and scientists to understand which genetic technology is useful and why, and allows fisheries geneticists to understand the management context for their research.

The workshop brought together stakeholders who were interested in the role of genetics in fisheries. An overview of the literature review and a summary of the interview responses were presented to the workshop. Much of the workshop was spent discussing, as a single group and as break-out groups, the major issue identified from interviews as limiting the effective use of genetic tools in fisheries: communication. Like the interview results, the workshop consensus was that the responsibility for better communication should be shared among stakeholders. The most effective partnership may be between fisheries scientists and geneticists, where scientists act as a conduit for genetic data via advisory groups to managers and *vice versa* where there is a knowledge gap that could be addressed by genetics. A number of strategies were identified to facilitate communication including the use of simple language, conducting science and stakeholder based workshops, and better integration of disciplines in research project teams.

The report provides an example of a communication tool (a 'field guide') that summarises genetic themes in a very simple and easy to understand format. It addresses many of the communication issues identified here and could readily be adapted to a web-based tool or app for managers and scientists.

The compelling conclusion from this project is that fisheries stakeholders agree that genetics offers a diverse collection of versatile and useful tools for informing fisheries managers about issues that have a biological basis. This project identified that poor communication was limiting the effective use of genetics in fisheries management in Australia. Examples of how this could be addressed are presented here, but further investment is needed to ensure that outcomes are maximised. In the medium to long term several emerging genetic themes have the potential to deliver significant benefit to key future issues facing fisheries managers such as fisheries status and dynamics, and climate change and adaptation.

The review and consultation process allows for better informed decisions regarding current and future applications of genetics tools to fisheries management and places funding agencies in a better position to develop an investment strategy in the area of applying genetics to wild fisheries management. To assist in this process, an Implementation Plan is also developed for four Key Areas: (1) 'Lack of effective communication between geneticists, other scientists, managers and other stakeholders', (2) 'Enhancement of information about fisheries stocks', (3) 'Provide estimates of population parameters, independent of stock assessment modelling' and (4) 'Ecosystem Based Fisheries Management support; particularly where genetics can provide information that is unobtainable or cost prohibitive by other means'.

KEYWORDS: Fisheries, management, genetics, stakeholders.

2   Acknowledgements

We wish to acknowledge the invaluable input of the geneticists, fisheries managers, stock assessment scientists, fisheries scientists and industry representatives who gave up their valuable time during the interview process to provide us with insight and greater knowledge.

Our thanks also go to the workshop participants who provided significant feedback on our findings and shared their opinions on the challenges facing fisheries genetics.

We also wish to thank the following experts who provided comment on early versions of the genetic review section of this report - Sharon Appleyard, Matt Barwick, Peter Baverstock, Damien Broderick, Dean Blower, Christine Dudgeon, Phillip England, Anders Goncalves da Silva, Malcolm Keag, Rosie Godwin, Michael Macbeth, Lisa Pope, Warwick Nash and Thuy Nguyen.

3   Background

In 2011, FRDC requested tenders to review genetics techniques in the context of fisheries management. Two separate proposals were initially received, but these were combined into a single successful proposal with a joint team from CSIRO, DEEDI and C$_2$O Fisheries. The Planned Outcomes for the review were designed to assist FRDC to make more informed decisions about current and future applications of genetics tools to fisheries management, and to develop an investment strategy in the area of applying genetics to wild fisheries management. The project was required to include a review plus a consultation process that would inform the role of genetics and its applicability to fisheries management. This report is the result of this tender process and successful funding application.

4　Need

The FRDC has commissioned a review of the role that existing and future genetic technologies may play in addressing critical challenges facing the exploitation of wild fisheries. Wild fisheries management has been assisted by genetic research for over 50 years, and in Australia this research has been largely funded by the FRDC. Both fisheries management and the methods of genetic analysis have changed significantly during this time. The capability of genetic technologies is ever broadening, whilst fisheries managers must address fundamental challenges such as assessing the impact of fishing on target species and the ecosystem, as well as increasingly diverse issues such as illegal trade. Given these dynamics, as well as perceptions that communication between fisheries managers and geneticists has been poor in some cases, there is a strong need to reassess the ways in which genetic research can contribute to fisheries, and for fishery managers and researchers, industry representatives and fisheries geneticists to critically examine each other's needs and capabilities.

There have been numerous recent reviews of the contributions of genetics to fisheries management overseas. However, these reviews may be difficult to access, they do not target an industry audience, and none focus on the Australian fisheries context. An Australian-focused assessment that is based on both literature surveys as well as strong stakeholder engagement will promote clear joint understanding of the needs and capabilities of fishing industry, fishery managers, fisheries science and fisheries geneticists respectively. It will lead to more coordinated and consistent approaches to the application of genetic technologies in Australia, greater uptake of research outcomes, and build an enduring platform for future successes in genetic research and fisheries management.

5   Objectives

The overarching goal of this project was to prepare a document that summarises past, present and emerging ways in which research using genetic technology can assist the Australian fishing industry to maintain productive and sustainable harvests. The objectives were:

1. Document existing and prospective biotechnologies and genetic analysis tools that are relevant to wild fisheries management, and their availability and application at a national and international level;
2. Document the FRDC's past and current investment in biotechnology and genetic tools used in wild fisheries management research;
3. Document the different biotechnology and genetic tools that are being used in wild fisheries management research in Australia, and the nature and location of key research groups;
4. Describe what management question each tool has been used for (e.g. stock structure, biomass estimation, product provenance, disease monitoring);
5. Identify those tools and approaches (existing and future) most likely to deliver significant advances in fisheries management;
6. Identify the potential for collaborations, which could improve the focus and impact of work in this area.

6 Reading Guide

The below flow chart provides a guide for reading the report. For non-specialists, it is not essential to read the literature review (Section 8.1), as a non-technical version ('field guide') of this review is available in Appendix H. Section 8.5 is a key section for managers and funding agencies as it links the genetic tools with the management issues.

SECTION	SECTION DESCRIPTION	SUGGESTED AUDIENCE
Section 8.1	**Literature review:** Technical summary of available genetic tools in a fisheries context	Geneticists Fisheries scientists
Section 8.2	**Research groups:** Summary of Australian genetic research groups within Australia	Geneticists Fisheries scientists Fisheries managers Funding bodies
Section 8.3	**Stakeholder interviews:** Summary of stakeholder perceptions about genetic tools, their use in fisheries, and management issues	Geneticists Fisheries scientists Fisheries managers Funding bodies
Section 8.4	**Workshop:** Summary of outcomes from the project workshop focusing on communication issues	Geneticists Fisheries scientists Fisheries managers
Section 8.5	**Linking genetic and management:** Overview of genetic tools and how they can be applied to management questions	Geneticists Fisheries scientists
Section 8.6	**Discussion:** Discussion across all the above sections in a broader context	Geneticists Fisheries managers
Appendix H	**Field guide:** User-friendly and succinct overview of genetic tools and their utility in fisheries	Fisheries scientists Fisheries managers Funding bodies
Appendix I	**Implementation plan:** Description of development pathways for effective future use of genetics in fisheries	Geneticists Fisheries scientists Fisheries managers Funding bodies

7   Methods

7.1   Literature Review

Two team members with significant experience in fisheries genetics (Jenny Ovenden and Oliver Berry) were responsible for compiling the review of genetic techniques in fisheries.

Current and future uses of genetics in fisheries were categorised into eleven genetic themes. The genetic themes were derived from interviews with fisheries geneticists in Australia and worldwide, from published literature and reports and from personal knowledge of work underway in Australia.

Sub-headings were used to describe and evaluate each genetic theme:

- How does it work and why is it important;
- How is it used for fisheries management;
- Availability and skill set required;
- Case studies (Australian and international, emphasising contrasts where appropriate);
- FRDC projects (a listing of past or currently funded FRDC projects);
- Technical challenges;
- Barriers to uptake in fisheries management; and
- Future (future prospects for contributions of that theme towards fisheries management).

The list of FRDC projects matching each genetic theme was compiled from a search of the web site (www.frdc.com.au). To ensure the list was complete, scientists in Australia that had been involved in past FRDC-funded projects were contacted.

Two rounds of peer review were undertaken on previous versions of the genetic review section (total 12 reviewers; Sections 7.1 and 8.1, and Appendix H). Reviewers consisted of workers in the field of fisheries genetics in Australia, fisheries managers and stakeholder representatives.

7.2   Interviews with stakeholders about the use of genetics in fisheries

Consultation with key fisheries stakeholder groups within Australia and internationally was primarily achieved using structured interviews, as well as a workshop at which preliminary analysis of interview findings was extended and discussed (workshop discussed in Sections 7.3 and 8.4). The stakeholder groups interviewed included fisheries scientists, geneticists, fisheries managers and fishing industry representatives (see Effort details on interviewees). The purpose of conducting the interviews was to qualitatively assess stakeholder attitudes and perceptions on the use of genetics in a fisheries management context, to determine if there were barriers to the uptake of genetic information, how this might be improved, and how genetics might best contribute to fisheries management in the future.

Interview questions were based around the following key areas of information: awareness/knowledge of genetic methods and applications; genetic tools used; perceptions about the use of genetics in fisheries; adequacy of communication among geneticists and other stakeholders; future genetic applications; and future management issues. The wording of the interview questions varied to ensure appropriateness for the stakeholder being interviewed. This resulted in three similar but different interview versions (fisheries managers/scientists, geneticists, and industry representatives). Specific interview questions are provided in Appendix D. In some cases, questions were made available in advance. All team members participated as interviewers.

The interviews were conducted from May – November 2011 and were generally conducted one-to-one either in person or over the telephone. Although the focus was within Australia, the project team also interviewed stakeholders in Europe, North and South America, the Western Pacific region, South Africa and

New Zealand, thereby providing the project with an international perspective on the issues discussed. Within Australia, we attempted to obtain interviews among the different stakeholder groups across all jurisdictions (e.g. Australian states, Australian federal, government and university sectors, indigenous representatives, conservation agencies, business leaders) to ensure responses to interviews were as representative as possible.

7.3   Workshops

On November 7, 2011, a workshop entitled "Scoping current and future genetic tools, their limitations and their applications for wild fisheries management – a workshop" was held at the Ecosciences Precinct, Dutton Park, Brisbane. The objectives of this workshop were to:

   a. Provide feedback to geneticists, managers and other stakeholders regarding the project's preliminary findings;
   b. Develop potential solutions to the key gap highlighted during interviews – communications (see Section 8.4); and
   c. Discuss and rank management challenges and identify if and how they may be addressed with genetic methods (see Section 8.3.4).

The latter would allow a clear prioritisation, from a manager's perspective, of the future challenges for fisheries management and link these to possible genetics methods. Approximately 25 people representing different Australian jurisdictions, science organisations and management agencies attended. The workshop was a mixture of presentations combined with comments, questions and discussion, and group break-out sessions to discuss and provide solutions to specific topics.

The Agenda for the workshop is provided in Appendix F and a list of participants in Appendix G.

7.4   Linking genetic and management themes

Fisheries scientists and managers identified eleven management themes that represent the most important issues in Australian fisheries management (Section 8.3.4). Those surveyed may have had a general knowledge of the role of genetics in fisheries management, but they were not aware of the eleven genetic themes as presented in this review. Managers and scientists ranked the management themes with no reference to the way in which genetics could contribute.

When evaluating whether a genetic theme could contribute information relevant to a management theme, we ranked it according to four key elements: readiness, utility, maturity and costs (see Table 6). Some genetic themes are widely available (high readiness score) and are highly likely to produce the information required (high utility score), while others are less available (low readiness score) and less well developed in Australia (low maturity score). Comparing utility and cost gives a rough estimate of the cost-benefit ratio for the use of a genetic theme to address a particular management issue.

7.5   Communication with stakeholders

A key component of this project was obtaining input from various stakeholders. Interviews were undertaken both nationally and internationally of geneticists, other scientists, industry and managers (see section 7.2). Mid project results were also provided to stakeholders for review and input in a workshop (see section 7.3), and the final results were extended at the Australian Society of Fish Biology Conference, 2012 in Adelaide. Stakeholders here included scientists (geneticists, stock assessment scientists, fisheries scientists) managers (both fisheries policy officers and fisheries managers) and industry (included vessel or licence owners and managers in fisheries businesses). A Field Guide has also been developed for quick reference (see section Appendix H).

Further extension of the outcomes of this project is planned as a series of actions within the key area 'Lack of effective communication between geneticists, other scientists, managers and other stakeholders' (see Appendix I).

8   Results and Discussion

8.1   Review of genetic analysis tools that are relevant to wild fisheries management: their availability and application at a national and international level

8.1.1   INTRODUCTION

Wild fisheries management has been assisted by genetic research for over 50 years (Ryman and Utter, 1987). During this time, both approaches to fisheries management and methods of genetic analysis have matured and changed significantly. The breadth of issues considered by fisheries managers has increased dramatically so that now, in addition to conventional management problems, issues such as ecosystem effects of fishing and surveillance of illegal fishing needs to be considered (Section 8.3.4). Similarly, genetics in the laboratory has undergone a revolution in the past two decades driven largely by advances in pharmaceutical and biomedical industries, and there have also been significant theoretical advances in the analysis of genetic data. This is reflected by the rapid growth in genetic research on wild fisheries in Australia (Figure 1).

In light of these changes in both the scope of management and scientific capability, there is a need to reassess the ways in which genetic research can contribute to fisheries. Fishery managers and researchers, industry representatives and fisheries geneticists need to be aware of each other's requirements and capabilities in order to make the most out of new genetic technologies. This report therefore includes a review of how genetic tools can be used to assist the management of wild fisheries in Australia. This section also evaluates the readiness, utility and maturity of genetic tools to address a range of research questions in fisheries management. This will allow fisheries managers and scientists to identify tools and approaches that are most likely to deliver significant advances in fisheries management, now and in the future, and to stimulate new collaborative thinking that could improve the focus and impact of work in this area.

The review is organised into eleven genetic themes, each of which encapsulates a genetic sub-discipline focused on specific types of biological or management questions relevant to fisheries. The themes were identified in a review of scientific literature and from interviews with stakeholders and geneticists (Section 8.3). Some themes are focused on a single genetic concept and outcomes for management (e.g. genetic effective population size estimates). Other themes focus on a management challenge and discuss genetic theory and methods that can usefully address that challenge (e.g. product provenance). While they provide a useful structure to exhibit the variety of genetic applications, the divisions between genetic themes are artificial, and there is much overlap and linkage between them.
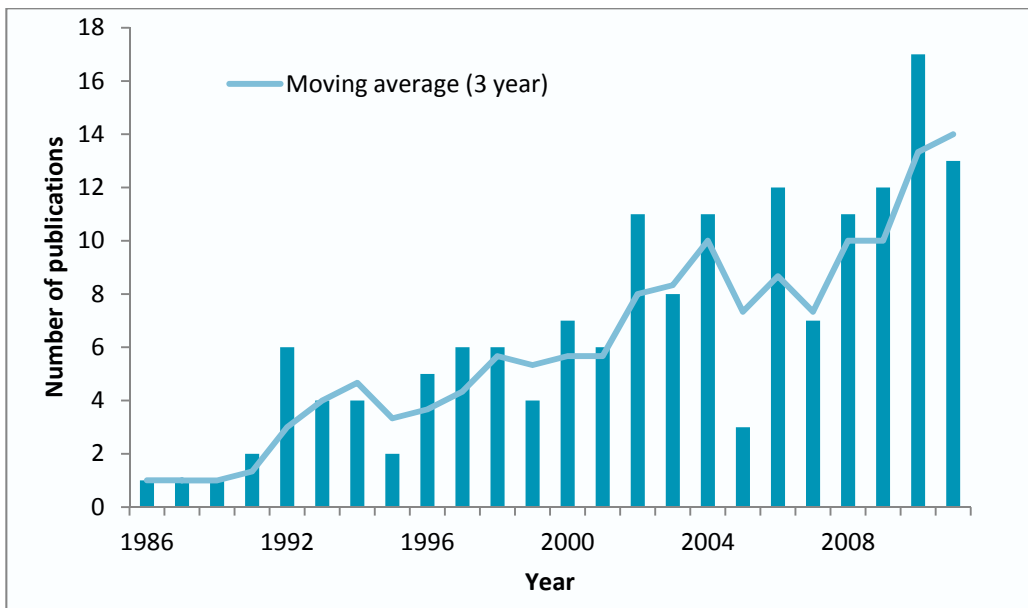
Figure 1. Number of peer-reviewed publications listed on the Web of Science Database related to fisheries management in Australia, and that involved genetic analysis (Search: TS=(fishery AND (genetic OR DNA)) AND AD=Australia). The total number of publications listed is 144.

The genetic themes are:

1. **The identification of fisheries stock structure.** Assays of the distribution of genetic variation may be used to divide the range of harvested species into demographically independent regions suitable for independent management.
2. **Genetic effective population size.** Estimates of genetic effective population size can be used to index changes in abundance through time, including prior to industrial fishing.
3. **Genetic mark-recapture for estimating mortality and abundance.** Novel genetic mark-recapture methods can directly estimate critical parameters in fished or bycatch species such as mortality, abundance and movement.
4. **Product provenance and fisheries surveillance using genetics.** Genetic analysis is a useful tool to support regulation, enforcement and surveillance. Given appropriate reference material, specimens may be assigned to species, population, family group or individual.
5. **Species recognition using genetics.** Increasingly, genetic analysis is being used as a tool for the discovery of new species and for the rapid identification of existing species via DNA barcoding.
6. **Fisheries-induced and natural selection.** Two issues are addressed here; the potential for harvest to increase the frequency of undesirable traits in harvested species and the use of genetic tools to identify adaptation to specific environmental conditions.
7. **Genetic effect of captive-bred fishes on wild conspecifics.** Interbreeding with captive-bred fish may change the genetic attributes of a wild population, potentially affecting their fitness and viability.
8. **DNA as a biomarker for age.** Preliminary research suggests telomeric DNA (see glossary of terms in Appendix C) has potential to estimate age, which would be a step forward for species that cannot be aged by conventional methods.
9. **Genetics for disease detection in wild fisheries.** Genetic tests can be applied to wild individuals and environments for disease surveillance and for understanding disease epidemiology.
10. **Mixed stock analysis using genetics.** A method to determine statistically the contribution of independent breeding stocks to a mixed exploited population.
11. **Genetics for environmental monitoring.** Genetics can provide ways to monitor the complex interactions between fisheries and the environment, such as food web analysis, remote detection of invasive species, and monitoring for environmental contaminants.

The Fisheries Research and Development Corporation (FRDC) has supported research in the majority of the genetic themes identified in this section (Figure 2). Support has focused largely on stock structure (genetic

theme 1) and disease detection (genetic theme 9), although a compelling case is presented here for diversifying funding by demonstrating how genetic tools can provide outcomes for many current and future issues in Australian fisheries management (Section 8.5). Projects funded by FRDC in the past are included in the description of the genetic themes below.
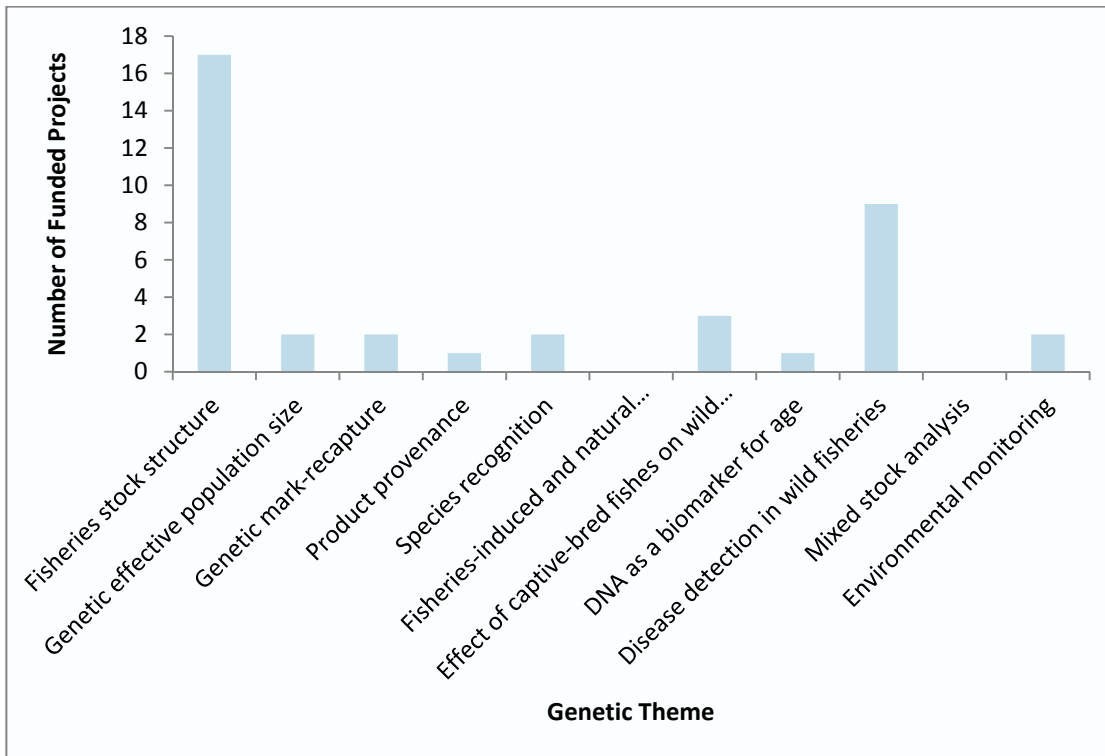
Figure 2. Allocation of financial support from the FRDC towards the eleven genetic themes described in this report. Analysis based on data retrieved from a search of the FRDC online project database (www.FRDC.com.au/research) with search items Fisheries AND (Genetics OR DNA) and through discussions with researchers in Australia.

The review presents general and specific ways in which the themes can be applied to fisheries management, as well as the strengths and limitations of each approach. Within each genetic theme, a summary of the underlying principles of the genetic methods is provided, but interested readers are encouraged to consult primary literature for further information. The review has endeavoured to cut through the jargon to focus on the key ideas that users of genetic information need to know, but there is a glossary in Appendix C, if required. In addition, a plain-English summary of the eleven genetic themes is presented as a 'field guide to genetics in fisheries' (Appendix H. For each genetic theme, a summary of the collaborative team skills needed to apply the technology in a fisheries setting is provided (Table 1). The possible future of the genetic themes is presented, trying to balance enthusiasm with realism.

Table 1. Possible team composition (by area of expertise; dark grey, essential; light grey, desirable; white, not required) for research aligned with the eleven genetic themes that contribute to wild fisheries management.

GENETIC THEMES	FIELD BIOLOGIST	FISHERIES SCIENTIST	FISHERIES MANAGER	TAXONOMIST	POPULATION GENETICIST	MOLECULAR GENETICIST	STATISTICIAN	MATHEMATICIAN	SOFTWARE ENGINEER	BIOINFORMATICS EXPERT	DATABASE MANAGER
1 Genetic analysis for the identification of fisheries stock structure	■	■		■	■		▨		▨		■
2 Genetic effective population size	■	■			■	▨	■	■	■		
3 Genetic mark-recapture for estimating mortality and abundance	■	■			■	■	■	■	■		■
4 Product provenance and fisheries surveillance using genetics	■	■		■		■					▨
5 Species recognition using genetics	■	■		■		■					▨
6 Fisheries-induced and natural selection		■			■	■	■	■			
7 Genetic effect of captive-bred fishes on wild conspecifics		■			■	■					
8 DNA as a biomarker for age	■	■		■		■	■			▨	
9 Genetics for disease detection in wild fisheries	■	■			■	■					
10 Mixed stock analysis using genetics	■	■			■	■	■				
11 Genetics for environmental monitoring and food-web analysis	■	■			■	■				■	

8.1.2 GENETIC THEME 1: THE IDENTIFICATION OF FISHERIES STOCK STRUCTURE

How does it work and why is it important?

The concept of a stock is central to the management of wild fisheries. Stocks represent demographically cohesive groups of individuals of one species. That is, changes to stock size are largely a function of local birth and death rates, not immigration and emigration. Stocks represent natural management units because a relationship between productivity and harvest rates can be established.

Stock delineation requires an understanding of population connectivity, which is inherently difficult to achieve in marine environments. In the past few decades, population genetic analysis has been energetically applied to this problem. The appeal of the genetic approach comes from the theoretical relationship between the number of migrants exchanged between stocks, the level of genetic difference ("genetic structure") between those stocks and the stocks' effective population sizes (genetic theme 2). Genetic difference is readily estimated through assays of genetic markers like microsatellites. Thus, genetic structure is a useful proxy for stock structure because genetic differences between regions imply a limitation to dispersal.

A variety of genetic tools are appropriate for this analysis, including genetic markers such as allozymes, microsatellites, AFLPs and mitochondrial and nuclear DNA sequences (see Appendix C). Generally, the more variable the marker and the more markers used, the more powerful tests to determine a significant genetic structure will be (Balloux and Lugon-Moulin, 2002), though there are exceptions (Hedrick, 2005). Although, large genetic differences can be identified with few markers, a large number of markers are required to identify small genetic differences. Practically, the optimum number of samples to analyse for an expected degree of genetic structure can be estimated using a power analysis given some empirical genetic data from the target population (Ryman and Palm, 2006). A large number of statistics are available for

characterising genetic structure. One of the most widely used is the standardised variance of allele frequencies (F_{st}; see glossary of terms in Appendix C).

An important feature of these conventional genetic approaches to measuring connectivity between stocks is that they measure long term (i.e. multi-generational) average levels of connectivity as opposed to short term "ecological" connectivity. In doing so, **these methods capture enduring patterns of connectivity**, but may miss short term and ecologically important connectivity. Non-genetic methods, such as otolith microchemistry and parasite abundance analyses are commonly used for ecological-level analyses. This report does not address the relative merits of these different approaches, except to note that best-practise stock delineation takes account of all lines of evidence to address management priorities on a case-by-case basis.

Analytical methods have been developed that do not rely on pre-defined stock boundaries to frame the analysis. These flexible approaches work by grouping individuals in such a way that the most genetically cohesive groupings are identified. In doing so, the analysis both identifies the number of discrete genetic stocks and maps their distributions (Pritchard *et al.*, 2000; Guillot *et al.*, 2005). They work best when individuals are sampled throughout the range of the target species. One strength of this approach is that it lends itself well to combining genetic information with geographic, oceanographic, or other environmental information to increase the explanatory power of the analysis to identify barriers to dispersal.

An extension of this approach is that each individual organism can be statistically attributed to one of the identified genetic groups based on its genetic affinities. In doing so, recent migrants and even the offspring of migrants can be identified and enumerated. Unlike conventional genetic analysis, these methods can directly estimate the number of migrants between populations on an ecological timescale, and so are highly compatible with non-genetic methods that work on that timescale (Cornuet *et al.*, 1999; Berry *et al.*, 2004; Manel *et al.*, 2005). Individual-focused approaches to measuring the origins of individuals have similarities to genetic theme 3 (Genetic mark-recapture), genetic theme 4 (Product provenance) and genetic theme 10 (Mixed stock analysis).

How is it used for fisheries management?

The identification of spatially or temporally discrete stocks is useful for fisheries management and the underlying data analyses, which include stock assessment and fisheries monitoring. Data limitations preclude formal stock assessments for many Australian fisheries species, but in such cases precautionary approaches can be applied based on known stock structure using spatially defined management and monitoring regimes.

Because stock delineation is difficult, genetic analysis plays a valuable role in this multidisciplinary field. The conventional strategy for conducting genetic assessments of stock boundaries involves: 1) collecting samples from throughout a region either opportunistically or based on existing concepts of stock boundaries; 2) characterising genetic diversity overall and within each potential stock, and 3) testing whether genetic diversity is distributed randomly with respect to the putative stock boundaries, or throughout the region of investigation. **Where genetic structure is detected, it is a strong indication of limits to dispersal and hence to the presence of separate stocks.** This information permits population models to be developed for each stock, and managers may use these models to evaluate alternate scenarios of harvesting prior to setting limits.

Availability and skill set required

As with all of the genetic themes described in this document, the design of experiments to define stock boundaries will benefit from being conducted in close collaboration with fisheries scientists and managers with knowledge of the species and environmental context being investigated. In the future, it is likely that genetic analysis will be better integrated with demographic and hydrodynamic modelling. Such analysis may require specialised statistical and bioinformatics skills (Table 1).

Case studies (Australian and International)

Genetic analysis of stock structure can reveal the most appropriate scale of management on a species-specific basis. This is illustrated by a series of genetic investigations of fished species co-distributed between northern Australian and Indonesian waters. The taxa studied included sharks, mackerel and lutjanids (snapper), and the molecular tools utilised included allozymes, microsatellite DNA and mitochondrial DNA sequencing. A great variety of population structures exist among the species in this geographic region, including within each of the taxon groups, such that, surprisingly, life-history traits, bathymetry and hydrodynamics are not always effective predictors of population genetic structure. For example, two shark species (*Prionace glauca* and *Sphyrna lewini*) showed no evidence of stock structure, whereas pronounced structure was evident in another species across the Timor Sea (*Carcharhinus sorrah*; Ovenden *et al.*, 2010). In the lutjanids, two co-distributed species showed strong correspondence in their stock structure (Salini *et al.*, 2006) with the Timor Sea once again providing a barrier to movement, as it does also in the benthic lutjanid *Pristipomoides multidens* (Ovenden *et al.*, 2004). In contrast, another co-distributed lutjanid, *Lutjanus argentimaculatus* exhibits no structure in this region (Ovenden and Street, 2003). Similar multi-species analyses have been conducted in south-western Australia (Ayvazian *et al.*, 1994; Watts and Johnson, 2004).

Investigation of population structure in salmonids (salmon, trout and charr) has been instrumental for both the development of fisheries genetic techniques (Utter, 1991) and the sustainable harvest of the resources. In part this is because of their enormous economic value, but it is also due to their unusual life history. Salmonids are renowned for their ability to return to their natal headwater streams to breed. This behaviour, coupled with relatively small breeding populations within each stream, typically results in high levels of genetic differentiation and corresponding stock structure between drainages (Allendorf and Seeb, 2000). Genetic structure is often evident not only spatially, but temporally, with different "runs" within a single drainage being effectively reproductively isolated from each other. Such high levels of fidelity mean that fine scale stock structure must be taken into account in salmonid management (Shaklee *et al.*, 1999). Furthermore, even during sea-going phases where fish from individual drainages are mixed, they can be distinguished based on their unique genetic signatures. This analysis forms the basis of mixed stock analysis (see genetic theme 10). Such fine-scale stock structure associated with drainages is uncommon in harvested species in Australia, although some estuarine species with non-dispersive larvae do approach similar levels of subdivision (Ayvazian *et al.*, 1994; Horne *et al.*, 2011).

FRDC Projects

- 1987/092 - Assessment of restriction enzyme analysis mitochondrial DNA for the identification of stocks of commercially important marine species and for the detection of genetic markers for the use in salmonid husbandry.
- 1991/034 - DNA studies on Northern Territory stocks.
- 1994/022 - Origin of recruits to the east coast yellowfin tuna fishery and the delineation of the structure of yellowfin stocks in the western Pacific.
- 1994/165 - DNA markers and genetic stock structure in commercial species of penaeid prawns in the east coast fishery.
- 1997/112 - Determining genetic stock structure of bigeye tuna in the Indian Ocean using mitochondrial DNA and DNA microsatellites.
- 1997/117 - Stock delineation of the pink ling (*Genypterus blacodes*) in Australian waters using genetic and morphometric techniques.
- 1998/159 - The stock structure of the northern and western Spanish Mackerel.
- 1999/164 - Application of molecular genetics to the Australian abalone fisheries: forensic protocols for species identification and blacklip stock structure.
- 1999/122 - Biology, management and genetic stock structure of mangrove jack (*Lutjanus argentimaculus*) in Australia.
- 2000/108 - Population structure of the Patagonian toothfish (*Dissostichus eleginoides*) in Australian waters.
- 2003/033 - Enhancement of saucer scallops (*Amusium balloti*) in Queensland and Western Australia - genetic considerations

- 2005/010 - Determination of management units for grey mackerel fisheries in Queensland and the Northern Territory.
- 2007/032 - Defining the stock structure of northern Australia's threadfin salmon species
- 2007/035 - Stock structure of sharks on the northeast Australian coast
- 2009/020 - Evaluation of population genetic structure in the western rock lobster.
- 2010/013 - Towards understanding greenlip abalone population structure.
- 2011/033 - Spatial patterns, landscape genetics and post virus recovery of blacklip abalone, *Haliotis rubra* (Leach), in the Western commercial fishing zone of Victoria.

Technical Challenges

Whilst genetic analysis potentially provides a rapid, and therefore cost-effective, way to define fishery stocks, it has limitations. In some cases, it may have low power to detect restrictions to demographically important immigration because of different thresholds for genetic and demographic cohesion. As the number of dispersers between stocks increases, a point is reached where stocks are no longer genetically distinct but they are still demographically de-coupled. This arises because genetic connectivity depends upon the *absolute* number of migrants between populations, whereas demographic connectivity depends on the *relative* contribution to population growth of migration versus local recruitment (Mills and Allendorf, 1996; Lowe and Allendorf, 2010). It follows that small and demographically insignificant absolute numbers of immigrants can homogenise genetic structure in large populations, meaning that genetic analysis has a bias towards failing to detect demographically independent stocks, and the bias is worse in large populations. This makes marine organisms particularly troublesome because populations tend to be large and rates of dispersal tend to be high.

Where genetic subdivision is detected, it is a strong indication of genuine limits to dispersal, and in the past this has generally been accepted as the basis for delineating different stocks. However, it has been recently argued that a more appropriate criterion is whether that limit to dispersal is demographically significant. Such criteria would depend upon the particular management objectives. The most effective way to understand links between demographic and population genetic processes is through coupled demographic-genetic simulations, which can set criteria for accepting stock structure based on case-specific conditions for the species of interest and the particular management objectives (Palsboll *et al.*, 2007; Lowe and Allendorf, 2010).

Barriers to uptake for fisheries management

There are practical as well as interpretive challenges (see above) to using genetic analysis for delineating stocks. Added to this is the potential for conflicting stock structures to be suggested by alternate modes of analysis such as parasite loads, tagging, otolith microchemistry, and in some cases, different genetic markers. Such discordant results reflect either differences in spatial resolution of the methods, temporal scale of connectedness, or different aspects of population cohesion, such as adult and juvenile dispersal capabilities. As such they may not represent conflicts, and which information is deemed most relevant will depend upon the management objectives. A practical challenge to using genetics to delineate stocks is whether fisheries managers have the capacity to manage resources at the spatial scales indicated by the stock structure. Another significant challenge is how to interpret population structure that does not conform to discrete units but instead exhibits an isolation-by-distance pattern where populations are progressively more genetically differentiated from each other as the distance between them increases.

Future

Conventional indirect approaches to detecting stock structure through genetic analysis will continue to be an indispensable part of wild fisheries management. It is likely that change in this field will largely be incremental, with increases in the power of the analysis through greater sample sizes and larger numbers of DNA markers (Waples and Naish, 2009). One shift in emphasis will be towards using DNA markers that are under selection as opposed to neutral markers such as microsatellites, which are commonly used at present (see genetic theme 6 Fisheries-induced and natural selection). As well as addressing Type I errors (i.e. genetic structure is present, but not detected), these markers may provide greater resolution of

demographically relevant rates of migration, and they will also be used to identify population sectors bearing significant adaptive differences that may be key to future adaptability of fisheries resources (e.g. water temperature). As discussed in genetic themes 6 and 7, adaptive markers will also be used to identify wild fish stocks that carry potentially useful adaptations for either aquaculture or re-stocking.

Many of these changes will be facilitated by the rapid development of next-generation DNA sequencing technologies, which are revolutionising all branches of molecular biology by providing vast volumes of DNA sequence data at a fraction of the cost of conventional DNA sequencing technologies (Mardis, 2008). Another important shift in emphasis will be greater integration of genetics into multidisciplinary assessments of stock structure and connectivity. For example, complementary analysis such as hydrodynamic simulations, micro-chemical analysis, fatty acid analysis, coupled demographic-genetic computer simulations, and Geographic Information Systems. Finally, genetic analyses are likely to rely much more on non-equilibrium models of population structure such as those discussed in genetic themes 6 and 7, which focus on the behaviour of individuals on ecological time frames rather than on the long-term average behaviours of entire populations.

8.1.3   GENETIC THEME 2: GENETIC EFFECTIVE POPULATION SIZE

How does it work and why is it important?

Large populations retain more genetic variation than small populations. This principle underpins the concept of genetic effective population size (N_e), which is a metric that describes the capacity of a population to retain genetic variation. N_e has two key applications to fisheries management. Firstly, change in the absolute abundance of a naturally occurring species can be reflected in changes in N_e, therefore N_e can provide a proxy for change in abundance. Secondly, levels of genetic diversity dictate the rate at which a species can adapt in response to environmental change, and so provides a measure of evolutionary resilience.

For the purposes of this review, we discuss two broad classes of genetic effective population size: contemporary (CN_e) and historical (HN_e). Contemporary estimates apply to N_e in the recent past (over several past generations or years), while historical N_e estimates apply to pre-exploitation (i.e. virgin) populations.

CN_e estimates (e.g. Waples, 1989; Waples and Do, 2008; Zhdanova and Pudovkin, 2008; Wang, 2009) take advantage of the subtle differences in genetic diversity between recruits and parents, which is driven by the number of parents that produce the recruits. For instance, if all recruits come from one pair, they are likely to exhibit less genetic diversity than recruits derived from a larger number of parents. The phenomenon, known as a sweepstakes effect, is common in marine species due to the large potential fecundity per individual and it is amplified by high mortality of larval and juvenile life stages. CN_e is a measure of the strength of this effect, as well as other factors that influence genetic diversity.

HN_e can be estimated from the magnitude of genetic diversity combined with a reasonable estimate of mutation rate. Individuals carrying new mutations (the raw material of genetic diversity) have more chance of leaving offspring in a large population rather than a small population; hence the mutation is likely to become common in the population adding to genetic diversity. Estimates are referred to as 'historical' because genetic diversity is the product of accumulation over a large number of generations and the estimates apply to the population a large number of generations ago.

How is it used for fisheries management?

Genetic effective population size is one of a suite of methods available for genetic monitoring (Schwartz *et al.*, 2006). Changes in population size can be inferred from changes in genetic diversity (e.g. expected heterozygosity and allelic diversity), allele frequencies and CN_e. Estimates of HN_e apply to a large number of generations in the past, so are not used for monitoring recent changes in abundance, but are potentially valuable for estimates of virgin biomass. Fisheries stock assessment modelling based on fisheries dependent data (e.g. catch per unit effort, CPUE) is the standard way of generating estimates of biomass or population size. Time-series estimates of N_e can be made in absence of CPUE or any other fisheries

dependent data. Thus, they are 'fisheries independent' sources of data and are potentially important in validating population trends predicted from stock assessment modelling.

Because estimates of HN_e represent long-term averages they have the potential to reveal historical abundances in species now heavily harvested. In doing so they may overcome the 'shifting baseline' effect. Demographic data are normally collected from a fishery resource after the onset of exploitation, and the collective memory of fishers often does not encompass pre-exploitation abundance or abundance changes over the course of a fishery. As pre-exploitation abundance estimates are generally not available, current levels of abundance tend to be taken as indicative of long-term abundance. The discrepancy between actual compared to perceived pre-exploitation abundance is the 'shifting baseline' (Lotze and Worm, 2009; Venkatachalam *et al.*, 2010). By definition, HN_e estimates are pre-exploitation, and thus have the potential to provide a measure of the extent of the decline of abundance and contribute to setting limits of fishing mortality.

At present, genetic estimates of effective population size (CN_e) play a large role in monitoring the possible decline of genetic diversity that occurs when fingerlings are produced in captivity, and then are released for re-stocking. This is discussed further in genetic theme 7 (Genetic effect of captive-bred fishes on wild conspecifics).

Availability and skill set required

A similar team is needed for this genetic theme as for genetic analysis of fisheries stock structure, which includes field biologists (for sample collection), fisheries scientists, and population geneticists (Table 1). The involvement of a fisheries manager is highly desirable. However, in addition to this standard team extra skills are needed for extension of theory into fisheries populations (statistician and mathematician, software engineer) and for dealing with tissue samples collected in the past (molecular geneticist).

Case studies (Australian and International)

Portnoy *et al.* (2009) studied the heavily exploited sandbar shark (*Carcharhinus plumbeus*) in embayments on the eastern coast of the US. Estimates of CN_e were similar to the magnitude of N_c (number of breeders). N_c in the population was extrapolated from mark-recapture estimates of the numbers of young-of-the-year, average yearly reproductive success of females and the adult sex ratio. The similarity demonstrated between CN_e and N_c for this elasmobranch is landmark for the application of N_e to marine species. For species with low fecundity and correspondingly low variance in reproductive success, this case study confirms that CN_e may have an important role in the assessment of abundance and hence biomass.

The ratio between CN_e and N_c in a study on tiger prawns was very different to sharks; 0.5 and 1.0 for sharks compared to 10^{-3} for prawns. Ovenden *et al.* (2007) studied tiger prawns (*Penaeus esculentus)* in Moreton Bay, Queensland to explore the usefulness of CN_e for fisheries management. The population was selected as a model system because it conformed to CN_e assumptions; it did not have overlapping generations and was likely to be closed to immigration. Overall, the study demonstrated that even with a large fisheries population of invertebrates, precise genetic estimates of effective population size could be made with eight microsatellite loci on a sample size of around 700 individuals. Furthermore, the estimates were stable between years. CN_e was 797 to 1,165 for year 2001 and 866 to 1,304 (95% CI) for year 2002, while census estimates were 648,898 for 2001 and 464,627 for 2002. The ratio between N_c (number of spawners) and CN_e was approximately 10^{-3}. Comparing census and CN_e estimates, it was possible to determine that the variance of reproductive success was large (Vk, 2,200), while the mean number of progeny per pair was likely to be two as demonstrated by the stability of the CN_e estimate across the two years. Interestingly, the HN_e estimates approximated CN_e estimates, suggesting long-term stability of abundance over evolutionary timescales despite high harvest pressure.

HN_e has been used to estimate abundance prior to harvesting and to recommend goals for population recovery. For example, HN_e estimates for Pacific gray whales led to an overall estimate of 96,000 individuals based on genetic diversity at ten microsatellite loci assayed in 42 individuals (Alter *et al.*, 2007). This was inferred to represent census size prior to exploitation, and was several times larger than the current estimate of population size based on survey data of about 22,000 whales. Interestingly, the survey

estimates are assumed to represent a 'recovered' population as harvesting has been effectively banned since 1949. However, the N_e estimates suggest the population is far from recovering to pre-whaling abundance. The authors acknowledged the uncertainty in these genetic estimates of abundance due to evolutionary (e.g. selective sweeps on genetic loci, population structure and mutation rates) and demographic (e.g. population expansions and bottlenecks and variance in reproductive success) forces. Overall, the effects of these factors would be to upwardly bias HN_e that would reinforce their conclusion that the current population has not recovered to pre-whaling abundances.

FRDC Projects

- 2001/018 - A new data source for fisheries stock assessments: Genetic estimates of the effective number of spawners.
- 2010/062 - Shark futures: Sustainable management of the NSW whaler shark fishery.

Technical Challenges

'The concept of effective population size (Ne) is elegantly simple yet rapidly becomes complex as simplifying assumptions give way to practical realities' (Waples *et al*., 2011).

The application of genetic estimates of effective population size is a rapidly developing area of theoretical and applied research. However, its routine application as a proxy for population abundance is limited at the moment by the uncertainty and variation in the ratio between *Ne* and *Nc* (census population size). For example, consider a marine population consisting of 1000 individuals. The population is outbred so individuals are unrelated to one another. All individuals participate in reproduction during the spawning season and on average each individual contributes one adult offspring to the next generation so that the population size is stable. The next generation consists only of offspring (i.e. parents die after spawning) and the population is closed to migration. Under these circumstances, the genetic effective size of the next generation is equal to the census size of the parental generation. Alternatively, and more realistically, in the parental generation some animals do not participate in reproduction or if they do, their offspring die before becoming adults in the next generation. Consequently some animals (i.e. families) contribute many more offspring to the next generation than others. In this case, the genetic effective size of the next generation is less than the census size of the original generation. For typical marine species, where fecundity and mortality are high and variable between families, the genetic effective population size can be three (Ovenden *et al.*, 2007) to five (Hauser *et al.*, 2002) orders of magnitude below census size. However, for less fecund species like sharks the variance is lower, and the ratio may approach unity (Portnoy *et al.*, 2009).

As in the example above, typically N_e is smaller than *Nc*. Researchers have been addressing the major factors influencing the ratio, such as the effect of unequal sex ratio (Waples and England, 2011), the degree to which generations overlap, variance in family size, fluctuations in N_c (Antao *et al.*, 2011) and the effect of immigration (Waples and England, 2011). Waples *et al.* (2011) have provided a method to directly compare estimates of the number of breeders obtained from genetic and demographic data. Future work using their *AgeN$_e$* software may test the expectation that the ratio varies systematically across species depending on life-history strategy. Portnoy *et al.* (2009) demonstrated that the ratio is close to unity in elasmobranchs that have a smaller variance of reproductive success, in contrast to marine fish where the ratio may be 10^{-5}. Simulation studies by Antao *et al.* (2011) showed that estimates of N_e track declines in census size suggesting that genetic monitoring could provide early warning of population depletion. This work needs to be validated with marine populations that would have higher abundances than threatened, endangered or protected (TEP) species that were used as examples. England *et al.* (2010) have made important steps forward in the use of N_e to detect incipient population fragmentation and Waples and England (2011) have explored conditions under which N_e can be estimated in metapopulations, a type of population structure commonly found in marine species. Finally, as census estimates of the number of breeders decline through time as a result of harvesting, the ratio to genetic estimates may change, which would have has implications for the use of N_e to track *Nc*. This was called 'genetic compensation' when it was demonstrated by Ardren and Kapuscinski (2003) for steelhead trout, a species where recruitment is largely determined by suitable spawning habitat.

Genetic effective population sizes are regularly lower than census population sizes, and until the mechanisms underpinning this can be generally understood the interpretation of N_e as a proxy for abundance should be carefully considered.

Estimates of CN_e and HN_e apply to individual populations, so baseline information on genetic population structure is an important pre-cursor to this work. The population to which HN_e estimates apply is likely to be spatially more expansive than CN_e, as the HN_e estimate sums across all processes that have influenced genetic diversity including past and present instances of migration (i.e. gene flow). Caution needs to be exercised in summing CN_e estimates for individual populations to produce an estimate for the species over its entire range, as the behaviour of CN_e estimates in metapopulations is not fully understood (Waples and Do, 2010; Waples and England, 2011).

Future

Waples *et al.* (2011) have recently produced a method (and software, *AgeNe*) for estimating genetic effective population size from life-history tables. Dual application of genetic and demographic estimates across species that vary in life-history and exploitation characteristics may assist in understanding the factors that drive the relationship between N_e and N_c. Implementing this method may have the added benefit of illuminating pathways for the integration of fisheries population models (e.g. stock-recruitment models) with estimates of N_e. Likewise, close comparisons between CN_e and estimates of abundance derived from genetic mark-recapture (genetic theme 3 below) have great potential to benefit both methodologies.

8.1.4   GENETIC THEME 3: GENETIC MARK-RECAPTURE FOR ESTIMATING MORTALITY AND ABUNDANCE

'Counting fish is like counting trees, except that are invisible and they keep moving' (John Shepherd in Hilborn, 2002)

How does it work and why is it important?

Estimating the abundance and harvest rates of fisheries and non-target species impacted by fishing is one of the key requirements for determining sustainable yields or sustainable environmental impacts. Yet, these parameters are inherently difficult to measure in the marine environment. This section introduces some recently developed and novel approaches that combine conventional capture-recapture modelling (CMR) with genetic analyses to directly estimate the abundance as well as other important population parameters of wild fish stocks. These methods can be grouped under the label "genetic tagging".

Genetic tagging has not been widely applied to marine organisms (Palsboll *et al.*, 2007). However, recently a series of approaches have been developed that draw together genetic analyses and CMR in novel ways to enable estimation of abundance and related population parameters in marine species, and which avoid some of the difficulties associated with conventional CMR, such as tag loss. **They offer direct and fisheries-independent methods to estimate abundance of wild fish stocks**, and therefore have the potential to be widely deployed for routine assessments of fisheries resources.

How is it used for fisheries management?

Capture-mark-recapture modelling (CMR) is a well-established set of statistical tools for estimating abundance and related population parameters in wild fish stocks (e.g. mortality, recruitment). CMR is particularly effective for organisms that are readily captured in easily defined regions (e.g. anadromous salmon) (Rodgers *et al.*, 1992). However, it is difficult to implement for most mobile marine organisms because of low rates of recapture and tagging-induced mortality (Thorrold *et al.*, 2002). Mortality is a particular problem for CMR investigations of wild fishes since capture often introduces significant trauma, especially in deepwater fishes (St John and Syers, 2005).

The use of natural genetic tags to identify individual organisms has been widely deployed for monitoring terrestrial wildlife in the past decade (McKelvey and Schwartz, 2004). Genetic tags are unique DNA fingerprints (genotypes) that are obtained from individuals by assaying variable DNA markers such as microsatellites. The high variability of these markers means that if enough markers are assayed all individuals can be distinguished. Two useful features of this approach are that unlike conventional tags, genetic tags cannot be lost, and second, monitoring need not introduce changes to behaviour or increase risk of mortality because usually DNA samples can be collected without capturing animals (e.g. from hair, faeces, remotely collected biopsies).

The data obtained from genetic tagging analysis is directly comparable with conventional tagging data, so many of the existing statistical CMR approaches can be applied to it. However, there are several important factors to be considered to ensure that bias is not introduced to the analysis. The two most significant issues are: 1) genetic tags must contain sufficient information to distinguish all individuals otherwise estimates of abundance will be underestimated; and 2) genetic tags must not contain errors, otherwise estimates of abundance will be over-estimated due to missed identification of recaptures. These issues are not specific to genetic tagging and established protocols exist to deal with them (Wilberg and Dreher, 2004; Lukacs and Burnham, 2005; Macbeth *et al.*, 2011).

Availability and skill set required

Genetic mark-recapture work brings together the specialist fields of population and molecular genetics, capture-recapture modelling and fisheries science. It requires a highly skilled team to integrate them effectively (Table 1).

Case studies (Australian and International)

The first use of genetic tags to understand the dynamics of wild marine organisms was an investigation of the abundance and migration patterns of North Atlantic humpback whales (Palsboll *et al.*, 1997). Based on 3060 biopsies collected at sites throughout the North Atlantic Ocean, 2,368 individuals were identified, including 692 recaptures. This permitted an estimate of 7,698 whales, which was higher than estimates based on photo identifications. It also demonstrated high fidelity of individuals to particular migration routes between summer and winter-feeding grounds, and differences in levels of feeding ground fidelity between males and females.

Typically, fished species are more difficult to obtain biopsy samples from than whales. Recently, two novel applications of genetic CMR have been developed in Australia. Genetagging (Buckworth *et al.*, 2012) has been applied to finfish, and involves "capturing" and "recapturing" fishes without landing them. It does so by collecting biopsies from fishes with specialised hooks (Buckworth, 2004) before immediately releasing them. The DNA contained in the biopsies is then analysed in a laboratory with DNA markers suitable for individual identification (e.g. microsatellites). The set of unique genotypes (DNA fingerprints) collected during one capture session is compared to sets of genotypes collected on subsequent sessions, or from the landed catch, to identify instances of recapture. The data can be analysed with conventional CMR modelling approaches to estimate harvest rate and abundance (Otis *et al.*, 1978; Pollock *et al.*, 1990), although it requires rigorous error-checking systems (see below). A particular advantage of genetagging over conventional tag and release for finfish is that capture is less likely to induce mortality than conventional tagging, and tags cannot be lost. Buckworth *et al.* (2012) have applied the method to Northern Territory populations of Spanish Mackerel (*Scomberomorus commerson*) to monitor real-time harvest rate.

Close kin genetics also relies on a mark-recapture analysis framework (Bravington and Grewe, 2007). It obtains unique genotypes from discrete parental and offspring generations and treats the offspring as a sample of the parental generation at the time of spawning, and the parents as a second sample of that parental generation. These samples can be taken lethally from landed individuals, so long as the investigation lasts only a single generation, or can be taken non-lethally via biopsies (e.g. genetag hooks). Parentage analysis (e.g. (Marshall *et al.*, 1998) is applied to the raw genetic data and parent-offspring relationships (equivalent to recaptures) are enumerated. Variants of capture-recapture modelling are applied to the parentage data to provide direct estimates of population abundance in the parental

generation. Related methods have been developed that can extend the method to also estimate recruitment, mortality, and sex ratio (R. Barker, Dept. Mathematics, Otago University pers. comm.). Bravington and Grewe (Bravington and Grewe, 2007) have applied close kin genetics to the Southern Bluefin Tuna (*Thunnus maccoyii*) to estimate spawning biomass. The use of parentage analysis is not unique to investigations of abundance. Methods such as this are increasingly being used to understand the extent of connectivity in marine populations in the context of the functions of marine protected areas (Planes *et al.*, 2009; Christie *et al.*, 2010), but equally could be applied to harvested species.

FRDC Projects

- 2002/011 - Department of Resources (NT) - GENETAG: genetic mark-recapture for real-time harvest rate monitoring. Pilot studies in northern Australia Spanish Mackerel fisheries.
- 2008/034 - CMAR - Fishery independent estimate of spawning biomass of Southern Bluefin Tuna through identification of close kin using genetic markers.

Technical Challenges

Assuming that appropriate biological samples can be obtained, there are a number of important technical challenges relating to the information content of the genetic tags that must be dealt with to ensure the reliability of the estimates obtained through genetic mark and recapture. Firstly, genetic tags must contain sufficient information to enable individuals to be distinguished (in the case of genetagging), and for parentage to be established with high certainty (in the case of close kin analysis). Less information is required to distinguish individuals than to assign parentage. In general, the information content of genetic tags is improved by increasing the number of markers, or by including markers bearing more variation. These issues are easily solved through calculation of summary statistics that establish whether a panel of markers provide sufficient power to distinguish individuals (e.g. probability of identity) and assign parentage (e.g. exclusion probability) for a given population and experimental design.

The second challenge is to minimise errors in the genetic tags because their inclusion will bias population estimates upwards (i.e. true recaptures will not appear as recaptures). Errors can be introduced into the raw data at the laboratory stage, and for genetagging a variety of data checking procedures exist (McKelvey and Schwartz, 2004; Macbeth *et al.*, 2011). Capture-recapture models have also been developed that can account for errors in the genetic tags (Lukacs and Burnham, 2005). Database errors are also a risk because both close kin and genetagging experiments have the potential to deal with very large datasets consisting of thousands of individuals and tens to hundreds of markers. Indeed, for abundant species sample sizes for close kin analysis may need to be several thousand in order to obtain sufficient recaptures for useful abundance estimates to be obtained. However, this is a general problem and not specific to this genetic application.

A major problem in identifying individuals and families from genetic data is the occurrence of 'shadows' or type I errors (genetic data from two samples is identical, but the samples represent two different individuals). The occurrence of type II errors (when genetic data from two samples is different, but the samples represent the same animal) is less frequent and is quantified by determining the genotyping error rate. Type I errors can be addressed with sound experimental design (increasing number and power of genetic markers) or during data analyses (Macbeth *et al.*, 2011).

Another technical challenge is that capture-recapture analysis requires specialised knowledge that is usually outside of the experience of population geneticists who have the skills to generate and analyse the genetic data. This challenge can be met by collaboration and discussion between population ecologists and geneticists.

Barriers to uptake for fisheries management

Both genetagging and close kin genetics have the potential to provide valuable baseline or monitoring data for wild fisheries that is difficult to obtain by conventional means. However, there may be both biological and financial barriers to its uptake for the management of wild fisheries. Genetic CMR is well suited to sedentary species that suffer high mortality upon capture (e.g. Dhufish, *Glaucosoma hebraicum*).

However, some marine species have life histories that present greater challenge. For example, as is the case for conventional CMR tagging, large populations of wide ranging species will require extensive effort to obtain sufficient recaptures for accurate and precise parameter estimation. Fish 'marked' with the genetag hook are not landed, so their physical characteristics cannot be recorded, meaning that there is little scope for adding individual co-variates to CMR models.

Close kin analysis relies on being able to distinguish parental and offspring generations and sampling the generations independently. Species without obvious age classes or spatial/temporal segregation by age are problematic. Similarly, parent-offspring pairs that occur together cannot easily be sampled independently (e.g. whales and calves, marine turtles and eggs). Because both genetagging and close-kin genetics employ a CMR analysis framework both are well suited to *a priori* power analysis that can provide indications of the sampling effort required to accurately and precisely estimate the population parameters of interest (White and Burnham, 1999).

Future

The future is bright for genetic CMR based methods of analysis and these methods have been greeted with optimism from industry. Equivalent methodologies are now in mainstream use in terrestrial environments. Compared to terrestrial species, aquatic species have higher abundances and many aspects of their biology are less well known, which makes the application genetic CMR more challenging. A number of research groups are working on similar analytical approaches worldwide.

8.1.5 GENETIC THEME 4: PRODUCT PROVENANCE AND FISHERIES SURVEILLANCE USING GENETICS.

How does it work and why is it important?

Effective regulation underpins the sustainable harvest of wild fisheries. The successful implementation of regulations relies on a means to reliably identify exploited organisms and their products. However, this can be difficult when diagnostic morphological characters are not evident, such as fish fillets or trunks that lack heads, guts and tails following processing at sea. Also of concern is the identification of the geographic origin of the product or whether several products represent a single organism. Genetic tools are irreplaceable in these situations.

Given the right information, genetics can trace relationships between tissue samples representing species, populations, family groups and individuals. Samples can be identified as coming from the same, or different, individuals; for example to trace product from a single individual in the market place. Likewise, samples from fish can be placed into groups of siblings, half-siblings and parents using genetic markers. A fish can be assigned as coming from a particular wild fisheries population or species. Reference samples are essential for the use of genetics to determine the population or species of origin. This means genetics can address the question 'Does this sample match this group?', but without reference data, it cannot answer the question 'What group does this sample come from?'

This genetic theme focuses on the many uses of genetics in determining fishery product provenance and touches on the many types of genetic methods that are relevant. The specific use of DNA sequencing for species recognition is discussed briefly here, but is dealt with in greater detail in the next section (genetic theme 5).

How is it used for fisheries management?

Genetic tools largely have post-harvest application, but there are some pre-harvesting uses. For instance, genetic tests for parent-offspring relatedness (e.g. Bailie *et al.*, 2011) are being used in Ireland to confirm the berried status of lobsters (*Homarus spp.*) by matching egg and adult tissue samples. A match allows the fisher to be compensated for releasing berried females without verification by a fisheries officer.

Product substitution, where a valuable food product is illegally substituted for a less valuable product, is a well-described problem in the seafood industry (Rasmussen *et al.*, 2009; Aranceta-Garza *et al.* 2011). The

practice results in consumer losses, devaluation of marketing tools, degradation of fisheries resources and potentially adverse effects on human health. Lack of standardisation between common, marketing and scientific names has been addressed for products sold in Australia with support from FRDC (Yearsley *et al.*, 1999; 2003). Ensuring the accuracy of labelling is recognised as a high priority by Australian industry (Bremmer and Snow, 2007).

Genetic analysis of samples is widely used to enforce accurate labelling of seafood (Asensio Gil, 2007; Rasmussen *et al.*, 2009). This is the most straightforward of the provenance testing procedures, and generally involves obtaining an mtDNA sequence from a specimen of interest and making a direct comparison to reference DNA sequence for known species (see genetic theme 5).

Another novel use is tracking the fate of individuals in the marketplace using microsatellite genotypes. In the Korean and Japanese whale markets it provided a means of independently estimating the true catch as well as monitoring supply chains (Dalebout *et al.*, 2002). The number of individuals for sale at any one time was estimated and the presence of the same individual among outlets suggested a common origin for processing. The information validated catch records and other official assessments of trade.

Genetic tools can be used to determine the population of origin. Many wild fisheries operate under a management system where biological or jurisdictional stock boundaries are important. A range of genetic tools has been employed to assist the enforcement of such regulations. Importantly, all rely on the existence of underlying genetic differences between temporally or spatially discrete units. This is the rationale behind the EU-supported FishPopTrace project (Martinsohn and Ogden, 2009; Helyar *et al.*, 2011) where reference genetic data have been collected across the spatial range of specific species. This allows individuals to be matched back to locations for enforcement and product tracing. Sophisticated statistical methods enable probabilities of origin to be determined and also enables particular stocks of interest to be excluded as origins (e.g. Cornuet *et al.*, 1999; Banks and Eichert, 2000).

Availability and skill set required

A standard team for this type of work would consist of population and molecular geneticists, taxon-specific fisheries scientists and taxonomists and ideally fisheries managers (Table 1). A database manager would be useful if large projects were undertaken with many taxa. Routine service provision in this field would require a different set of skills and equipment. For example, high throughput and rapid turnaround of results may be necessary. Labs may require national certification of facilities and operating procedures. **The advice or involvement of legal experts may be needed if the results are presented as evidence in court.** Access to reference data is critical. This may be based on voucher-specimens (for species identification), or it may be population samples from relevant reference populations (determining the geographic origin). These references may be freely available from online genetic databases (species identification; GenBank (Benson *et al.*, 2010) and BOL, www.boldsystems.org), or need to be prepared for a specific application (assigning the geographic origin).

Case studies (Australian and International)

Cod products are highly sought after in the British Isles and Atlantic Cod (*Gadus morhua*) has experienced extensive fisheries collapses (Walters and Maguire 1996). Miller and Mariani (2010) conducted a investigation to determine the species identity of cod products on sale in Ireland. They purchased fresh, frozen and smoked Atlantic cod products from local fish shops and supermarkets, largely in Dublin. Against expectations, DNA analyses showed that around 10% of fresh product and up to 30% of smoked product were mislabelled. The products were from a range of similar species, including Pacific cod and cod relatives. One potential consequence of such mislabelling is generation of false perceptions among consumers about the availability of the product and health of wild stocks (Miller and Mariani 2010). The outcome of the study will be to increase accountability in product labelling that will lead to an increase consumer confidence in labelling. Ultimately and with the provision of the right information, the consumer can chose to purchase if a product is from a sustainably managed fishery.

An analysis of mtDNA sequence variation demonstrated widespread mislabelling of premium fish products in the Australian marketplace (Anon, 2004). The laboratory method employed (PCR-RFLP; see Appendix C),

is an inexpensive approach to detecting DNA sequence variation, but requires the establishment of a baseline dataset for the species of interest. Overall, 76.8% of products were correctly labelled, however the levels of compliance varied greatly between species, being highest for barramundi (87%) and lowest for red emperor (59%) and dhufish 53%). Compliance also varied significantly among wholesale, retail and food service sectors, with the food service sector showing the worst compliance (64%).

Currently in Queensland it is illegal to possess female mud crabs (*Scylla serrata*). Genetic methods were used to achieve a successful prosecution in the case of female possession. The defendants claimed that females in their possession were derived from the Northern Territory coast of the Gulf of Carpentaria, where there are no gender-specific possession rules. Genetic analysis of the females revealed that they possessed a mtDNA haplotype (COI region) that was previously shown by Gopurenko and Hughes (2002) to be unique to Queensland populations on the north-eastern coast. The outcome set new standards in fisheries enforcement in Australia. Both fishermen received fines worth tens of thousands of dollars.

Assigning bycatch to species and population of origin is relevant to ecosystem-based fisheries management. Globally, albatrosses and other pelagic seabirds have declined as the result of mortality associated with longline fisheries (De Roy *et al.*, 2008). Because these species are highly mobile and because bycatch carcasses may be highly degraded, it is difficult to assign mortality rates to species or specific breeding populations. Genetic tools demonstrated that the species, subspecies, breeding colony and gender of albatrosses could be assigned with high accuracy (e.g. *Diomedea spp.* and *Phoebastria nigripes*) (Walsh and Edwards, 2005; Burg, 2007).

FRDC Projects

- 2005/011 - Development of Field Implemented Fillet Identification (FIFI) for coral reef finfish.

Technical challenges

Precise identifications cannot be made without appropriate reference data, so the breadth of reference data needs to be carefully considered when using genetic tools for product provenance. The user may be alerted to missing reference data when an unmatched sample lies between several reference species on a phylogenetic tree or cannot be assigned to a population with high confidence. The consequences of false negative or false positive identifications need to be considered on a case-by-case basis.

The extent to which the method can be used to determine the population of origin of an unknown sample depends on the genetic distinctiveness of the population compared to others. Genetically distinctive populations of wild fisheries are not as frequent or as easily characterised as some freshwater or terrestrial populations, where dispersal barriers are more common and population sizes may be smaller.

Reference data for genetically distinct populations needs to be validated regularly, as temporal changes in gene frequencies and gene composition can occur due to a variety of processes (drift, selection, immigration with breeding, mutation). Reference data for species are more stable, but it is essential that they are formally associated with a specimen that has been identified to the highest available taxonomic standard. Care is needed when using on-line databases. For instance, taxonomic assignment of nucleotide sequences on GenBank (Benson *et al.*, 2010) are not 100% reliable (e.g. Siddall *et al.*, 2009).

Barriers to uptake for fisheries management

While genetic data often provide uniquely accurate provenance information, the costs of identifications may be a drawback for product provenance and surveillance work. Costs include determining the genetic characteristics of the unknown sample, collecting and maintaining the reference data, maintenance of the laboratory and salaries of experienced personnel performing the identifications and interpretation and reporting of results. Costs of genetically testing the unknown and reference samples are decreasing as methods become more automated, but the other costs are generally fixed. Costs associated with other analytical methods using in fisheries science (e.g. isotope analyses of otoliths, trace element testing of environmental samples) are often higher than genetic costs on a per sample basis.

Availability of skilled personnel and equipped laboratories to perform the identifications is a limiting factor. Many laboratories in universities, museums and government institutions are equipped to collect genetic data, but few have access to the appropriate reference data and have the skills to perform the identification. **In Australia, there is no organised network of laboratories for forensic genetic analysis of non-model fisheries or wildlife species.**

Identifications need to stand up to cross-examination in court. As the use of genetic data becomes more common, it may become less likely that the defendant will plead not guilty knowing that they are up against genetic data (as often happens now). Lawyers and barristers for the defendants will become more knowledgeable about the use of genetic data and may call expert witnesses. No laboratories in Australia have certification for genetic analyses of non-model species. Procedures that are common in human forensic laboratories, such as chain-of-evidence, sample-logging and blind verification of results, are not in place for fisheries species. The lack of facilities may continue in Australia until the demand increases.

Future

Larger companies may consider it prudent to develop in-house capability for product provenance, or specialist private-industry providers of this service may be established. One possibility is that processing companies may take the initiative to certify their premium products in terms of their origins and identities as part of a catch documentation scheme (CDS, Baker, 2008) or certification by the Marine Stewardship Council. Similar approaches have been used by the Norwegian whaling industry to register all legally killed individuals with a microsatellite DNA genotype (Palsboll *et al.*, 2006), and there is a close parallel in certification of timber products (e.g. Double-Helix Track Technologies, Singapore).

The assignment of individuals to stocks or to specific family relationships is now largely conducted with microsatellite DNA markers because of their relative ease of development and genotyping. SNP markers may take over in the future because they are better suited to automation, are less prone to error, and references are easily transferred between laboratories or genotyping technologies (Helyar *et al.*, 2011). Some current barriers to the use of SNP may be overcome within five years (e.g. development of SNP *de novo*, SNP genotyping technologies), but it will take longer to develop appropriate reference data. SNPs will not replace DNA sequencing for species identifications and there has been little or no development of SNPs for individual and family group identification in non-model organisms.

Developments in gene discovery and genetic engineering may lead to the bespoke genetic marking of fisheries product from aquaculture and wild fisheries. As well as having application to product provenance, this activity would be the precursor to property rights over fisheries strains and stocks.

8.1.6 GENETIC THEME 5: SPECIES RECOGNITION USING GENETICS

How does it work and why is it important?

Australia's coastal and offshore waters are poorly explored by global standards, and the documented species biodiversity is growing rapidly. Many aspects of fisheries management rely on the accurate identifications of both harvested and non-harvested organisms. For example, mapping species distributions, the discovery of cryptic species, recognising larval stages, detecting toxic algal blooms, the identification of bycatch, and the construction of foodwebs on which ecosystem models are based (see genetic theme 11). In this section we illustrate how DNA analysis is increasingly being deployed as a rapid, universal, and highly accurate tool to assist with the recognition[1] of species.

Taxonomic classifications are largely based on morphological data and rarely are classifications proposed using DNA data alone. DNA data can alert taxonomists to the presence of new taxa, which may provide impetus to investigate the specimen further. DNA data can normally be collected regardless of the type of

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[1] To avoid the implication that DNA data alone can be used to taxonomically describe new species, and to reflect the general usefulness of DNA as a tool for identifying species, we have used 'species recognition' rather than 'species identification' in this section.

specimen or its state of preservation (fossils generally excluded) and provide a great deal of information about the specimen, in contrast to morphological characters that can be data-poor.

The advantages of DNA as a data source have been incorporated into the 'barcoding' approach (e.g. (Hebert *et al.*, 2003). 'Barcoding' is the use of a specific mtDNA sequence (cytochrome oxidase subunit 1; COI) to identify species. However, in theory, any gene-region can be used. Generally, a user obtains DNA sequence from their sample, matches it against reference sequence (e.g. Barcode-of-Life Database) or in-house data. If a match is made, species identity can be inferred.

In collaboration with Australian and international colleagues, Ward has led the collection of reference data for the recognition of fisheries species in Australia (Ward *et al.*, 2005; Ward *et al.*, 2009). These extensive baseline data are an invaluable resource. This program is incorporated into the International Consortium of the Barcode of Life, which has well-established quality assurance processes to ensure the accuracy of reference data, such as linking all DNA sequences to museum voucher specimens, and documenting the biological and collection data associated with each specimen.

How is it used for management?

Determining an organism's identity is fundamental to any biological investigation, including fisheries research. Individuals harvested from a fishery or unintentionally caught or affected (e.g. by-catch and threatened, endangered and protected species) need to be identified to species to maintain accurate catch records and to assist with fisheries enforcement. DNA can be useful if a specimen lacks the morphological characters for routine taxonomic identification (e.g. fish fillet), or if morphological characters cannot be easily distinguished (e.g. pre-caudal vertebral counts in whaler sharks) or if no diagnostic morphological characters are known (e.g. cryptic species). Seafood marketing requires species identification to provide consumer confidence in quality, and labelling regulations are strictly enforced (see product provenance, genetic theme 4).

Availability and skill set required

A team approach to this work would encompass fisheries geneticists, scientists and managers along with taxonomists and a database manager for large projects (Table 1).

Case studies (Australian and International)

Many freshwater species in North America support significant recreational and commercial fisheries, yet biodiversity is in decline. April *et al.* (2011) gathered sequenced (mtDNA COI) of 752 species of freshwater fish from North America. Their study produced reference data that allowed 90% of the species to be recognised using DNA sequence. For the remaining 10%, taxonomic issues and possibly issues associated with the genetic marker used (mtDNA) interfered with species recognition.

Using DNA species recognition, the frequency of Common Blacktip sharks (*Carcharhinus limbatus*) in northern Australian fishery was found to greatly exceed previous estimates (from less than 1% to around 50%) and the range of Australian blacktip sharks *Carcharhinus tilstoni* was shown to extend further south than expected (Ovenden *et al.*, 2010).

FRDC Projects

- 1993/064 - Stock structure and species identification of school and gummy sharks in Australia.
- 2007/035 - Description of the stock structure of Queensland's east coast shark populations

Technical Challenges

DNA-based species recognition (DNA barcoding) is a widely accepted genetic tool. However, in a minority of cases, its accuracy may fall below what is required, or identifications may not be possible using the data collected. The mtDNA genome is maternally inherited so inter-specific hybridisation is an issue. The problem with hybridisation is that mtDNA can be permanently exchanged between closely related species, leading to incorrect identifications. Although hybridisation is a natural process, it is relatively rarely detected and its overall occurrence is unknown. Another natural phenomenon, the retention of ancestral

polymorphism (where mtDNA sequence differences between species have not developed due to recent speciation), mimics the appearance of hybridisation and has the same issues for species recognition. Finally, mtDNA can be transferred to nuclear DNA (Moulton *et al.*, 2010; Hazkani-Covo *et al.*, 2011) by cellular processes that are largely unknown. If this happens, the genetic distinctness of species can become obscured because nuclear mtDNA copies may not show the expected correlation with species taxonomy. The above caveats aside, large empirical datasets reveal that the accuracy of DNA barcoding is greater than 90% in almost all taxa (see above).

 'Barcoding' can also fail when the species is not represented in the database, or has been entered into the database under the wrong species name (e.g. Siddall *et al.*, 2009). The International Barcode of Life Consortium (www.ibol.org) is working hard to improve species coverage, but database errors are harder to correct. Phylogenetic analysis of reference and unidentified DNA sequences is a powerful way of detecting and addressing these errors.

Barriers to uptake for fisheries management

DNA-based species recognition is a useful tool for alerting managers to the presence of cryptic species, which pose a particular challenge for management. The lack of observable morphological or phenotypic differences between cryptic species means that sample identification is difficult, but species identification is essential for collecting accurate data on age, growth and fecundity. DNA sequence analysis may provide a means to accurately distinguish cryptic species so that reliable diagnostic morphological characters can be identified (Garci-a-Rodriguez *et al.*, 2008).

When DNA and morphological distinctiveness don't correspond, a likely explanation is unrecognised cryptic species. In many cases it is resolved once taxonomic voucher specimens are examined and hidden morphological characters are uncovered (e.g. the "madtom" catfishes , Egge and Simons, 2006).

Other barriers include those listed above for product provenance (genetic theme 4), including cost of service, lack of coordination between government and private laboratories and lack of quality assurance processes that are needed to produce results that can be used as evidence in court.

Future

Species recognition using DNA is a burgeoning scientific field. It is probably the most rapidly growing area where genetic tools are being taken up for fisheries management. Fisheries species are particularly well represented in international DNA databases because of the ongoing, dedicated program designed to establish this baseline (Ward *et al.*, 2009). This resource will facilitate a growing uptake of barcoding technology in fisheries management, and enable more accurate and consistent attributions of catch and bycatch than have been possible in the past.

The integration of DNA characters into formal taxonomic descriptions is a relatively new development, but important for establishing reliable reference data. However, if genetic taxonomy moves into the world of genomics, then the most appropriate DNA sequence for inclusion would be the entire mitochondrial and nuclear genome sequences. This may soon be possible, given the rate at which technology is moving forward.

The number of taxonomists is declining, which will impact on natural resource and biodiversity management, particularly in regions such as the Indo-pacific where much remains to be discovered. Recruitment of taxonomists may be improved by combining conventional taxonomy and genomics.

8.1.7 GENETIC THEME 6: FISHERIES-INDUCED AND NATURAL SELECTION

 'Unnatural selection generally acts at cross purposes to the long-term goal of sustainable harvest of wild populations and can reduce the frequency of phenotypes valued by humans' Allendorf and Hard 2009.

How does it work and why is it important?

Evolutionary processes have rarely been considered in the management of wild fisheries. However, there are three ways in which understanding evolutionary processes are likely to become increasingly important. The first concerns the potential of fishing to introduce undesirable evolutionary changes to harvested populations. The second concerns the use of genetic indicators of local adaptation to assist with the delineation and identification of stocks. The third concerns to use of molecular and phenotypic markers to monitor the evolutionary impacts of climate change.

Fishing-induced selection: Fishing mortality is often many times larger than natural mortality. Furthermore, fishing mortality is non-random with respect to phenotypes. Thus, fishing has the potential to exert "unnatural" selection on life-history traits if those traits have any genetic basis. This process can have implications for fisheries because the **traits favoured by fishing are likely to be undesirable in terms of the long-term sustainability of fisheries.** For example, because fishing often targets larger individuals, it inevitably selects for a reduced size at maturity, which can ultimately reduce the productivity and stability of fisheries. Alternatively, the traits favoured by fishing may be those that are not favoured by sexual selection, also leading to lower productivity. Even where fishing is not selective for particular traits like size, and merely results in higher mortality overall, it has the potential to promote evolutionary change towards earlier maturation (Allendorf *et al.*, 2008). Importantly, although evolutionary change in fisheries can occur rapidly (within decades), theoretical models demonstrate that it may be much slower to correct once harvest effects are removed (Walsh *et al.*, 2006).

Local adaptation and identification of stocks: Translocation experiments across a variety of taxa demonstrate that most organisms exhibit some level of adaptation to local conditions. As discussed in genetic theme 7 (Genetic effects of captive-bred fishes), taking account of local adaptations increases the success of translocation and re-stocking initiatives, and can also inform selection of aquaculture broodstock. One implication of this for wild fisheries management is that it emphasises the importance of preserving genetic diversity so that it is available to respond to environmental change. **Preserving genetic diversity requires the maintenance of large and regionally representative populations (Allendorf and Luikart, 2007).**

As discussed for genetic theme 1, genes under selection can be used to delineate stocks at greater resolution than is possible with conventional "neutral" DNA markers. Whole genome sequencing technologies make it possible to identify genes under selection, even for species without existing genomic information (Storz, 2005), and there is a growing list of candidate genes with known functions that relate to key environmental variables (De-Santis and Jerry, 2007; Nielsen *et al.*, 2009).

Monitoring evolutionary responses to climate change: Like fishing-induced selection, climate change has the potential to introduce novel and strong selective forces on marine and aquatic organisms. When confronted with a changing climate, organisms could respond in one of four ways: 1) decline and/or become extinct; 2) respond by plastically adjusting their phenotype; 3) moving to more suitable environments; and 4) adapting genetically to the new conditions. Climate change therefore has the potential to significantly affect the distribution and abundance of marine and aquatic organisms, including important fisheries species in Australia (Neuheimer *et al.*, 2011). Detecting responses to climate change or forecasting how organisms will respond offers a way to identify species at risk and to adjust management strategies accordingly (Hansen *et al.*, 2012). Genomic analyses, especially where they are applied to both historical and contemporary samples in combination with aquaculture experiments potentially offer a way to detect and predict responses to climate change (Nielsen *et al.*, 2009).

How is it used for fisheries management?

Fisheries managers are likely to pay increasing attention to evolutionary processes in wild fisheries management in the future. There are few, if any current examples where these genetic concepts are being incorporated into management.

Availability and skill set required

Research in this genetic theme requires sophisticated combinations of experimental molecular and quantitative genetics as well as evolutionary biology. Verification of fishery-induced selection and trait heritabilities requires experimental manipulations, design and analysis, as well as access to long-term data on phenotypes and environmental conditions. The identification *de novo* of genes under selection requires expertise in outlier loci analysis, bioinformatics skills in genome assembly and mapping. Collaboration with specialist bioinformaticians may be appropriate (Table 1).

Case studies (Australian and International)

Fishing-induced selection

Theory predicts that high levels of harvest can result in rapid evolutionary effects (Swain *et al.*, 2007). Such change has been observed in a variety of organisms (Allendorf *et al.* 2008). The best-known examples of fishing-induced selection come from heavily exploited North Atlantic fish populations such as the cod (*Gadus morhua*), North Sea Plaice (*Pleuronectes platessa*), and Atlantic Salmon (*Salmo salar*). In the case of the northern cod, centuries of exploitation have led to its life history shifting towards maturation at earlier stages and smaller sizes in spite of environmental conditions favouring the opposite trend (Olsen *et al.*, 2005). In the case of Atlantic salmon, heavy angler exploitation of early runs in three Irish fisheries has shifted the peaks of catch progressively later in the season, which is outside the preferred angling season (Quinn *et al.*, 2007).

One example from Australia that may be explained by an evolutionary response to fishing is the Western Rock Lobster (*Panulirus cygnus*). The size at sexual maturity in this species has declined substantially in the past 35 years, and it has been argued that this may be at least partially a response to extremely high annual exploitation of adults (~75%), together with a minimum carapace length of 76mm in harvested animals (Melville-Smith and de Lestang, 2006; Allendorf *et al.*, 2008). One difficulty with this interpretation is that the change also coincided with increases in water temperatures over this period, which is expected to produce a similar pattern (Melville-Smith and de Lestang, 2006). Further work is required to establish the relative importance of phenotypic plasticity, environmental or fishery induced selection.

Local adaptation and identification of stocks

The Atlantic Cod (*Gadus morhua*) and European Flounder (*Platichthys flesus*) are examples of species where conventional DNA analysis with neutral microsatellite DNA markers detected almost no genetic differences among regions, but genes with known function (i.e. under natural selection) show strong spatial differences. For the cod, genetic differentiation at nine neutral microsatellite DNA markers was negligible (F_{st} = 0.003; see Appendix C for definition of F_{st}), but with the Pantrophysin gene (Pan I) substantial differentiation was observed (Fst = 0.261). The basis for this differentiation is that frequencies of Pan I genetic variants are affected by temperature, salinity, and depth (Ãrnason *et al.*, 2009). Similarly, in the European flounder genetic differentiation among regions was very low (Fst = 0.02), but the heatshock protein Hsc70 exhibited high levels of structure (Fst = 0.45). Further, analysis of gene expression profile provided strong evidence of differential expression in many genes (Larsen *et al.*, 2007). In these examples, the strongly differentiated DNA markers can be used to identify stocks that experience unique environmental conditions, and that retain genetic variants suited to those conditions. They can also be used as diagnostic markers for the provenance of individual fish (see genetic theme 4).

Monitoring evolutionary responses to climate change

At present no clear molecular evidence exists for the evolutionary effects of climate change on fishes (Nielsen *et al.*, 2009). As illustrated above, the Pantrophysin (Pan I) gene has been shown to vary spatially in the north-eastern Atlantic with sea surface temperature (Ãrnason *et al.*, 2009). However, an investigation that used historical otoliths to detect temporal change in the Pan I gene in response to changes in sea surface temperature showed that frequencies of different gene variants were stable over time (1928 - present) (Nielsen *et al.*, 2007).

None - but see 2010/521 FRDC-DCCEE: vulnerability of an iconic Australian finfish (barramundi, *Lates calcarifer*) and related industries to altered climate across tropical Australia.

Technical Challenges

Fishing-induced selection

Disentangling natural environmental effects and also phenotypic plasticity from fishing effects is difficult, and may require long-term datasets and experimental manipulation to resolve conclusively. However, precautionary management plans should still be developed that seek to ameliorate the evolutionary effects of fishing (Allendorf *et al.*, 2008).

Local adaptation and identification of stocks

Whilst there is a growing list of candidate genes with known links to environmental adaptation, in most cases the genetic basis for adaptation is complex, and involves multiple genes and regulatory mechanisms. Screening for genes under selection can be achieved in a variety of ways, including AFLPs, SNPs, RAD-tag next-generation sequencing, and microarray analysis together with outlier analysis (Allendorf *et al.*, 2010).

Monitoring evolutionary responses to climate change

Like fishing-induced selection and identifying local adaptation, making clear links between environmental parameters, selection, and adaptive change is technically very difficult and has rarely been achieved (Hansen *et al.*, 2012). Long-term temporal investigations of genomic change may be possible in many fisheries species because of archived otolith and scale samples (Nielsen *et al.*, 2009).

Barriers to uptake for fisheries management

Evolutionary processes have rarely been a consideration in the management of wild fisheries, and most are yet to adopt strategies that guard against evolutionary responses to exploitation. Yet, the evidence for selective effects of harvest is overwhelming (Allendorf *et al.*, 2008; Allendorf and Hard, 2009). A major challenge will be to make fisheries managers and scientists aware of the selective effects of fishing and their potential to impact on productivity. This may require greater emphasis on long-term planning than is common practice.

In light of the potential for evolutionary processes to reduce the productivity of fisheries, how can they be detected and how can they be ameliorated? Some key case studies have delivered compelling evidence for evolutionary responses to fishing through combinations of experimental manipulations and estimation of reaction norms (Olsen *et al.*, 2005), and provide practical guidelines for its detection. Similar approaches could be applied to detecting the effects of other environmental changes, such as climate change. In addition, the growing availability of genomic resources can provide direct access to genes selected for by fishing, thus providing a way to monitor changes by screening temporal or spatial collections. Measures to reduce the risk of evolutionary change in fisheries include: reducing the selectivity of fishing methods, and maintaining large populations that retain the full range of phenotypes for natural and sexual selection to act upon, either by setting appropriate quotas or by implementing no-take areas that retain unselected phenotypes. Reviews on this topic are provided by (Allendorf *et al.*, 2008; Allendorf and Hard, 2009; Hansen *et al.*, 2012).

Future

Virtually all research on the selective effects of harvest in fisheries, and on the effects of changing climate on adaptation in fish has been conducted in the northern hemisphere; hence there is greater awareness of the phenomenon in that region. Awareness is likely to increase in the southern hemisphere, but may require convincing demonstration in southern hemisphere fisheries. Understanding and identifying adaptive traits is likely to be of increasing importance for the genetic identification of fisheries stock structure, the selection of broodstock for re-stocking (see genetic theme 7), and for monitoring and

predicting the effects of climate change on fisheries species (Hansen *et al.*, 2012). Next-generation genomic sequencing tools will be a key resource for describing evolutionary processes in southern hemisphere marine and freshwater species. They will be most effective when used in combination with experimental manipulations and when applied to historical sample collections.

8.1.8 GENETIC THEME 7: GENETIC EFFECT OF CAPTIVE-BRED FISHES ON WILD CONSPECIFICS

How does it work and why is it important?

Reproduction in captivity inevitably leads to a difference between captive-bred fish and fish in the wild. Captive-bred fish accumulate genes for survival in captivity (Frankham, 2008). They also acquire genes for traits related to profitability (e.g. growth) as a result of selective breeding and genetic modification (i.e. transgenesis). When captive-bred offspring are produced for release in the wild quality assurance programs can minimise the adverse effect of natural selection (e.g. Rowland and Tully, 2004) by appropriate choice of broodstock from the wild and by husbandry procedures. However, genetic changes in offspring are inevitable and unpredictable.

Genetic leakage occurs when captive-bred individuals interbreed with wild conspecifics following accidental or deliberate release. The result is free-living individuals with admixed genomes; like hybrids, these individuals have a mixture of two genomes. Over subsequent generations, natural selection may remove admixed individuals if they have lower fitness and if they are common, their removal will have a large effect on population size and genetic diversity. Out of 70 studies, Araki and Schmid (2010) found 23 studies where captive-bred and wild stock differed in fitness, and 28 studies where levels of genetic variation were lower in captive populations. There were no studies where captive-bred individuals had a higher fitness in the wild.

Captive-bred animals have the opportunity to interbreed with wild conspecifics when they are purposely released (e.g. for re-stocking) or when they escape from aquaculture. If this occurs in open systems (characterised by high levels of genetic connectivity, such as inshore marine populations), the movement of liberated captive-bred animals is likely to be widespread and so is the potential for genetic leakage.

Inbreeding is another outcome of genetic leakage that occurs when captive bred animals are released into the range of conspecifics. Inbreeding has deleterious effects on reproduction and survival; for instance sperm production, mating ability, female fecundity, juvenile survival, age at sexual maturity and adult survival (Frankham *et al.*, 2002; Frankham, 2005). Inbreeding levels are often high in captive bred populations, because the genetic effective size (see genetic theme 2) of a captive population is substantially lowered by the selective use of a small number of brood stock as well as natural selection (Frankham, 2008). When large numbers of captive bred offspring that have a low N_e are released into the wild, the overall N_e of the admixed (i.e. native plus captive bred individuals) population is lowered increasing the possibility of inbreeding (Ryman and Laikre, 1991).

More research is occurring on genetic leakage and the risk it poses to wild fisheries in Europe (e.g. Danancher and Garcia-Vazquez, 2011) and North America than in Australia. Aquaculture is more extensive in the northern hemisphere and anthropogenic alteration to freshwater, estuarine and inshore fish habitats is more common as well, leading to a larger number of re-stocking programs.

How is it used for fisheries management?

Fisheries and conservation managers understand **genetic leakage is potentially detrimental to wild fisheries populations**. For example, the Western Australian Department of Fisheries web site discusses the impact of barramundi aquaculture on the biodiversity of native species. Australia's Biodiversity Conservation Strategy 2010-2030 (Natural Resource Management Ministerial Council, 2010) recognises genetic diversity as one of three types (genetic, species and ecosystem) to be conserved to ensure environmental health and resilience to threats.

Examples of aquaculture species in Australia that may escape and interbreed with wild populations include abalone, yellow-tail kingfish and barramundi.

Environmental impact statements and risk assessments are commonly undertaken before proceeding with re-stocking and aquaculture that could lead to genetic leakage.

If captive-bred animals are released purposely to re-stock a wild population, the groups must be matched closely. The failure of re-stocking programs for Pacific Salmon in north-western United States may have partly been due to the release of animals with genotypes that were poorly matched to their environment (Allendorf and Waples, 1996).

Availability and skill set required

To investigate cases of genetic leakage, population geneticists need to work with field biologists and fisheries scientists as well as fisheries managers (Table 1).

Case studies (Australian and International

The Eastern Freshwater Cod (*Maccullochella ikei*) is an endangered fish in the Clarence River system in northern New South Wales. It is culturally significant to local communities and a favoured recreational fishing target. Some populations have been augmented by the release of hatchery-reared fingerlings. The genetic effects could be assessed because tissue samples were collected before and after re-stocking. There was a significant loss in both genetic heterozygosity (21%) and number of alleles (24%) in the populations in the Mann and Nymboida Rivers since the commencement of re-stocking (Nock *et al.*, 2011). The majority of this was due to genetic swamping (where captive-bred outnumbered wild fish) rather than genetic leakage, because interbreeding was unlikely to have occurred. However, the decline in genetic diversity is an alert for future conservation actions involving release of captive-bred animals.

Micro-tagged barramundi were released in the Johnson River (North Queensland) and have been recorded from the commercial catch, showing survival. Research is underway to determine if they are reproducing in the wild (FRDC 2009/040).

Steelhead (ocean) trout are a strain of Rainbow Trout (*Oncorhynchus mykiss*) that feed in the oceans and return to freshwater each year to breed. Unlike Pacific salmon, they make several spawning trips between the sea and freshwater. They are highly desirable as food and sports fish. In North America, steelhead and Pacific salmon populations are enhanced by the release of five billion captive-bred juvenile fish per year. While these juveniles are meant for harvest, captive-bred fish do reproduce in the wild and interbreed with native fish. Araki *et al.* (Araki *et al.*, 2007; Araki and Schmid, 2010) studied the success of captive-bred fish when they reproduced in the wild compared to wild fish. They found that for each generation of captive rearing, the subsequent reproductive success in the wild was reduced by about 40%. The most plausible explanation was a reduction in survival in the wild. In other words, the captive-bred fish were genetically different to wild fish, and offspring of crossbred fish were less able to reproduce in the wild than offspring of wild parents. Given continual contributions from captive bred fish, the overall fitness of the wild population would progressively decrease. In the longer term, the population would become more and more reliant on enhancement to maintain adequate numbers.

FRDC Projects

- 2009/040 - Fish stocking programs - assessing the benefits against potential long term genetic and ecological impacts
- 2007/057 - Towards responsible fish stocking: Identifying management concerns and appropriate research methodologies
- 1994/005 - Feasibility of Enhancing Abalone Stocks by Larval Seeding.

Technical Challenges

Determining the extent of genetic leakage may require extensive resources in some cases. For example, Bourret *et al.* (2011) used a comprehensive set of genetic markers (112 SNP and eight microsatellite loci)

and historical samples collected from 1980 to 2005 to conclude that escapees from Atlantic Salmon farms in the Bay of Fundy (Canada) had interbred with wild salmon causing a loss of adaptation and decline in abundance in the wild population. However, it is relatively rare that declines in abundance of natural populations can be linked by research to genetic leakage rather than to the effect of other anthropogenic and ecological forces. Linking a population decline to genetic leakage beyond reasonable doubt would require expert experimental design and substantial resources.

There are no predictive tools to assess whether genetic leakage will occur, or to predict its effects. Past experience, however, would suggest that captive-bred fish become adapted to conditions in captivity; that these conditions are different from those in the wild; and that admixing of captive-bred fish with wild populations (whether accidental or intentional) can reduce the fitness of these admixed stocks.

Barriers to uptake for fisheries management

The major challenge for fisheries management is balancing the economic and social need for the process responsible for genetic leakage (i.e. re-stocking or aquaculture) against its potentially deleterious effects.

Risk analysis needs to be performed before genetic leakage occurs, as deleterious effects are difficult, or impossible, to undo. If the endemic breeding population is adversely affected by re-stocking, then the local resource may become dependent on re-stocking to maintain a 'fishable' population. Once re-stocking is underway, high public fisher and community support makes it politically difficult to stop, even if the adverse effects are thought to be repairable.

If re-stocking is considered to be socially or economically undesirable, management tools (e.g. reducing fishing effort on natural populations) or alternate strategies (e.g. habitat restoration) could be considered as alternatives.

Future

Genetic leakage is likely to increase in Australia. Many Australian state governments support and carry out re-stocking freshwater habitats. It has been proposed in New South Wales for inshore marine habitats. There has been a marine trial of re-stocking in Queensland (Butcher *et al.*, 2003) and seeding of marine scallop populations has occurred in Western Australia. The number of species in aquaculture in Australia is increasing, including Australian species cultured within their endemic range.

If appropriate genetic reference data were available from each farm, there is potential for genetic methods to be used to assign aquaculture escapees back to farms and for prosecution to be considered.

As genetic leakage leads to fish with admixed genomes it is possible (but unlikely) that admixed offspring could be favoured by natural selection instead of being selected against. Theoretically, these novel types could increase the likelihood of survival of a population when challenged with environmental change. This process requires further systematic study.

CSIRO has developed a molecular technology called 'sterile feral' that is designed to prevent a species grown in captivity having detrimental environmental effects if it escapes (Thresher *et al.*, 2009). Genetic engineering techniques are used to insert a set of genes into the genome of the target brood stock, which causes offspring to develop to maturity only in the presence of a substance available in captivity. This substance would not be available in the wild, and this would prevent the escapees from reproducing. Further research is needed to test its reliability.

8.1.9   GENETIC THEME 8: DNA AS A BIOMARKER FOR AGE

How does it work and why is it important?

Estimates of individual growth rates and age are an essential component of fisheries stock assessment. Growth estimates require the ages of individuals in days, months, or years. Biomarkers for age are important because some species are difficult and expensive to age using conventional methods. For example, the age of finfish can be estimated from rings in otoliths or scales. However, other harvested

marine taxa such as crustaceans and molluscs do not have otoliths or equivalent structures. There is considerable interest in the development of biomarkers to age these organisms.

DNA has potential as a biomarker for age because chromosomal DNA of some species has been found to decrease in length by a small amount at every cell division during the life of an animal. This is because of incomplete replication of full length DNA during cell division. The cell deals with this in several ways, including having expendable DNA at the end of chromosomes that can decrease in length without affecting chromosomal function. This telomeric DNA consists of a particular DNA sequence ('TTAGGG' in vertebrates) repeated thousands of times and interlaced with proteins. As well as buffering the chromosome against shortening, telomeres cap chromosome ends to prevent physical damage. In germ line cells, an enzyme called telomerase maintains telomeres at the same length, but it is generally not active in regular body cells.

The principle of using telomeres to estimate age is that if the rate at which telomeric DNA shortens is known, then the age of an individual can be estimated from its telomere length (age$_{DNA}$). If the method could be implemented using tissue samples obtained non-lethally, age could be estimated for species of high conservation importance or where only remotely-taken tissue is available (e.g. genetag hook tissue biopsies).

How is it used for fisheries management?

A DNA biomarker for age potentially allows growth to be estimated by comparing weight or size of a single sample of individuals from the fishery with their age$_{DNA}$. If a relationship could be established between age$_{DNA}$ and size or weight, or if instantaneous age structure could be estimated, this would be immediately useful for fisheries stock assessment.

Availability and skill set required

This type of research would require collaboration with molecular geneticists and fisheries scientists and managers. Statistical assistance is also necessary. Bioinformatics skill would be required if genomic resources were utilised (Table 1).

Case studies (Australian and International)

In Australia, there are several groups interested in DNA as a biomarker for age with variable results. One study, in particular, showed considerable potential. In abalone from Tasmania, there was an inverse relationship between telomere length and shell size (r^2= 0.833, P < 0.001) (Ovenden and Godwin, 2011; Godwin *et al.*, In preparation). The average coefficient of variation between experimental replicates was low (9%). The full potential of the method for age estimation in wild-harvested abalone requires development beyond this pilot study. A weak correlation between age and telomere length was detected in another mollusc species, Sydney rock oysters (Godwin *et al.*, 2012). However, a relationship between telomere length and body size was unable to be demonstrated in five Australian commercial crustacean species (Godwin *et al.*, 2011). Two confounding issues were identified for crustaceans; extracted genomic DNA degraded during storage in the laboratory (mimicking the effect of telomere attrition) and telomeres in these species were long making them difficult to analyse in the laboratory. There have been two studies on the relationship between telomere length and age in pinnipeds. A study on harp seals showed no correlation between age as estimated from counts of growth layers in teeth and telomere lengths (Lydersen *et al.*, 2010). However, Australian sea lions adults could be distinguished from pups and juveniles on the basis of their telomere lengths (Izzo *et al.*, 2011).

In the first application of DNA as a biomarker for age in wild animals, Pauli *et al.* (2011) described a method to estimate the age-class of a species of small mammals. They combined telomere length measurements with other biological parameters in a Bayesian network. Martens are small predatory mammals that are trapped in North America for fur production, so large numbers of tissue samples were available across a wide geographical range. They can be reliably aged with dental techniques and have a maximum life span of 13 years. Depending on what type of extra biological data was available (e.g. body size, sex), the telomere length had a 75-88% accuracy in assigning animals to either juvenile (<1 year) or adult (> 1 year)

ranging up to a 90-93% accuracy for assignment to five discrete age classes (0, 1, 2, 3 or 4+). Telomere length alone was a poor predictor of age.

FRDC Projects

- 2007/033 - Development of a DNA based aging technique for use in fisheries assessments.

Technical Challenges

It took nine years for the proposal of Haussmann and Vleck (2002) about the use of telomeric DNA as a biomarker for age to be demonstrated in a naturally occurring animal population. The key to the success of Pauli *et al.* (2011) was combining predictions of age$_{DNA}$ with relevant biological measurements on their target small mammal species in a Bayesian network model. Accuracy of age$_{DNA}$ was significantly higher when population density, gender and species identity were included. Pauli *et al.* (2011) argued that population density was important because it integrated a number of physiological characteristics that influence the rate of telomeric DNA attrition, such as overall habitat quality (animals in poor habitat had higher rates of DNA attrition) and density-dependent effects such as age-structure (martens in good habitat have more offspring). Although males and females had similar telomere lengths, gender improved the predictive model possibly because female martens are the sole caregivers that increased their nutritional and physiological demands.

Covariance of telomere length with factors other than chronological age has been emphasised in reviews by Monaghan (2010) and Dunshea *et al.* (2011). Telomere length appears to measure cumulative biological stress (e.g. physiological stress, chronic disease and body condition), which (if known) may be important for managing exploitation of a wild fishery. For example, shellfish such as abalone or scallops on the verge of senescence as predicted by telomeric DNA may be given a higher priority for harvest.

More specific technical challenges face the development of this theme for fisheries science. The fisheries species where age and growth information is most needed also tend to be those that are not (or cannot be) kept or grown in captivity. These species also may not have hard parts that can be sectioned for ring counting as an alternative method of estimating age. For these species (e.g. spanner crabs), it is challenging to determine the rate of telomeric DNA attrition with age, because there are no animals for which age is known. Solutions may include using the rate of DNA attrition for closely related or similar species, or studying the attrition rate in marked animals from which regular tissue samples are taken non-lethally.

The cost and efficiency of assaying individuals for telomere length is another significant challenge. In a recent FRDC-funded study, the cost per animal was $37 using the Southern blotting method in September 2010 (Ovenden and Godwin, 2011). The recent successful study of Pauli *et al.* (2011) used PCR instead of blotting technology, which may be more cost effective. The increasing availability of genomic resources for non-model species may assist with developing PCR protocols.

Barriers to uptake for fisheries management

The main barrier to uptake is that not enough is known about DNA as a biomarker for age in fisheries species. There are many challenges to its potential use in fisheries management. These include the need to model the effect of error in growth determinations from age$_{DNA}$, the start-up costs that would apply to each new species and the ability to use fine-scale spatial information on variation in growth in conventional stock assessment modelling.

Future

While telomeric DNA shows promise as a biomarker for age, there are other molecular methods that may be worth exploring. Transcriptional profiling (TP) of electron transport genes showed an age-related decline in expression in humans, mice, flies and worms (Zahn *et al.*, 2006). This method measures the level of gene expression in a pathway that is essential to cell survival. Using this method based on eight genes in mosquitoes, 87% of the variance in gene expression was explained by age (Cook *et al.*, 2006; 2007). The other biomarker for age may be age-related changes to the degree of DNA methylation in non-expressed genes. Methylation is a chemical change to the cytosine (C) nucleotide in DNA that occurs during the

lifespan of an individual. Among fisheries species, there has been no developmental work on biomarkers for age, other than telomeric DNA. So, the potential of transcriptional profiling and methylation for fisheries species, although promising, remains to be assessed.

There has been much speculation about the occurrence of telomeric sequence within, as well as at the ends of chromosomes, which could interfere with its usefulness as an age biomarker. The nature of DNA sequence upstream from telomeric DNA would be invaluable for designing PCR assays for telomere length. Genomic information would provide information on how telomeres vary between chromosomes. However, fisheries species represent a large number of diverse taxa and we predict that genomic resources will be available for only 50% of these within ten years.

8.1.10 GENETIC THEME 9: GENETICS FOR DISEASE DETECTION IN WILD FISHERIES

How does it work and why is it important?

Genetic analysis is widely used to diagnose and monitor diseases in wild fisheries populations and the environment. In this theme, the genetic tools do not target the fisheries species, but the organisms that cause disease. Many FRDC projects in this genetic theme have been funded under the Aquatic Animal Health Subprogram.

The diseases studied in Australia are linked to growth in captivity (e.g. abalone aquaculture), importation of food for aquaculture, or they are not linked to human activity, but appear to be a natural phenomenon (e.g. Queensland grouper). The diseases may be endemic or introduced.

Genetic tools are used because they can be highly sensitive and specific to diseases and have the potential to quantify the abundance of disease organisms. Non-genetic tests (e.g. immunological) are also used. Both types of tests are used for diagnosis and monitoring. Genetic tests are readily developed from genomic information of the disease organism (e.g. Corbeil *et al.*, 2010).

How is it used for fisheries management?

Management agencies use genetic tools to diagnose and then take action following a disease outbreak. For example, if genetic test were available to determine the presence of the disease it could be deployed for surveillance. A disease could be caused by an organism unknown to science, in which case it would be necessary to isolate and identify the disease, using a range of tools which would include DNA analyses (see genetic theme 5). Once this was completed, a diagnostic test could be developed.

Management action following the detection of a disease would be considered if it was likely to reduce population size, cause adverse health outcomes in consumers (e.g. humans, aquaculture stock), or spread through the environment Appropriate management actions would include a reduction in permitted harvest, closure of the affected fishery or exclusion of fishing activity in an affected area. Ongoing monitoring with genetic methods would trigger modifications to these and other management actions if the status of the disease altered.

Availability and skill set required

A qualified molecular geneticist with experience in disease analyses would be required to do this work along with fisheries biologists and managers. Capability in handling environmental biosecurity issues on a local and broader scale would be essential, including appropriate laboratory facilities and experienced personnel. Diagnostic laboratories require highly stringent quarantine conditions and generally will conduct analysis under accredited laboratory protocols. Initial isolation and identification of disease vectors is a highly specialised task relying on a range of methods, some of which include genetic analyses. Accredited laboratories in Australia include the CSIRO AAHL Australian Fish Diseases Laboratory (http://www.csiro.au/services/AAHL-fish-diseases-laboratory.html). For ongoing monitoring, high throughput, rapid turnaround analysis would be important.

Case studies (Australian and International)

In late 2005 and during 2006, a disease was detected in abalone (*Haliotis laevigata x H. rubra*) farms in western Victoria. It was identified as a herpes-like virus by electron microscopy and is now referred to as abalone viral ganglioneuritis (AVG). The disease became common in wild populations of both abalone species along the Victorian coastline, causing high mortality. It has been detected in two processing facilities in Tasmania and in wild Tasmanian populations. A quantitative PCR 'Taq-man" assay was developed by Corbeil *et al.* (2010) and a group led by the Australian Animal Health Laboratory (CSIRO Livestock Industries, Geelong, Victoria). The assay is being used to confirm that individuals with symptoms have the disease and for surveillance of wild and farmed populations throughout Australia.

Genetic tools can also be used to detect parasites as well as viruses and bacteria. The myxozoans are a large group of economically important, microscopic parasites of fishes. One species (*M. cerebralis*) causes whirling disease in Rainbow Trout, which is not necessarily fatal, but severely reduces survival. Another parasite of this group (*Kudoa thyrsites*) causes unsightly white cysts and soft texture of Atlantic salmon flesh. It lowers market value but seldom causes death of the salmon. Another extensively farmed species in North America, Gilthead Sea Bream (*Sparus uruta*), experiences infections of three species of myxozoans causing histopathological damage and mortality. The detection and diagnosis of these infections was hampered by the complex life cycle of the parasites across hosts and the movement within hosts from invasion sites to target tissues. DNA-based assays were developed from 18S rDNA sequences. These assays can detect all life-stages of the parasite and were essential to understanding the life-history and pathology of the disease. Non-lethal tests have been developed so that samples can be collected from valuable individuals (e.g. brood stock) using intestinal swabs. Fish health laboratories routinely use these tests for diagnostic studies (Kent *et al.*, 2001).

FRDC Projects

- 2001/630 - Aquatic Animal Health Subprogram: validation of DNA-based (PCR) diagnostic tests suitable for use in surveillance programs for marteiliosis of rock oysters in Australia
- 2007/006 - Aquatic Animal Health Subprogram: Development of molecular diagnostic procedures for the detection and identification of herpes-like virus of abalone (*Haliotis spp.*)
- 2007/007 - Aquatic Animal Health Subprogram: Optimisation of PCR tests for diagnosis of megalocytivirus (*Gourami iridovirus*) and cyprinid herpesvirus 2 (goldfish herpesvirus)
- 2007/225 - Metazoan parasite survey of selected macro-inshore fish of south-eastern Australia, including species of commercial importance
- 2008/030 - Aquatic Animal Health Subprogram: Development of a DNA microarray to identify markers of disease in pearl oysters (*Pinctada maxima*) and to assess overall oyster health
- 2008/031 - Aquatic Animal Health Subprogram: Investigation of Chlamydiales-like organisms in pearl oysters, *Pinctada maxima*.
- 2008/041 - Aquatic Animal Health Subprogram: Tools for investigation of the nodavirus carrier state in marine, euryhaline and freshwater fish and control of NNV through integrated management
- 2009/032 - Aquatic Animal Health Subprogram: Characterisation of abalone herpes-like virus infections in abalone
- 2010/034 - Aquatic Animal Health Subprogram: Investigation of an emerging bacterial disease in wild Queensland gropers, marine fish and stingrays with production of diagnostic tools to reduce the spread of disease to other states of Australia.

Technical Challenges

The technical challenges of using genetic tools for disease detection in wild fisheries are largely the same as non-genetic tests, which are common to all epidemiological studies on naturally occurring populations. It is difficult to effectively monitor large areas for disease outbreaks, particularly when the occurrence of the disease may be sporadic, spatially confined and at low levels. Procedures for dealing with Type 1 (false negative) and type 2 (false positive) errors must be developed and implemented. New genetic tests must be developed, evaluated and tested if organisms are novel.

Barriers to uptake for fisheries management

When technical challenges are met, managers need to evaluate alternative strategies to control and contain the disease. This includes determining when to take action; for example, at the outset, or when a testing routine is established and results are validated. There is little general monitoring for diseases in wild fisheries in Australia and no general strategy to follow when they are detected.

Future

The need for management of diseases in wild fisheries populations may increase in Australia. More Australian species will be grown in captivity, where conditions can favour build-up of disease organisms despite best-practice husbandry procedures. Escapees into the natural range of the species are an ideal mechanism for the spread of disease into the wild.

Natural systems are susceptible to environmental change, which could increase disease prevalence. In September and October 2011, fisheries authorities closed Gladstone Harbour in central Queensland to commercial and recreational fishing due to the occurrence of red-spot disease, lesions and parasitic flatworms in many species. Investigations are ongoing and the cause has not been determined.

8.1.11 GENETIC THEME 10: MIXED STOCK ANALYSIS USING GENETICS

How does it work and why is it important?

Mixed stock analysis (MSA) determines the relative contribution of one or more recognised stocks to a fishery. Stocks, representing breeding populations, may be located away from the fishery, are presumably genetically stable from year-to-year and may be composed of individuals that return each year to breed. The classic example of species with this type of life-history are the Atlantic and Pacific Salmon (*Salmo salar* and *Oncorhynchus* spp. respectively). MSA proceeds by first obtaining the genetic characteristics of the fishery, then comparing those characteristics to reference genetic samples from source stocks. Through use of statistical mixture modelling techniques scientists can determine for example, that a fishery consists of 80% from stock A and 20% from stock B.

Mixed stock analysis has similarities with other themes. In product provenance (genetic theme 4), individuals are identified as recaptures or assigned to families, populations or species. This is a similar approach to mixed stock analysis, but on the scale of individuals not populations. Mixed stock analysis can also be used to determine the recruitment and breeding success of hatchery-derived individuals following re-stocking (Genetic effective of captive-bred fishes on wild conspecifics, genetic theme 8).

Mixed stock analysis requires the genetic characterisation of the breeding populations and it is essential that they are genetically distinct. Chemical composition of otoliths is also used to characterise breeding populations (e.g. Thorisson *et al.*, 2011) often in combination with genetic data. The choice of how to characterise the breeding population depends on which data types provide the greatest contrast.

How is it used for fisheries management?

Mixed stock analysis is relevant to species that breed in one location and move to another location to feed, and where exploitation occurs in the feeding phase. It allows management of the feeding population to protect breeding populations. Mixed stock analysis is widely used in North America for the management of the coastal populations of Pacific salmon and in Europe for salmonid and cod species. This method is not currently used in Australia, because of a lack of knowledge of the life-history of local species. It may be needed in the future, however for species such as shark and billfish.

Availability and skill set required

To implement mixed stock analyses, a team would need to consist of field biologists, fisheries scientists, population geneticists and fisheries managers. Involvement of a statistician would be desirable for advanced data evaluation (Table 1).

Case studies (Australian and International)

Mixed stock analysis is extensively used in the northern hemisphere with salmonid species, but this does not help to illuminate the typical Australian situation. In the absence of the application of this methodology in Australia, we have chosen an example of mixed stock analysis of Atlantic Cod (*Gadus morhua*), whose life history is fully marine.

Ruzzante and colleagues (2000) used six microsatellite loci to genotype cod sampled from spawning grounds in spring and summer on the western Atlantic coast of Canada. Several genetically distinct, temporally stable spawning stocks were identified within and around the mouth of the Gulf of St Lawrence within a range of approximately 600 km. Cod sampled from the fishing ground in winter were found to represent fish from the various spawning stocks. Contributions from the spawning stocks to the fishing ground varied from 8% (from south-central Newfoundland) to 71% (from northern Gulf of St Lawrence).

The northwest Atlantic cod stock is around 1% of 1977 abundance and exploitation has ceased. But, if fishing was reopened, the mixed stock analysis would predict that the northern Gulf spawning stock would be significantly impacted while other spawning stocks would be less affected. There would be scope to adjust the levels of exploitation to conserve various spawning stocks. Beyond that, the study demonstrated that the cod spawning stock consists of several genetically distinct populations that would have benefited from separate management arrangements (genetic theme 1: Genetic analysis for the identification of fisheries stock structure).

FRDC Projects

It has not been implemented in Australia.

Technical Challenges

The implementation of mixed stock analysis is not technically challenging, but it is resource-intensive. Standard statistical methods (e.g. maximum likelihood) are used to estimate proportions of breeding stocks during the aggregation (or feeding) phase. If the composition of the aggregated stock is expected to change with time, then samples would need to be genotyped in real-time and the results provided in a timely fashion for management decisions.

Barriers to uptake for fisheries management

Mixed stock analysis (MSA) is widely used outside Australia. **If MSA were ever needed here, there would be a strong precedence for its uptake by fisheries managers in Australia.** If the composition of the fished population was changing through time and management decisions needed to be made rapidly, this would be challenging for management. It would have considerable flow-on effects for fishing effort and enforcement on a fine-spatial scale.

Future

There are few harvested species in Australia with separate breeding and feeding ranges. As elsewhere in the world, some species of sharks in Australia appear to return to certain locations to mate and give birth (e.g. bull sharks in northern Australia, Tillett *et al.*, In press) (e.g. white sharks in southern Australia, Blower *et al.*, In press), which implies that removing individuals from non-breeding locations may deplete breeding populations. Some other Australian commercial fisheries species have life-histories encompassing freshwater, estuarine and marine habitats (e.g. *Mugil cephalus, Lutjanus argentimaculatus, Scylla serrata*) that may potentially require mixed stock analysis if habitat partitioning was demonstrated between breeding and feeding phases. Tropical Rock Lobster (*Panulirus ornatus*) undergo a breeding migration from the Torres Strait and northern Great Barrier Reef towards the Gulf of Papua (Dennis *et al.*, 2001), but only one breeding stock has been identified.

8.1.12 GENETIC THEME 11: GENETICS FOR ENVIRONMENTAL MONITORING AND FOOD-WEB ANALYSIS

How does it work and why is it important?

As fisheries increasingly adopt the principles of ecosystem-based management, tools to monitor the interactions between fisheries and the environment are more in demand. However, these interactions are diverse, complex, hard to observe, and therefore difficult to accurately characterise. This section profiles several emerging applications of genetic analyses that can be loosely grouped under an environmental monitoring heading, and which have the potential to provide high resolution understandings of ecological processes in marine and aquatic environments. The first application summarised here is food web analysis, the second is the detection of invasive species, and the third is monitoring of environmental quality through ecotoxicogenomics.

How is it used for fisheries management?

Food-webs

The direct effects of fishing on the abundance of target species are well known, but fishing may also have undesirable indirect effects on ecosystem function. Where fisheries selectively harvest species, there is the potential to alter flows of energy through ecosystems and to induce cascades of ecological change. Importantly, such changes may be irreversible if new stable community equilibria are reached. Well-known examples are the creation of urchin barrens in south-eastern Tasmania by heavy fishing of benthic predators (Ling *et al.*, 2009), and the increase of benthic invertebrates such as snow crab that has coincided with the crashes of cod stocks in Nova Scotia (Frank *et al.*, 2005).

Detecting such changes, or pre-emptively determining the likely indirect consequences of fishing through the implementation of ecosystem models (e.g. Atlantis;Fulton *et al.*, 2011) requires an understanding of foodwebs. Foodwebs map out networks of predator-prey relationships amongst ecosystem components, and because of the complexity and diversity of marine foodwebs they are difficult to generate. DNA analyses have attributes that make them well-suited to foodweb analysis, providing much greater taxonomic resolution and capacity for high-throughput than conventional methods based on morphological analysis of stomach contents or on isotopic signatures. They also are less reliant on expert taxonomic knowledge and can resolve diets even when no morphological features are evident.

DNA-based foodweb analysis is a specialised example of DNA barcoding as described in genetic theme 5. It may be applied to environmental samples, such as plankton, or to gut content samples. Typically it involves extracting DNA from the environmental or faecal samples and obtaining diagnostic DNA sequences from a partial or complete assemblage of the items contained in that sample. For dietary studies such analysis historically was restricted to simple diets and small numbers of samples. For investigations of the dynamics of phyto or zooplankton, the analysis typically involves intensive microscopy. The time required for microscopic sorting of dietary or environmental samples can be extensive. The development of next-generation DNA sequencing technologies together with large databases of reference sequences now provide opportunities to rapidly and exhaustively sample complex diets or environmental assemblages from hundreds of samples.

Detecting invasive species

Early detection of invasive species provides the best opportunity to contain or eradicate them. However, invasive species may be rare and cryptic during this phase making them difficult and expensive to detect via conventional trapping or observational techniques. This is particularly true in aquatic environments. The high sensitivity of the polymerase chain reaction (PCR) to minute quantities of DNA shed by organisms into the environment means that in certain situations DNA analyses can provide a rapid, accurate and easily deployed means to detect invasive species. Environmental DNA (eDNA) testing typically involves extracting mass DNA from water samples and applying specific tests developed for target species to those samples. The same approach is equally applicable to the detection of rare or cryptic native species.

Ecotoxicogenomics

Because fish can be readily captured and identified, they potentially provide useful indicators of environmental quality. Conventional approaches to this analysis typically assay tissues for the presence of toxins that accumulate over time. More recently, it has been shown that fish exposed to toxins exhibit characteristic gene expression profiles in genes associated with detoxification metabolic pathways. Gene expression analysis potentially provides a rapid approach to detecting the impacts of environmental pollutants in aquatic and marine environments that could supplement existing methods.

Availability and skill set required

This assemblage of approaches requires experienced geneticists, field biologists, fisheries scientists and managers as well as taxonomists (Table 1).

Case studies (Australian and International)

Food-webs

Deagle *et al.* (2009) provide a compelling demonstration of the power of next-generation DNA sequencing to reveal the diet of an important marine predator in great detail. Analysis of faecal samples from Australian fur seals provided over 20,000 DNA sequences that distinguished over 60 prey species. The diet diversity was very similar to one determined from morphological analysis over a period of three years. However, the diet resolved through DNA analysis was more detailed than the morphological analysis and enabled the identification of soft-bodied or cartilaginous species that conventional analyses could not identify. Another encouraging aspect of this analysis was that it provided information on the relative contributions of prey species to the diet. Other examples of DNA-based dietary analysis in Australian marine species include the arrow squid (Braley *et al.*), the seven-gill shark (Barnett *et al.*, 2010) and the little penguin (Deagle *et al.*, 2010). Numerous "eco-genomic" or "meta-genomic" studies that characterise entire organismal communities have been carried out on plankton in the northern hemisphere (Creer *et al.*; Fonseca *et al.*).

Detecting invasive species

eDNA has been effectively used to delimit the range of two species of invasive carp in a large river and canal complex in the north-east USA (Jerde *et al.*, 2011). These species (silver and bighead carp) have impacted fisheries and environmental quality in this region and their ranges continue to expand. eDNA testing detected both species ahead of the expected invasion front. In comparison to the conventional method of detecting carp via electrofishing, eDNA had a consistently higher catch per unit effort, and detected carp in locations up to eight months before they were detected via conventional means. Many examples of eDNA analysis have been applied to ballast water for the detection of planktonic stages of economically important invasive species. Australian examples include the invasive gastropod *Maoricolpus roseus* (Gunasekera *et al.*, 2005), and the Pacific Oyster *Crassostrea gigas* (Patil *et al.*, 2005). Another application that is relevant to wild and cultured fisheries management is the detection of toxic algal blooms before they become widespread and result in fish kills or closures of fisheries (Baxa *et al.*, 2010).

Ecotoxicogenomics

The Fathead Minnow (*Pimephales promelas*) is widely used as a model for ecotoxicological surveillance in the USA. Assays based on quantitative PCR (qPCR) have been developed that detect gene expression changes in this species when it is impacted by environmental contaminants (Gust *et al.*, 2010). Similar tests have been developed for the Delta Smelt (*Hypomesus transpacificus*) that detect the deleterious impacts of copper exposure.

FRDC Projects

- Food-webs: 2004/013 - Towards integrated multi-species management of Australia's SE reef fisheries.
- eDNA: 2011/016 - Location and transport of early life stages of Dhufish (*Glaucosoma hebraicum*).

- Ecotoxicogenomics: None

Technical Challenges

Food-webs

Next-generation DNA sequencing has a relatively heavy bioinformatics emphasis, and may require collaboration between molecular scientists and bioinformaticians. Appropriate reference DNA sequences may not be available for many dietary items or plankton species, particularly for species collected in unexplored deep-water environments.

eDNA

These methods are highly sensitive to low concentrations of DNA. Therefore, precautions need to be taken to avoid sample cross-contamination. Generally, these methods are best suited to well-defined water bodies such coastal embayments and man-made structures where the probability of encountering diagnostic DNA molecules is higher than in open systems. Nevertheless, qPCR methodologies are well-suited to establishing detection sensitivities that can permit *a priori* estimation of whether an assay is likely to be effective in a particular setting. An important aspect of developing diagnostic tests for invasive species is the extensive testing for species-specificity that is required before tests are deployed in the field.

Ecotoxicogenomics

These analyses are reliant on an understanding of the molecular pathways involved in detoxification of pollutants. Candidate genes will be known for most organisms used as model species.

Barriers to uptake for fisheries management

Food-webs

DNA-based foodweb analysis provides information upon which ecosystem-based management decisions can be made. The high taxonomic and temporal resolution provided by these methods enables highly complex ecosystem models to be constructed. The demand for this level of complexity will vary according to the purpose of the ecosystem model under consideration. Nevertheless, taxonomic, spatial and temporal resolution can be improved by pooling data.

eDNA

This is an enabling technology that may lead to more accurate and cost-effective surveillance for both invasive and non-invasive aquatic and marine species than existing methods. Aside from investment in development of novel diagnostic tests, there should be few barriers to its uptake by fisheries or environmental managers.

Ecotoxicogenomics

The applications of this technology are likely to largely be in an aquaculture setting, or to supplement existing ecotoxicological analysis rather than in wild fisheries.

Future

Both food-web and environmental DNA analysis are likely to receive increasing attention for the management of wild fisheries. The high taxonomic resolution of DNA-based food-web analysis, together with the potential for generating quasi-quantitative data will enable longitudinal studies of change in foodweb structure. Highly detailed dietary data will become indispensable for the parameterisation of ecosystem models such as Ecopath and Atlantis (Pauly *et al.*, 2000; Fulton *et al.*, 2011). Next generation sequencing technology will be an essential tool, as will quantitative PCR, which can be utilised in the field for near real-time results. The costs associated with generating dietary profiles are likely to diminish significantly. Standardisation of PCR primer sets and laboratory protocols will be required if quantitative comparisons in space and time are to be made.

Elsewhere in this report, the eleven genetic themes are matched to current issues in fisheries management (Section 8.5). The list of current management issues was compiled as part of this project (Section 8.3.4). High-level issues across genetic themes that are important to strengthening the role of genetics in fisheries management are outlined and evaluated in the overall discussion (Section 8.6).

8.2   Nature and location of key research groups

There are at least 24 scientists conducting genetic research on naturally occurring fisheries species in Australia (Table 2). Some of these also work with captive aquatic species. Both university and government sectors (state and Commonwealth government) are represented. The listed researchers are based in all states and territories, except Northern Territory and the Australian Capital Territory.

This list is not exhaustive, but is presented as an example of the distribution and abundance of fisheries geneticists around Australia. These geneticists work with a much broader group of scientists, industry and managers. It was compiled in February 2012.

Table 2. Some Australian geneticists working with wild fisheries populations.

NAME	RESEARCH GROUP	TYPE OF INSTITUTION	UNIVERSITY NAME OR NAME OF EMPLOYER, CITY	STATE
Adam Stow	Department of Biological Sciences	University	Macquarie, Sydney	New South Wales
David Roberts	School of Biological Sciences	University	Wollongong, Wollongong	New South Wales
Cathy Nock	Plant Science	University	Southern Cross, Lismore	New South Wales
Lynne van Herwerden	School of Marine and Tropical Biology	University	James Cook, Townsville	Queensland
Cynthia Riginos	School of Biological Sciences	University	Queensland, Brisbane	Queensland
Jane Hughes	Molecular Ecology Laboratory	University	Griffith, Brisbane	Queensland
Dean Jerry	School of Marine and Tropical Biology	University	James Cook, Townsville	Queensland
Luciano Beheregaray	Molecular Ecology Laboratory	University	Flinders, Adelaide	South Australia
Chris Burridge	School of Zoology	University	Tasmania, Hobart	Tasmania
Karen Miller	Institute for Marine and Antarctic Studies	University	Tasmania, Hobart	Tasmania
Jennie Chaplin	School of Biological Sciences and Biotechnology	University	Murdoch, Perth	Western Australia
Jason Kennington	School of Animal Biology	University	Western Australia, Perth	Western Australia
Meagan Rourke	Aquatic Ecosystems	Government	Primary Industries	New South Wales
Steve Donnellan	Evolutionary Biology Unit	Government	South Australian Museum, Adelaide	Queensland
Jenny Ovenden	Molecular Fisheries Laboratory	Government	Department of Employment, Economic Development and Innovation, Brisbane	Queensland
Simon Goldsworthy	Pelagic Ecology	Government	South Australian Research and Development Institute, Adelaide	South Australia

NAME	RESEARCH GROUP	TYPE OF INSTITUTION	UNIVERSITY NAME OR NAME OF EMPLOYER, CITY	STATE
Mark Adams	Evolutionary Biology Unit	Government	South Australian Museum, Adelaide	South Australia
Simon Jarman	Science	Government	Antarctic Division, Hobart	Tasmania
Brett Ingram	Fisheries and Aquaculture	Government	Department of Primary Industries	Victoria
Peter Grewe	Marine and Atmospheric Research	CSIRO	CSIRO, Hobart	Tasmania
Phillip England	Marine and Atmospheric Research	CSIRO	CSIRO, Hobart	Tasmania
Robert Ward	Marine and Atmospheric Research	CSIRO	CSIRO, Hobart	Tasmania
Sharon Appleyard	Marine and Atmospheric Research	CSIRO	CSIRO, Hobart	Tasmania
Oliver Berry	Marine and Atmospheric Research	CSIRO	CSIRO, Perth	Western Australia

8.3 Interviews with stakeholders about the use of genetics in fisheries management

8.3.1 INTERVIEW RESULTS

A total of 88 stakeholders were interviewed with 63 of those from within Australia and 25 international (Table 3).

Table 3. Summary of the numbers of different stakeholder groups interviewed by each Australian jurisdiction and internationally. Industry representatives were not allocated to a jurisdiction as most of them overlapped two or more. Fisheries managers includes managers and policy makers as these often overlapped.

REGION	JURISDICTION	GENETICISTS	FISHERIES SCIENTISTS	FISHERIES MANAGERS	INDUSTRY	TOTAL
Australia	Tas	5	4	2		
	Vic	0	1	2		
	NSW	2	1	2		
	Qld	3	2	6		
	NT	0	1	2		
	WA	1	1	4		
	SA	3	1	3		
	C'wealth	0	3	2		
	Totals:	14	14	23	12	63
International		12	12	1	0	25
Totals:		26	26	24	12	88

Awareness and use of genetic tools and applications

The first interview question sought to ask fisheries managers, fisheries scientists and industry representatives about their awareness of the different genetic tools available. The question firstly asked specifically about the use of genetics in elucidating the spatial structure of stocks based on the assumption that this area of fisheries genetics application is the most widely known. The results therefore indicate that 100% of interviewees are familiar with the use of genetics in analysis of spatial stock structure. The second part of the question was open-ended in asking about knowledge of any other genetic methods and applications known. Although interviewees were given time to respond to these questions, the full extent of an individual's knowledge of genetics in fisheries was unlikely to be captured. However, across the full sample of interviewees the general patterns in knowledge is assumed to be accurate. In interviews with geneticists they were asked only about which genetic tools they worked with. The responses from interviewees were grouped using the 11 genetic themes presented in the literature review (Section 8.1).

Interviewee responses

Most genetic research themes were recognised or practised by fewer than half of interviewees in all stakeholder groups, both nationally and internationally. Within Australia in particular, examples of the application of genetic information in fisheries management were lacking and were mainly confined to only two themes: *Identification of Stock Structure* and *Effect of Captive-Bred Fishes on Wild Populations*.

Geneticists

Of the genetic tools used by geneticists (by genetic theme) the identification of spatial stock structure was the most common both within Australia and internationally (Figure 3). Genetic tools covering most of the genetic themes were relatively commonly used; however, disease detection was not being used by any of the geneticists interviewed. Notably mixed stock analysis techniques are commonly used overseas but not in Australia. This is likely to be heavily influenced by salmonids which are endemic to the northern hemisphere. They exhibit the life history characteristics for which mixed stock analysis is designed. That is, each population is strongly linked to a particular river system, each with a distinguishing genetic signature, and adult fish return to these rivers of origin for spawning. Many stocks of some species randomly mix during the intermediate marine phase of their life cycle. Further, these species tend to be data-rich, as a consequence of their economic importance. Use of tools under the themes *DNA as a biomarker for age* and *Environmental monitoring and food webs*, although not commonly used, were only used in Australia (Figure 3).
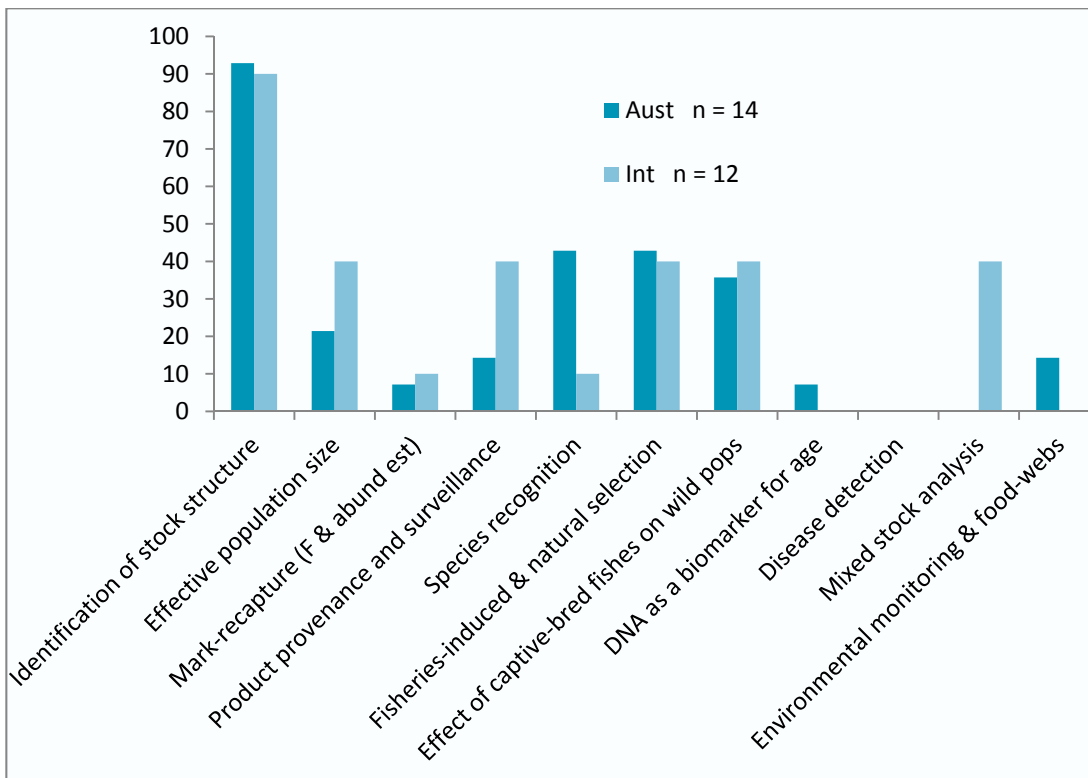
Figure 3. Genetic tools employed by Australian (Aust) and international (Int) geneticists grouped by genetic themes. Frequencies are expressed as a percentage of the total interview sample for Australian and international interviews with geneticists.

Fisheries Scientists

The awareness by fisheries scientists of the breadth of genetic tools available was generally moderate to poor, both nationally and internationally (Figure 4). The tools recognised reflected those most commonly used by geneticists, although many scientists mentioned less frequently used (and perhaps less developed) techniques such as *Mark-Recapture* and *DNA as a Biomarker for Age*. This may reflect the novelty and potential in these relatively new areas of genetic research for fisheries.
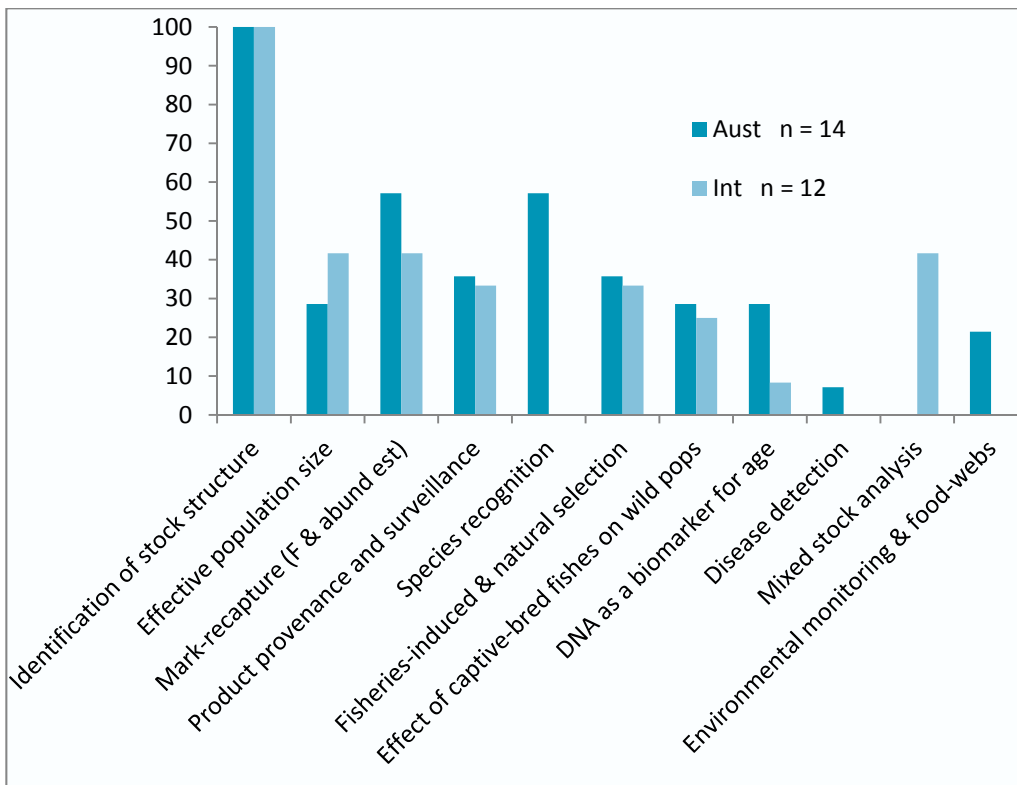
Figure 4. The awareness of genetic tools (grouped by genetic themes) by Australian and international fisheries scientists. Frequencies are expressed as a percentage of the total interview sample for Australian and international interviews with fisheries scientists.

Fisheries Managers

Australian fisheries managers were generally aware of genetic tools for fisheries applications but few were familiar with a large number (Figure 5). Due to stock enhancement efforts and genetic research to 'domesticate' different species in captive-bred situations in many parts of Australia, awareness of the *Effect of Captive-Bred Fishes on Wild Populations* theme was relatively high. The next highest ranked theme was *Mark-Recapture,* which was mentioned by approximately 1 in 3 managers interviewed.
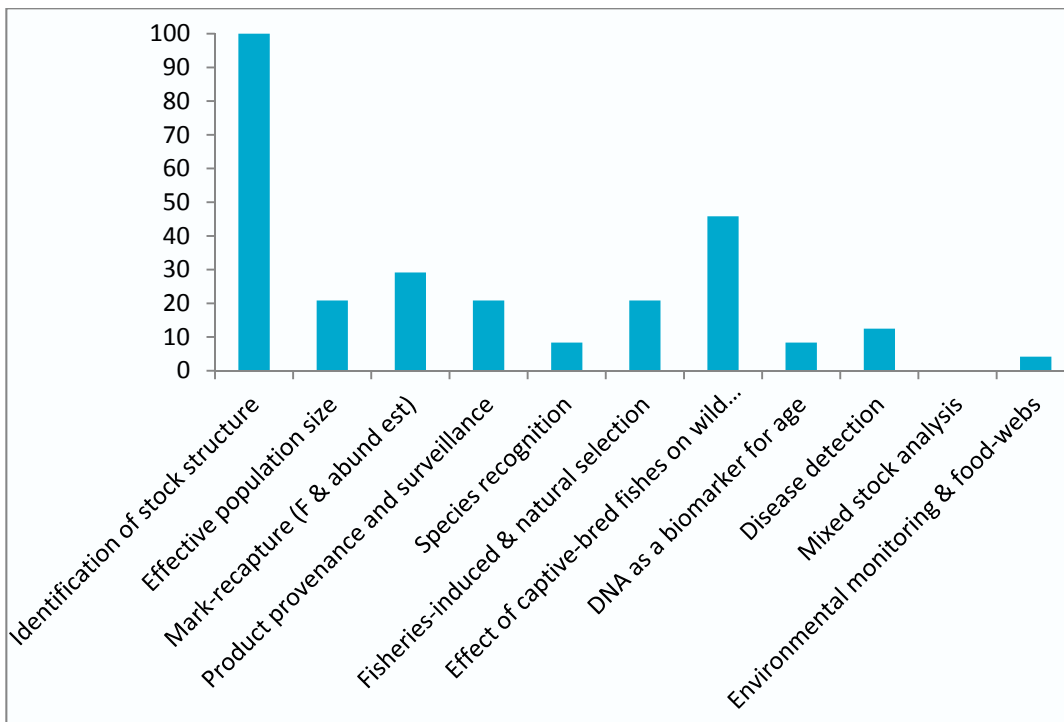
Figure 5. Australian fisheries managers and their awareness of genetic tools grouped by genetic themes. Frequencies are expressed as a percentage of the total number of interviews (n = 23).
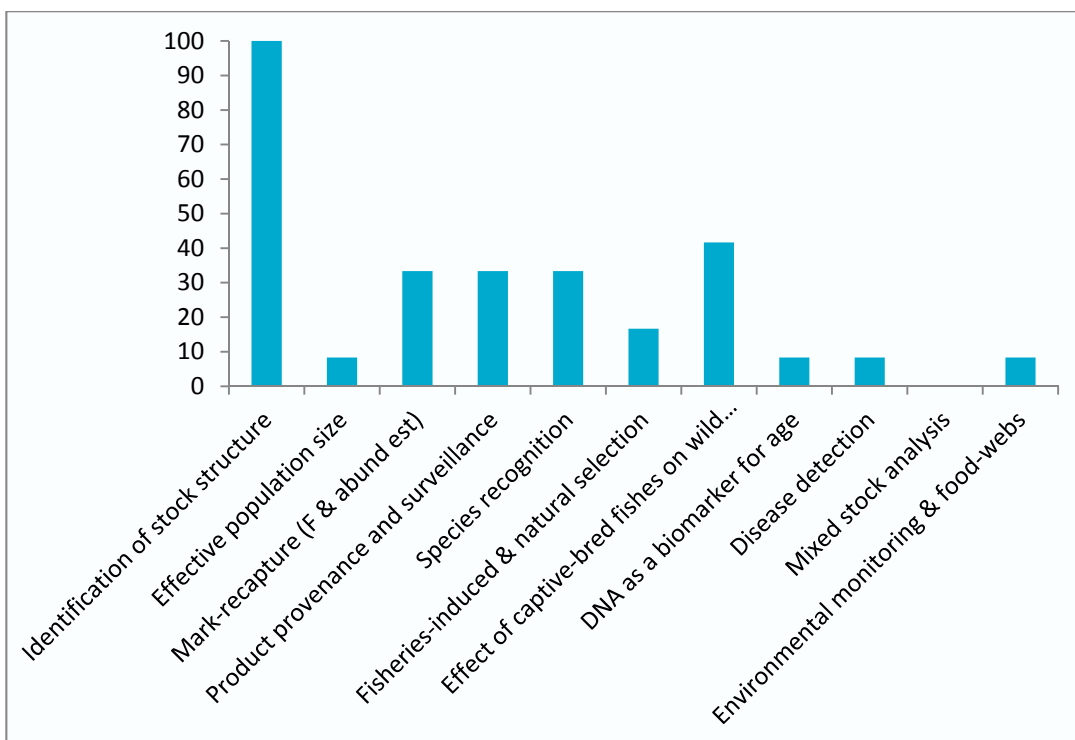
Figure 6. Australian fisheries industry representatives and their awareness of genetic tools grouped by genetic themes. Frequencies are expressed as a percentage of the total number of interviews (n = 12).

Industry

Many of the fishing industry representatives interviewed were either a member of fishery advisory committees or had been at some time in the past, so their level of awareness of genetics in fisheries was similar to that of fisheries managers (Figure 6). In fact some of these representatives have been actively involved in genetic research projects and their technical knowledge was extensive.

8.3.2 PERCEPTIONS ABOUT THE ROLE OF GENETICS IN FISHERIES MANAGEMENT

This question was again tailored to each stakeholder group but essentially asked the interviewee whether they or others thought genetics had a role to play in fisheries management and how positively (or not) they felt genetics was received by fisheries managers. The question also asked if and how the role of genetics in fisheries could be improved (see specific questions in Appendix D). Because these questions were open-ended in nature, we present the responses to the first part of this question as being either positive or negative.

Interviewee responses

The role of genetics in fisheries was viewed more positively by industry and management than by fisheries scientists nationally and internationally (Table 4). The basis for a positive perception by interviewees was that they either recognised genetics as having several useful applications, or more specifically that genetics was informative about the spatial structure of populations. Where there was a negative perception of genetics by interviewees, several reasons were provided as the basis for this response. These perceived barriers to more effective use of genetics in fisheries management included:

- A general lack of understanding of the potential value of genetic information.
- A perception that genetic studies are expensive.
- A perception that genetic results are often "oversold".
- A lack of consistency in interpretations of genetic results by researchers.
- That genetic information is far outweighed by other management decision considerations.

Geneticists felt that the reception of genetics results by fisheries managers was generally positive. However, there was a difference between Australian and international interviewees. Within Australia, genetics results were perceived to be more poorly received by fisheries managers than internationally (Table 4). Some geneticists both in Australia and overseas felt that there was still some scepticism of genetic information by fisheries managers. Within Australia several interviewees related experience of a lack of uptake of genetic results in management decisions due to lack of confidence in genetic information. Conversely many of the international interviewees indicated that the perception of genetics has shown significant improvement through time, probably due to legislative changes in some countries that require explicit consideration of genetic information in fisheries management. A possible contributor to the difference between Australian and international experiences is the high profile of species such as salmon, where genetic information is well documented and considered highly robust.

All interviewees generally felt that the role and effectiveness of genetic information in fisheries management could be improved. The suggestions of how this could be achieved could be grouped into three major categories: communication, technical and other. Communication strategies were clearly identified as the key area where the greatest improvement in the use of genetics would be realised (Figure 7). These included suggestions such as: improved communication of results to broad groups of stakeholders using plain (i.e. without jargon) language; greater communication among fishery scientists, geneticists, fishery managers and industry; a need for greater understanding of the utility of genetic methods by stakeholders; and greater accessibility to genetic research and researchers. Technical issues were also suggested as a key area where improvement is needed and included suggestions such as: making genetic techniques cheaper; more robust and reliable techniques; and more robust sampling designs. The few miscellaneous alternative suggestions were grouped in the 'Other' category.

Table 4. Stakeholder perceptions of the role of genetics in fisheries management. NB. Due to either neutral responses or duplicate responses (both +ve and –ve) the sum of interview responses does not always equal the total number of interviews.

STAKEHOLDER	POSITIVE		NEGATIVE		INTERVIEWS
	#	%	#	%	
Industry	11	91.67	1	8.33	12
Fisheries scientists (Aust.)	8	61.54	5	38.46	13
Fisheries scientists (Int.)	8	66.67	5	41.67	12
Fisheries managers	22	91.67	2	8.33	24
Overall	49	80.33	13	21.31	61
Geneticists (Aust.)	10	76.92	4	30.77	14
Geneticists (Int.)	8	88.89	1	11.11	11
Overall	18	81.82	5	22.73	25
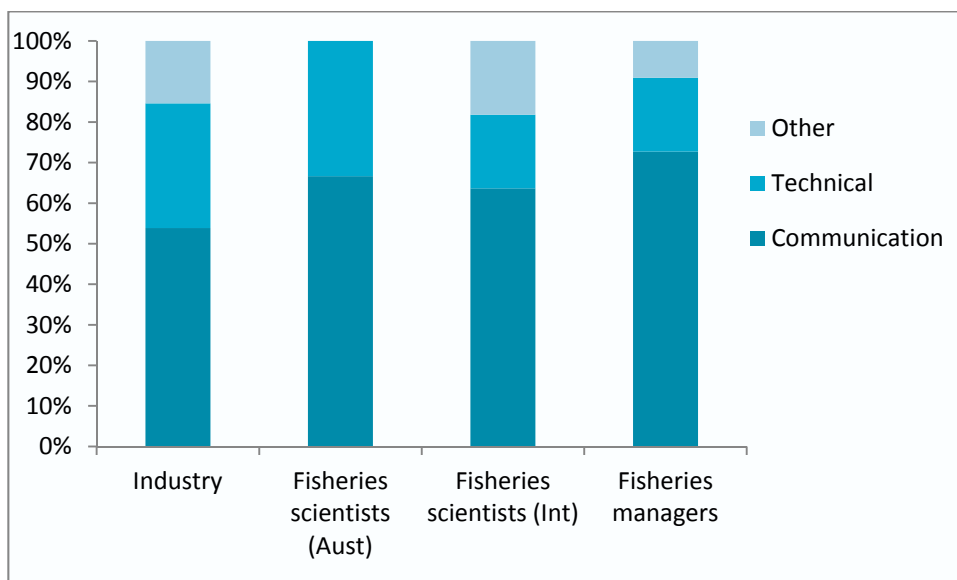
Figure 7. Suggestions from key stakeholders on how to improve the perception and/or effectiveness of genetics in fisheries management. Suggestions are grouped into three categories: communication, technical issues and other.

8.3.3 COMMUNICATION AMONG GENETICISTS, FISHERIES SCIENTISTS, MANAGERS AND INDUSTRY

This question specifically asked interviewees if they thought communication among fisheries scientists, geneticists, industry and fisheries managers could be improved and if so, how. All those interviewed responded "Yes" to the first part of the question. The suggestions of how communication could be improved were grouped into three different categories based on the stakeholder responsibility for adoption of the communication strategies suggested. These categories were: scientists' responsibility (including fisheries scientists and geneticists), managers' responsibility, and responsibility of BOTH scientists and managers. These suggestions are grouped accordingly below.

Interviewee responses

Geneticists used both direct and indirect methods to communicate genetic results to fisheries managers and other stakeholders. Some used several methods while some only used single methods. These methods

included: formal meetings such as workshops, conferences and advisory groups e.g. Resource Assessment Groups (RAGs) or Management Advisory Committees (MACs); informal meetings; project reporting requirements; journal publications; popular articles; and sometimes informal phone and email contact. Some had no contact with managers and relied on publication of peer-reviewed journal articles only. Most interviewed geneticists were not engaged in formal arrangements for communicating research to managers.

The suggestions from stakeholders on how to improve communication varied greatly and for ease of presentation we have grouped suggestions as much as possible while trying not to lose useful information. Indeed, the final list could be condensed further. Of all the stakeholder suggestions on ways to improve communication, over half require the responsibility of scientists to take action, while approximately a third of the suggestions require joint responsibility of both scientists and managers (Table 5). The most common suggestion overall was the need for clearer communication methods to ensure audiences and end-users fully understand the subject matter. In the case of scientists it is the need for being able to use non-technical language and being fully transparent while for managers it is about ensuring management needs are clearly articulated. What is clear from the interviews is that stakeholders feel that to improve communication both the scientific and fishery management community need to be actively involved in the process with much greater integration of the two groups, although individual actions may also make a positive difference.

8.3.4 FUTURE MANAGEMENT ISSUES

This question asked interviewees about what they felt were the key fisheries management issues, now and into the future. **These issues did not need to relate directly to genetic analysis or biological systems.** Geneticists were asked a different but complementary question about how genetic tools would be used for fisheries management in the future. Interviewees could list as many management issues as they wanted.

The principal topics of importance for fisheries management identified by scientists, managers and industry in interviews varied considerably. For convenience of analysis, we grouped topics together under eleven broad management themes listed below with a descriptive definition of each theme following. We note that themes are inter-related and in some cases, the boundaries between themes are indistinct, so they may not be mutually exclusive. Although not all of the management themes identified during interviews relate to scientific enquiry and have potential relevance to genetics, here we present full results across all themes due to the likely broad interest and importance of fisheries stakeholder views on fisheries management generally.

1. Population ecology/life history/stock structure
2. Fishery status and dynamics
3. Impact of fishing (bycatch, TEP, artificial selection, trophic dynamics)
4. Climate change and adaptation
5. Post harvest
6. Biosecurity risks
7. Enhancement
8. Management frameworks
9. Social impact
10. Economic impact
11. Fisheries extension

Table 5. Summary of suggestions on how to improve communication among fisheries scientists, managers and industry and the number of interviewees from each stakeholder group who made the suggestion (fisheries scientists – FS; fisheries managers – FM; Industry – Ind). Suggestions are grouped on the basis of which group is responsible for adopting the strategies.

SUGGESTIONS AND RESPONSIBILITIES	FS	FM	IND	TOT
SCIENTISTS				
Scientists/geneticists communicate in layperson language, highlight uncertainties/limitations and management implications	5	10	3	*18*
Managers/industry engaged/consulted in research projects		4	4	*8*
Scientists better understand management questions and the management process	5	2		*7*
Improve accessibility of information about available genetic (and other scientific) tools and past research		4	2	*6*
Scientists approach managers more (e.g. science groups should establish a science extension role)	1	1	1	*3*
More communication using technology such as visual tools (e.g. simple graphics, YouTube)	1		2	*3*
Project extension using industry articles, fact sheets, etc (in basic language)		2	1	*3*
Better integration of scientists from different disciplines (geneticists, fisheries and stock assessment scientists)	3			*3*
Scientists present relevant research to fisheries management audiences		2		*2*
Scientists need to be better trained in communicating with managers	1			*1*
		Total:		**54**
FISHERIES MANAGERS				
Managers communicate to the wider fishing community better (clearer objectives, needs)	2	6		*8*
Managers need to understand the science better	3	2	1	*6*
Better training of managers (science education, fisheries management training)	2	1	1	*4*
Managers attend scientific conferences more		2		*2*
Managers approach scientists more	1			*1*
		Total:		**21**
SCIENTISTS <u>AND</u> MANAGERS				
Establish formal processes for scientist (including geneticists)/manager engagement (RAGs, forums, committees, etc)	4	2	2	*8*
Communication efforts need to be two-way (open and constant dialogue)	2	4		*6*
Regular workshops/forums for managers and scientists		5	1	*6*
More relationship building	1	2		*3*
Integrate managers and researchers within agencies more	1	1		*2*
Both sides understand each other's needs better	2			*2*
Decision-making needs to be a collaborative process	1			*1*
Develop a public access database for all stakeholders	1			*1*
		Total:		**29**

Using these management themes we contacted interviewees after the interview process had been completed and asked them to rank what they felt were the top three management themes (1 = most important, 2 = 2nd most important, etc) and the bottom three management themes. We then collated these responses and, using a simple scoring system, generated a relative ranking of the respective management themes from 'most' important to 'least' important. For the scoring system, for the top three ranked themes the one ranked first was scored 3 points, second was scored 2 points and third 1 point. For the bottom ranked themes the lowest was scored -3 points, the second lowest -2 points and the third lowest -1 point. Scores were collated across all themes and standardised against the theme with the lowest score. It should be noted that after this ranking process the management themes were reviewed and changed slightly, with the *Impact of fishing* being added (this was to separate the topics Effects of fishing upon fished stocks and Fleet dynamics). We were still able to include this theme in the final rankings using a proxy score by adding up the management issues from the interviews that belonged in the *Impacts of fishing* theme and, as a percentage of the management theme mentioned the most (*Management frameworks*), convert this to a score in the final rankings. In using this approach we assumed interviewees would have ranked the *Impact of fishing* management theme consistently with how many management issues they identified during interviews belonging to that theme, relative to other themes. In this section we also present where genetics can play a potential role in relevant future management issues (themes).

Management theme definitions

Management Theme 1: Population ecology/life history/stock structure

This theme embraced management questions related to attributes of the fished species and the ecosystem that determine the bounds of management – the desirable level of fishing, including the productivity of a species or system. Species recognition was recognised to be a fundamental need in this area (e.g. for cryptic species). Other examples included the need to define spatial relationships and movement, growth and reproductive characteristics, for modelling and assessment. The theme also included the need to develop knowledge of ecosystem relationships (e.g. food webs, trophic relationships).

Management Theme 2: Fishery status and fleet dynamics

All areas of importance that relate to identifying the impact of fishing and its status on target and bycatch species were grouped together. This includes estimating exploitation rates, fishing mortality rates, absolute or relative abundance, often relative to reference points (such as biomass when the fishery is producing maximum sustainable yield). Also included were more complicated topics such as fishery dynamics (the interrelationships over time and space of both the fished species and fishing) and issues such as the problems of increasing fishing power and effort creep.

Management Theme 3: Impact of fishing (bycatch, TEPs, artificial selection, trophic dynamics)

This theme encompasses issues around the impact of fishing on non-target species and the ecosystem as a whole. This includes, for example, the direct impact of fishing on bycatch species, including Threatened, Endangered or Protected species (TEPs), and the physical effects of fishing operations. The latter might include the physical impacts of fishing such as contact with the bottom by traps, trawls and anchors, or the mortality of seabirds through strikes on rigging or trawl warps. Also included are effects mediated through ecosystem interactions. These might include increases in shark, crab and seabird numbers due to trawler discards, but decreases in predatory fish species due to competition with the fishing operation.

Management Theme 4: Climate change and adaptation

Management questions about environmental effects on populations, particularly those explicitly related to climate change, were placed in this theme. Examples include both the need to study and predict responses such as range change, and the impact of increasing cyclones on seagrass beds.

Management Theme 5: Post harvest

There were several problem areas identified that relate to improvements in economic performance via post harvest management of fishery products. These topics include species identification, traceability and provenance, quality control and market chain analysis, and product presentation.

Management Theme 6: Biosecurity risks

Problems related to this theme included the risk and damage due to invasive species (e.g. tilapia) and disease introductions.

Management Theme 7: Enhancement

This theme included both the need for and effective ways to study and improve techniques for stock enhancement, and means to mitigate problems that it might engender. Also included in this topic was the alteration of habitats with the intention of stimulating an increase in the size or quality of the target population (e.g. the addition of nutrients or the provision of forage species for a prized predatory species). Related problems were the translocation of fish or the deliberate selection or genetic enhancement of wild stocks

Management Theme 8: Management frameworks

We grouped responses in this theme that were to do with the fabric of management. This included legislative, administrative and communication structures that are related to the obligations and objectives of fisheries management. This fabric also includes the organisational structures and arrangements by which visions and objectives of management are translated into sets of rules for the management of the fishery. These rules might include management control rules (i.e. management responses to given sets of circumstances or observations), regulatory systems such as regulations and compliance rules, and arrangements for communication between the various parties affected by and engaged in management (e.g. management advisory committees) and the channels via which they inform the managers of fisheries.

Thus, examples within this included broad topics such as the development of sustainable and robust harvest strategies, ecosystem-based management, and policies for co-management. More specific examples included the development of approaches for applying Individual Transferable Quotas (ITQs) in multi-species fisheries and the recognition of threatening processes and mitigation.

Management Theme 9: Social impact

We included in this theme those issues which were to do with social and cultural attitudes to seafood and to fishing: to fishery product values as food both nutritionally and also the cultural significance of fishing. The latter includes maximising and recognising the contribution of fishing and the fishing industry to social values, the role of fishing in ensuring food (food security), and the recognition of industry achievements. We also included stakeholder attitudes and perceptions and the need for efforts to improve these.

Management Theme 10: Economic impact

This theme captured the recognition of needs around optimising fishery economic benefits. This included the development of understanding within the industry about the details of economic functioning within the fishing industry, and explicitly enhancing factors affecting profitability. For example, improved economic performance might be achieved via product innovation or marketing to produce better unit prices, or the reduction of costs, or reducing competition for the resource through controls on effort.

Management Theme 11: Fisheries extension

Problems placed in this theme related to communication of information between management and stakeholder groups and the general public. It includes the need for better delivery and explanation - even translation - of research results, providing better uptake of research outputs. Specific problems within this theme include public misconceptions regarding fishery impacts and the impacts of management strategies (e.g. MPAs).

Interviewee responses

Future fisheries management issues

The types of management issues listed were not necessarily consistent among the different stakeholder groups. Within Australia, issues under *Management frameworks* were listed the most by fisheries scientists, managers and industry (Figure 8). Generally, the numbers of issues raised for each of the management themes were similar for scientists and managers, although managers were more likely to mention *economic* issues than scientists, and industry members raised *economic* issues about twice as often as managers. Apart from one fishery scientist, industry was also the only group to list *Fisheries extension* issues. Among the fisheries scientists interviewed, management issues raised by international scientists were less diverse than Australian scientists with 4 of the 11 themes not represented by international interviewees. The top 3 management themes mentioned by international scientists were the same as those for Australian scientists. However, by far the most popular theme mentioned by international scientists was *Fishery status and dynamics* (75%) followed by *Management frameworks* (42%). This pattern was the reverse with Australian scientists (57% and 79% respectively). This possibly reflects the different (earlier) stages of fisheries establishment and data collection in Australia compared to the rest of the developed world.
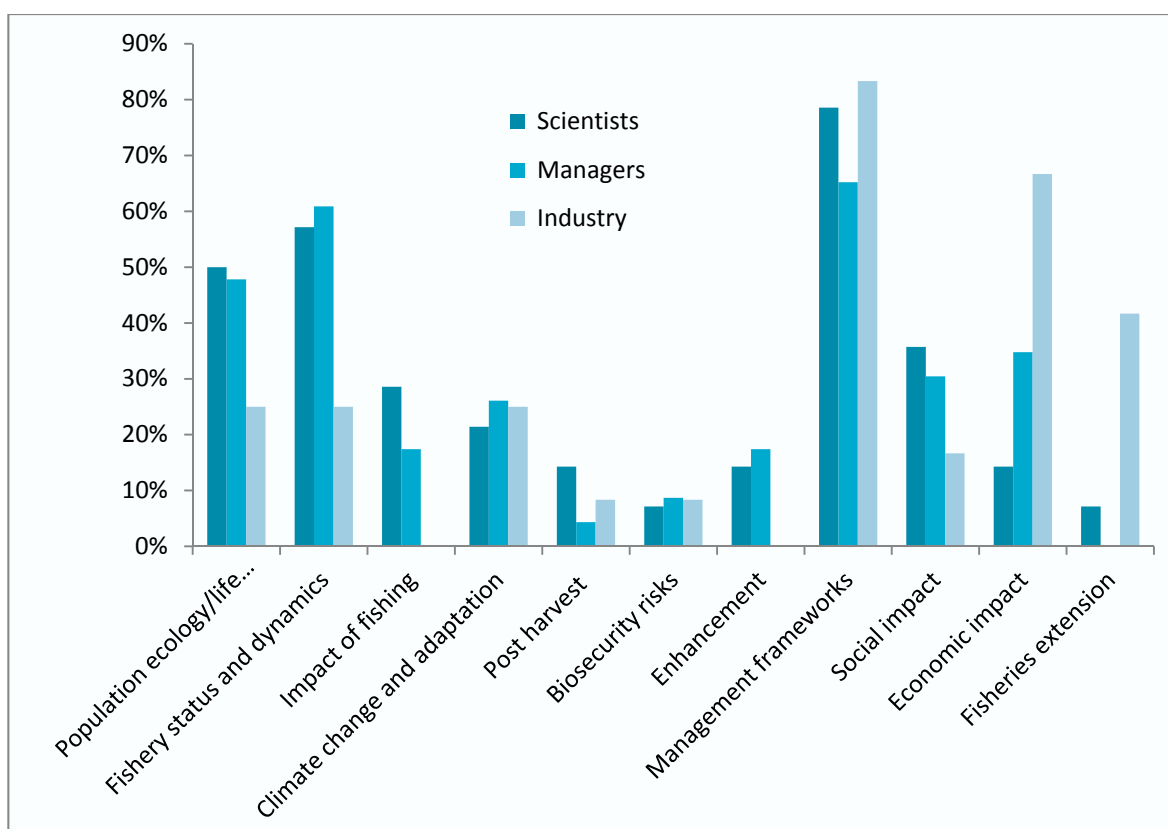
Figure 8. Frequency that management issues relating to the respective management themes were mentioned by interviews with Australian scientists, managers and industry. Frequencies are expressed as a percentage of the total number of interviews conducted with each stakeholder group.

Rankings of fisheries management themes

Overall, the two management themes that were considered as representing the most important future management issues were *Management frameworks* and *Fishery status and dynamics*. These were followed by *Population ecology/life history/stock structure*, *Impact of fishing*, *Economic impact*, C*limate change and adaptation* and *Social impact*. It should be highlighted that these rankings are relative only and that all management themes are important at different times and circumstances. In fact during the ranking process all management themes were scored in the top three most important management themes by at least

some stakeholders. The two themes that, overall, stakeholders appeared to have approximately equal opposing views on were the social and economic themes, particularly the *Economic impact* theme.
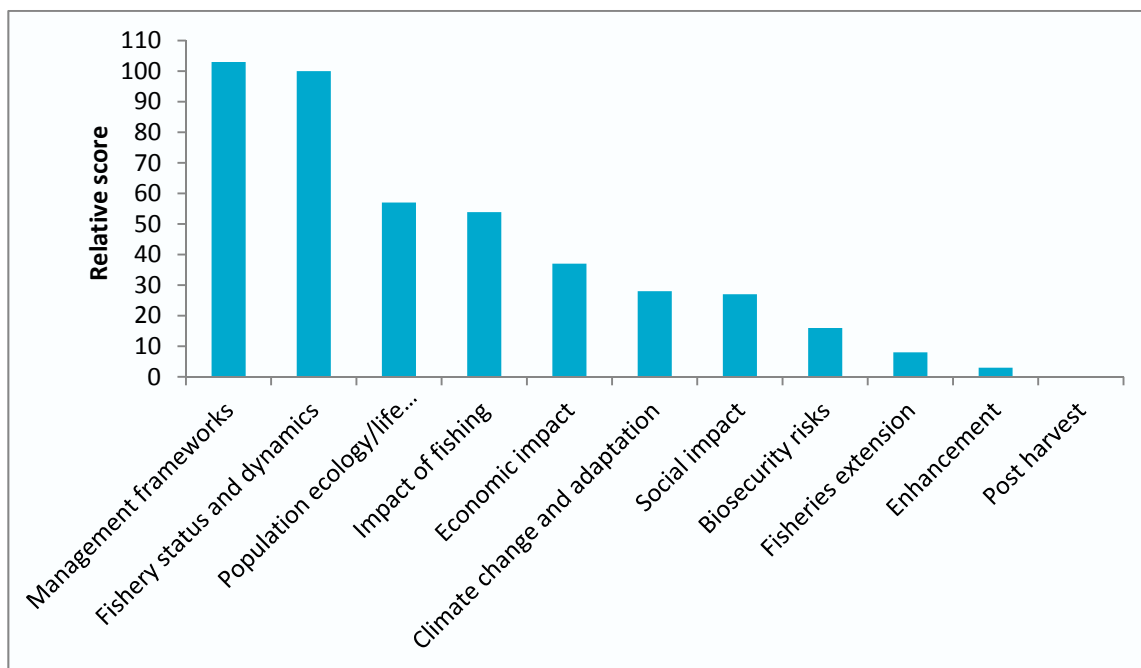
Figure 9. Relative rankings of management themes in order of decreasing (relative) importance going from left to right as determined by stakeholders. Ranking scores are standardised against the least important theme = 0. NB. The ranking for the Impacts of fishing theme is based on a proxy score (see main text).

Future genetic applications in fisheries management

The focus is on the 7 management issues that were related to scientific enquiry and potentially are relevant to genetic analysis. Geneticists foresaw changes in emphasis in the ways that genetic analysis would be utilised for fisheries management in the future. Historically, the geneticists interviewed worked on management applications relating to the theme *Population ecology/life history/stock structure*, and primarily this was on species stock structure (Figure 10). In the future many felt that conventional genetic applications to this management theme, although likely to remain an important area of future genetic research overall, would become less dominant. The other major difference was a significant increase in research on issues relating to the management theme *Climate change and adaptation* (Figure 10). Few of the geneticist responses talked about climate change issues directly but rather stated that questions about adaptive traits and selection were likely to be important in future genetic applications. The potential for increased use of genetic tools for environmental monitoring into the future was also apparent from the interviews (not evident in Figure 10). Four of the management themes are not directly influenced by genetic information so did not receive comment. They are included in Figure 10, however, for consistency with previous figures in this section.
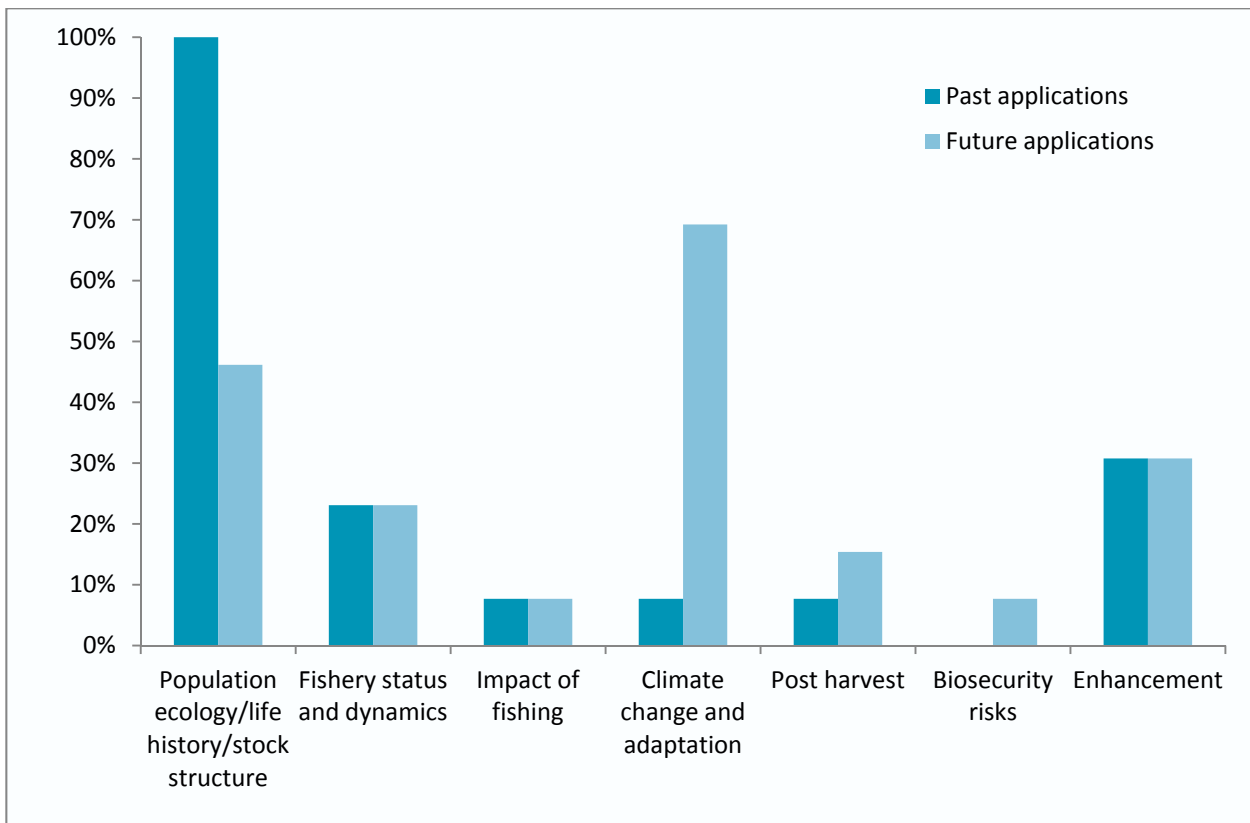
Figure 10. Comparison of Australian geneticists past applications of genetic tools to management with what they view as the future use of genetic tools for fisheries management. Responses are grouped into the respective management themes. Frequencies are expressed as a percentage of the total number of interviews conducted. Only the 7 management issues that were related to scientific enquiry and potentially are relevant to genetic analysis are included.

8.3.5 CONCLUDING REMARKS

The interviews conducted during this project provided a unique insight into the perceptions of different fisheries practitioners about a number of issues. Not only did the interviews deal with perceptions of the use of genetics in a fisheries context, but also on more general and encompassing issues such as communication among stakeholders and future management issues and therefore, likely directions for prioritising research funding. The key conclusions from the interviews were that:

- The level of understanding of key fisheries stakeholders on the availability and capabilities of genetic tools was low;
- Key fisheries stakeholders generally saw value in the use of genetics in fisheries management but felt the overall perception and use of genetics can be improved;
- The most important strategy for improving the role that genetics can play in fisheries is through better communication about the capabilities and limitations of genetic research, and about the needs of management;
- Non-geneticist stakeholders believed that the major communication improvement required is articulation of genetic information using non-technical language;
- While there were divergent views about whose responsibility it should be to improve communications among stakeholders, overall the consensus was that the responsibilities for improving communication should lie with both scientists (including geneticists) and managers, potentially through formal arrangements.

8.4 Workshop discussion on the communication gap

The key gap identified by stakeholders was a lack of effective communication between geneticists, other scientists, managers and other stakeholders. The workshop presented a number of options identified by interviewees for addressing this key communication gap. Three working groups provided guidance as to:

1. Who is responsible for communication - geneticists, managers, or shared with fisheries scientists as well as industry stakeholders? Should it be science-led or stakeholder-led?
2. What should be communicated?
3. How to facilitate increased communication and whether other fields (e.g. fisheries stock assessment) could be used as models.

8.4.1 WHO IS RESPONSIBLE FOR COMMUNICATION?

While there was no consensus on this matter, most participants agreed that the role of communicating the usefulness of genetics to fisheries management, and results of genetic studies, rests with all players. Despite this general view it was recognised that, because managers must take into account diverse policy drivers (including social, political and economic factors), they increasingly are drawing on the knowledge and experience of others (e.g. including scientists). Geneticists and scientists should therefore be pro-active in lobbying managers about the merits of genetic research when providing advice on strategic research directions that incorporate genetic information

When one investigates the practicalities of the above, it is clear that geneticists rarely have direct links with the management/science interface (e.g. they are rarely members of Assessment or Management Advisory Groups). Managers also have too little time to learn about every aspect of the different fields with which they interact. **This means that the most effective partnership is likely to be between fisheries scientists and geneticists, where scientists act as a conduit for genetic data via advisory groups to managers.** This approach may be challenging for geneticists, as within the workshop there was a view expressed that about 50% of fisheries scientists were sceptical about the role of genetics.

For this relationship to take place, a common understanding of fisheries science and genetics is required – a responsibility of both parties. This could be achieved using a hierarchical approach starting with this small FRDC project team, broadening the approach to the different groups (which contain the different stakeholders) including funding agencies where relevant.

8.4.2 WHAT IS THE BEST PROCESS TO FACILITATE COMMUNICATION?

From both the interviews and the workshop, there was generally a positive attitude towards genetics as a tool in fisheries research. Even though communication was seen as a major gap, **the positive view across several sectors is evidence that focusing on this aspect would be beneficial.** Advice from the workshop centred on a mixture model of geneticists learning to communicate in a policy and management environment, embedding key stakeholders in genetics projects, crafting publications aimed at managers, and the running of more genetics-focused workshops:

A high priority from workshop participants (especially from managers) was a need for a guide to genetics aimed at fisheries managers. It should include what works and what does not. This could be in the form of a guide book, a website or an app. The advantage of the latter two publication methods is that one can inherently create better cross linkages making the guide richer. An app has broader use because it is portable, but would require more computer literacy than a website. Managers would benefit from a table that matches management themes to genetic themes (this could be electronic). The summary of genetic themes in fisheries (Table 4) could be used as a basis for this.

1. The results collected from genetic studies often need to be modified to produce a message suitable for a wider audience. Many geneticists are unused to communicating beyond the scientific community. A point expressed by several participants was that geneticists could benefit from mentors. This approach was used in Western Australia to spread the word about stock assessment.

The role of the mentor in WA was to provide geneticists with a role model, training and opportunity to communicate to different audiences. This will enable geneticists who traditionally communicate to a technical audience to extend their work to stakeholders such as fishers and managers. There are excellent examples of programs and personnel within the field that can be drawn upon to provide advice and mentorship. Rather than relying on this mentoring taking place within each organisation, it is advisable to create active linkages to funded mentoring programs, such as through management agencies.

2. Two types of communication workshops were proposed. The first focuses on sharing knowledge within the scientific community so that other scientists are exposed to genetics, which is important because these scientists are often embedded in, or are closer to, the management interface. This is because the major mechanism of connecting genetics into the management system proposed above is through other scientists who are more part or the management process (e.g. Advisory Committee science members). The second type of communication workshop is aimed at the different stakeholders and uses a different communication approach.

   a. Focused science workshops on what genetics can offer fisheries science and management would be useful. They could be part of fisheries and modelling conferences e.g. ASFB or AMSA.

   b. Further stakeholder-oriented workshops are needed for communication involving a wide participant list, including fishers and industry. Communication should focus more on the best method of communicating complex methods (including genetics) so inclusion of science communicators in the planning would be essential. A useful topic for a workshop could be 'Latest techniques in fisheries science, including new questions' and genetics would be a major part of this. The most important aspect to include is the management questions, and managers information needs. A workshop could encompass both of these aspects. Case studies could also be used to demonstrate what can be achieved.

3. Integration of fisheries managers into research projects can be successful when it comes to disseminating results, but they need a real role and not just be numbers on a steering committee. Likewise, the managers need to be able to commit time and resources to the process of research.

4. Effective communication methods are essential to spread the message of the usefulness of genetics. Dedicated fisheries writers are needed.

5. Geneticists should not be afraid to exploit the novelty and 'wow' factor of their work, however they also need to not oversell their methods. In the interviews, this issue was often mentioned.

6. Scientists, including geneticists, should not be afraid to say where genetics won't work or where it isn't relevant. Genetics is not the only scientific tool for managers.

7. Genetics in fisheries management is newer than stock assessment modelling. There is an inevitable time lag in take-up of more sophisticated methods. A good example is the change in attitude of freshwater management bodies in NSW, which consist largely of interested fishers. They began by calling for very basic information, but quickly progressed towards calling for genetics research, which showed rapidly increasing levels of sophistication.

8.5   Linking genetic methods to management themes

Managers need the latest social, economic and biological data to support decision-making about sustainable and profitable harvesting. Genetic tools are a diverse collection of methods that yield useful biological data. Earlier in this report, genetic tools were characterised into eleven genetic themes depending on their characteristics and downstream application (Section 8.1 and Appendix H). In this section, ways in which genetic themes can be used to address management themes (issues) were described and analysed. Which management themes were the most important at present were identified (Section 8.3.4), and the eleven genetic themes were rated according to the effort required for implementation and the likelihood of yielding valuable information for that management theme.

 Genetic themes can provide useful biological data for seven of the eleven management themes identified in this report. Those management themes are:

- Population ecology/life history/stock structure (management theme 1),
- Fishery status and fleet dynamics (management theme 2),
- Impact of fishing (bycatch, TEP, selection, trophic dynamics) (management theme 3),
- Climate change and adaptation (management theme 4),
- Post harvest (management theme 5),
- Biosecurity risks (management theme 6), and
- Enhancement (management theme 7).

Genetic themes play no role in the following management themes, which have a social or economic basis.

- Management frameworks (management theme 8),
- Social impact (management theme 9),
- Economic impact (management theme 10) and
- Fisheries extension (management theme 11).

The genetic themes from Section 8.1 are

1. The identification of fisheries stock structure
2. Genetic effective population size
3. Genetic mark-recapture for estimating mortality and abundance
4. Product provenance and fisheries surveillance using genetics
5. Species recognition using genetics
6. Fisheries-induced and natural selection
7. Genetic effect of captive-bred fishes on wild conspecifics
8. DNA as a biomarker for age
9. Genetics for disease detection in wild fisheries
10. Mixed stock analysis using genetics
11. Genetics for environmental monitoring

Table 6. Summary of role that genetic themes can play in current fisheries management issues. Role is expressed as readiness (availability of expertise at multiple sites in Australia), utility (likelihood that a genetic tool will provide a direct response to the management issue), maturity (practical and theoretical tools are immediately available) and costs (based on estimate of genetic consumable costs only, without infrastructure or salary costs). Attributes are represented by horizontal bars on a scale between 1 and 5. See colour code below for each attribute. Some genetic themes cannot address some management challenges (blank). There are four management challenges that cannot be addressed using genetics, and these are not included in this table (see text).

GENETIC THEMES	MANAGEMENT THEMES (MT)						
	Population ecology/life history/stock structure (MT 1)	Fishery status and fleet dynamics (MT 2)	Impact of fishing (bycatch, TEP, selection, trophic dynamics) (MT 3)	Climate change and adaptation (MT 4)	Post harvest (MT 5)	Biosecurity risks (MT 6)	Enhancement (MT 7)
1. Genetic analysis for the identification of fisheries stock structure	●						●
2. Genetic effective population size		●	●				
3. Genetic mark-recapture for estimating mortality and abundance		●	●				
4. Product provenance and fisheries surveillance using genetics.		●	●		●	●	●
5. Species recognition using genetics	●	●	●		●		
6. Fisheries-induced and natural selection			●	●			
7. Genetic effect of captive-bred fishes on wild conspecifics							●
8. DNA as a biomarker for age	●						
9. Genetics for disease detection in wild fisheries						●	
10. Mixed stock analysis using genetics		●					
11. Genetics for environmental monitoring and food-web analysis	●		●	●		●	●

Legend (horizontal bars): Readiness — Utility — Maturity — Cost

The role that genetic themes could play in fisheries management issues is summarised in Table 6, and further elaborated below. **A fisheries stakeholder (e.g. manager or scientist) could use Table 6 to understand which genetic theme could be used to address a management issue.** Likewise, a geneticist working with natural resources could use Table 6 to extend outcomes of their research into specific areas of interest to fisheries managers. For fisheries stakeholders, there is a short synopsis of each genetic theme (Appendix Has well as a full review (Section 8.1) in this report. For geneticists, current issues in fisheries management are described in Section 8.3.4.

Link between population ecology/life history/stock structure (management theme 1) and genetic themes

Like the next two management themes, this theme is readily addressed by genetics

The link between this management theme (*Population ecology/life history/stock structure*) and genetics includes genetic theme *The identification of fisheries stock structure*, which is a well established, well focused and reasonably inexpensive set of methodologies (Table 6). This was acknowledged by managers and scientists interviewed as part of this project (Section 8.3).

Correct species recognition is essential for the collection of information about ecology, life history and stock structure, so the genetic theme *Species recognition using genetics* plays a key role. The expertise to do this in Australia is readily available and is highly likely to produce an accurate result. The cost is low.

Life history of fisheries species can be studied using DNA as a surrogate for age (*DNA as a biomarker for age*), in the same way that otoliths are used to age individuals. This genetic theme, however, is not widely available in Australia, methods are poorly developed and it is expensive at the moment.

Other attributes of fished species, and the ecosystem that sustains them, can be studied with the genetic theme *Genetics for environmental monitoring.* This genetic theme is currently expensive and underdeveloped in Australia, however it holds great promise for the future. Fisheries are increasingly adopting the principles of ecosystem-based management, which requires managers to take account of diverse, complex and difficult to observe ecological processes. The diversity of biological information that genetic analyses can provide suggests that this tool will become a valuable contributor to ecosystem- based management though such applications as characterising foodwebs, stock structure analysis, and estimation of abundance.

Link between fishery status and fleet dynamics (management theme 2) and genetic themes

Five of the eleven genetic themes can provide information that is relevant to this management theme.

Like stock structure studies, the effect of fishing on target and bycatch species cannot be studied unless the taxonomic status of individuals has been correctly determined. *Species recognition using genetics* is a widely available, focused, mature and inexpensive set of methods for this. Likewise, genetics can be used to assign individuals to population of origin (*Product provenance and fisheries surveillance using genetics*) and can be implemented at any point along the chain of processing, marketing or consumption. Although inexpensive, this genetic theme is not as widely available or as well developed in Australia as *Species recognition using genetics*.

Aspects of fishery status such as instantaneous harvest rates and abundance can be quantified using genetic themes such as *Genetic mark-recapture for estimating mortality and abundance* and *Genetic effective population size*. Implementations of these genetic themes vary in cost. *Genetic mark-recapture for estimating mortality and abundance* requires the analysis of a large number of individuals for a reasonable expectation of recapture in numerically large fisheries populations and hence is expensive and time-consuming. The methods return different information about fishery status, with *Genetic mark-recapture for estimating mortality and abundance* being more focussed on data that can be directly incorporated into fisheries stock assessments. *Genetic effective population* size methodology is more 'off-the-shelf' in Australia than *Genetic mark-recapture for estimating mortality and abundance*, and requires a number of assumptions in order to incorporate its outputs into conventional fisheries stock assessments. Neither method (genetag or close-kin) that form part of *Genetic mark-recapture for estimating mortality and abundance* has been widely applied. Both would benefit from peer-review and scientific publication.

The impact of fishing on various spawning populations can be determined using genetics (*Mixed stock analysis using genetics*), provided baseline genetic data is available on spawning populations and the spawning populations are genetically differentiated. This type of analysis is not currently implemented in Australia, but if it was needed (e.g. eastern compared to western gemfish stocks in Bass Strait) it could be readily implemented in a focussed way using methods developed overseas and at a relatively low cost.

Link between the impact of fishing (bycatch, TEP, selection, trophic dynamics) (management theme 3) and genetic themes

This management issue is also readily addressed using genetics. It has links to six genetic themes.

Genetics is ideally suited to determine the taxonomy of the bycatch or TEP species (*Species recognition using genetics*). It is an accurate, inexpensive and well-targeted way to do this. Likewise, genetics can be used to determine the population of origin from bycatch or TEP species from tissue samples in many states of preservation (*Product provenance and fisheries surveillance using genetics*). This is relatively inexpensive but requires a start-up phase to collect baseline data that may delay outputs.

In the same way that G*enetic effective population size* and *Genetic mark-recapture for estimating mortality and abundance* can be applied to target fisheries species, they can also be selectively applied to bycatch and TEP species. *Genetic mark-recapture for estimating mortality and abundance* may be more relevant to these species as population sizes will be smaller and hence fewer individuals will need to be examined to find recaptures. Similarly, the smaller population sizes may make *Genetic effective population size* methods more useful and easier to apply. However, the application of these themes would be dependent on the ability to encounter, sample and re-sample the animals in the first place. It is unknown whether remote sampling methods that have been successfully used for terrestrial populations (e.g. faecal or hair sampling) would be applicable to aquatic species, although sloughed skin is regularly collected from cetaceans.

The impact of fishing is expected to exert a considerable selective force on the resource. For example, individuals are expected to adapt by swimming faster to escape trawl nets or to reproduce at smaller sizes if larger individuals are selectively removed by fishing. Genetics (*Fisheries-induced and natural selection*) represents the major method available to quantify, forecast, and potentially ameliorate these effects. However, the field is not well developed in Australia and is likely to be relatively expensive to implement.

Genetics can be used for environmental monitoring and food web analyses to determine the impact of fishing on the ecosystem (*Genetics for environmental monitoring*). This area has great promise (high potential utility), but at the moment it is underdeveloped (low maturity and readiness) in Australia. Conventional, microscope-based methods have serious inadequacies for producing food webs for developing ecosystem models. These types of models are being used more and more in Australia, which will drive developments in this genetic theme (*Genetics for environmental monitoring*).

Link between the climate change and adaptation (management theme 4) and genetic themes

Tools to study this management theme are urgently sought as its importance is escalating. Two genetic themes are relevant now, and we expect other genetic themes could become relevant as the field develops in the future. For example, climate change is likely to affect the reproductive capacity of fisheries populations, in which case genetics could be a valuable monitoring tool (e.g. *Genetic effective population size* and *Genetic mark-recapture for estimating mortality and abundance*).

Genetics for environmental monitoring and food web analyses have the potential now to detect changes related to climate change. Populations will adapt to climate change as a result of natural selection, and this could be studied using the genetic theme *Fisheries-induced and natural selection*. However, in comparison to overseas research, the readiness, utility and maturity of these genetic themes to study climate change and adaptation are low and urgently need further development.

Link between post harvest (management theme 5) and genetic themes

This management issue is specifically addressed by two genetic themes. The driver behind their development was, in part, the need for fisheries post harvest analyses.

The two genetic themes are 1) *Product provenance and fisheries surveillance using genetics* and 2*) Species recognition using genetics*. Both themes have the highest utility score indicating that they will provide direct resolution to post harvest problems such as species labelling, traceability, provenance and market chain analysis. In common with Management Themes 5 and 6, *Species recognition using genetic*s has the highest readiness score because the capacity to do these analyses is common in genetics labs across Australia. *Product provenance* has a lower readiness score because it has a greater reliance on the

collection of appropriate base-line data. The relative cost of both themes is low and their utility is high, giving them a favourable cost-benefit ratio.

Link between biosecurity risks (management theme 6) and genetic themes

There are two aspects to this management theme; invasive species and diseases. Genetics has an excellent capacity to provide information on both aspects.

One genetic theme (*Genetics for disease detection in wild fisheries*) is specifically focused on identifying, detecting and monitoring the presence of disease in wild fisheries. There are several laboratories in Australia with the capability to do this work. The costs are relatively low, however they will vary depending on the disease organism. For example, viral detections tend to be more costly.

Two other genetic themes can address problems associated with invasive species. Both *Product provenance and fisheries surveillance using genetics* and *Genetics for environmental monitoring and food-web analyses* can detect the cryptic presence of invasive species (for example, from unidentifiable tissue samples or from DNA collected from the environment) and thus can be used to monitor their spread. *Product provenance* and *Environmental monitoring* are ranked equally for utility, but the latter has a lower readiness and maturity score. Genetic techniques for analysing degraded and very dilute DNA from the environment are under continual development. *Product provenance* can also determine the source of the invasion by matching invaders to genetically characterised potential source populations. Both genetic themes are relatively inexpensive.

Link between enhancement (management theme 7) and genetic themes

Like post harvest issues (*Product provenance and fisheries surveillance using genetics* and *Species recognition using genetics*), the enhancement management theme is directly targeted by a genetic theme; the *Genetic effect of captive-bred fishes on wild conspecifics* as well as two other genetic themes. *Genetic effect of captive-bred fishes on wild conspecifics* provides a way to monitor the effect of enhancement on native species, which could lead to mitigation action. It has a high utility ranking meaning that its highly likely that appropriate information will be provided, and experienced researchers are readily available in Australia. The costs are relatively low.

Baseline information on fisheries stock structure is important information for stock enhancement activities and has been routinely applied in many Australian examples. Thus, the genetic set of methods encompassed by *The identification of fisheries stock structure* is relevant here. These methods are widely available in Australia and highly likely to yield a result, particularly in freshwater systems (e.g. Murray Darling Basin), where physical isolation in separate drainages leads to significant genetic differences between regional populations.

Another genetic tool that is relevant to this management issue is *Product provenance and fisheries surveillance using genetics*. This theme can be used to monitor the survival of captive-bred individuals that are released for enhancement, and detect offspring if reproduction occurs. This capability is not well developed in Australia (Table 6).

8.5.1 CONCLUDING REMARKS

The majority of the management themes identified in this report (seven of eleven), and all the biological themes (seven of seven) can be supported by genetic analyses, and in most cases in multiple ways (Table 6). In some projects, it may be cost-efficient to collect data for more than one objective; for example, genetic data could be feasibly collected in one project to address *Product provenance and fisheries surveillance using genetics, Species recognition using genetics* and *Mixed stock analysis using genetics*. However, the way in which genetic themes are combined and deployed in practise will depend on many factors including the type of genetic data needed, details of the management challenge and based on consultation between stakeholders and geneticists.

Genetic methods can be also in combination with non-genetic methods. A good example of this is the combination of genetics, otolith microchemistry and parasite abundance to define stock structure. This is holistic approach has consistently yielded the best results for fisheries stock delineation. However, linking genetic and non-genetic methods used in fisheries science is not considered in any detailed way here. There are excellent Australian and international examples of this approach (Buckworth *et al.*, 2007; Abaunza *et al.*, 2008; Welch *et al.*, 2009).

The rankings of genetic themes (i.e. by readiness, utility, maturity and cost, Table 6) could be used to select the most appropriate genetic way to address a particular management issue. In practise, however, there are many scientific, technical and fisheries issues to be considered. For example, the genetic theme *Genetic mark-recapture for estimating mortality and abundance* has a higher utility rank than *Genetic effective population size* for the management theme of *Fishery status and fleet dynamics* (MT5). But, the cost of *Genetic mark-recapture for estimating mortality and abundance* may be higher than *Genetic effective population size*. In other cases, genetic themes have low rankings for readiness, utility and maturity and high associated costs, but they may represent the only way (genetic or otherwise) to studying important issues; for example, *Fisheries-induced and natural selection* as part of management theme 6 (*Impact of fishing*) and 7 (*Climate change and adaptation*). Thus, linkages discussed in this section and in Table 6 should be considered as guidelines and detailed consultations with experts are needed to design focussed, productive research projects. Overall, the relative importance of a genetic theme depends on the type of management issue being considered, the project objectives and project performance criteria. The gap analysis presented elsewhere (Section 8.2) provides specific and general advice on how get the most out of investment in genetics research, now and in the future.

It is also tempting to use Table 6 to make a statement about which genetic themes are the most widely used and hence may be the most important. But, this is not advisable. For example, two similar genetic themes (*Product provenance and fisheries surveillance using genetics* and *Species recognition using genetics*) are applicable to five current Australian management themes. It would be misleading to assume these are the most important genetic applications to fisheries management, however. Most published papers, and most funding for fisheries genetics, are directed towards a single genetic theme (*Genetic analysis for the identification of fisheries stock structure*) that addresses management theme 1 (*Population ecology/life history/stock structure*). Some genetic themes may rapidly increase in importance as studies on climate change, fisheries-induced selection and ecosystem-based management become more common and relevant to fisheries management.

There are several important caveats to this section. The rankings of genetic themes by readiness, utility, maturity and cost are largely subjective. While two members of the project team with considerable experience in genetics compiled them, the rankings have not been extensively externally reviewed. The relative costing of genetic themes was problematic. In Australia, many fisheries species are new to genetic studies, which means that they have little (if any) genomic resources (e.g. genetic markers, whole genomes, sequence data). The lack of this carries a significant start-up cost for research projects. Some species have genomic resources (e.g. prawns, tunas and billfish), so start-up costs for projects on these species across many genetic themes would be lower. The other caveat is that the linkages between genetic and management themes have been described in terms of today's genetic capabilities and management needs. In the near future, genetics may play an increased role in many more management issues; for example, in the field of climate change and food web analyses.

8.6   Discussion

While fisheries management has been drawing on genetic research for several decades, both have undergone massive changes during this period. Fisheries managers today are forced to deal with many more issues than in the past, and genetic research technologies have developed enormously. **However, genetic analysis has never been better equipped to assist with wild fisheries management in Australia.** Proof of this comes from the spectrum of pressing issues in fisheries management that genetic tools can address (Section 8.5), as well as the growing diversity of technical and analytical genetic methods (Section 8.1 and Appendix H and the great rate of technological change.

Two major technical developments in pharmaceutical and medical industries are impacting genetics in fisheries, and this impact is likely to grow. The first is the development of 'next-generation' DNA sequencing technologies (Appendix C), which can provide large volumes of DNA sequence data for non-model organisms at a fraction of the cost of conventional DNA sequencing. This resource will benefit fisheries genetics by reducing the cost of genetic marker development and increasing the power of the analysis because more markers and samples will be assayable. It will also facilitate new types of analysis, such as those focused on functional genomics or environmental monitoring. The second important development is the increased automation of laboratory procedures through use of robotic workstations. This has the potential to reduce the cost and increase the repeatability of analyses, and is well suited to ongoing monitoring projects where large numbers of samples are processed and where data needs to be produced in a timely manner for management decision-making.

Genetics in fisheries will be increasingly used as a monitoring tool. Many genetic themes reviewed here (Section 8.1) can be deployed in ongoing monitoring programs; for example, estimating abundance and spawner numbers through genetic mark-recapture (Section 8.1.4) determination of product provenance (Section 8.1.5) and disease detection (Section 8.1.10). Indeed, the majority of genetic themes have an application to monitoring. This is a relatively new way of applying genetics, as genetic information in Australian fisheries has traditionally been used to gather baseline information; for example, identifying fisheries stock structure (Section 8.1.2) and collecting reference data for species recognition (Section 8.1.6). In the past, baseline research has typically been funded by one-off grants of three years duration. In the future, a significant question will be whether funding bodies and research institutions are willing to support ongoing genetic monitoring as well as baseline research. The problem here is that monitoring is normally regarded not to be research (although research is needed to set up new monitoring techniques) and the responsibility for monitoring is thought to lie with state governments and other jurisdictions. It seems certain, however, that developed and emerging genetic technologies will be ideal tools for fisheries monitoring and their cost-effectiveness will only improve due to technological advances. If adopted, this will likely require support and funding from State/Territory governments.

The single biggest issue identified as limiting the effective use of genetic tools in fisheries management was poor communication between research and other sectors (Section 8.3 and 8.4). Although all stakeholders saw value in genetic data, there was clearly a lack of knowledge among end-users of the recent technological developments in genetics and a lack of awareness of the capability of genetics to address fisheries management issues.

Stakeholders identified several aspects underlying poor communication: i) genetics information is too often conveyed with highly technical language, ii) genetic research failed to deliver practical management outcomes, and iii) that information about genetic tools and how they can benefit fisheries is not easily accessed. Like many specialised scientific disciplines, the science of genetics is highly technical and understanding the basic concepts can be challenging. Fisheries managers therefore rely on geneticists and fisheries scientists as guides for genetic principles and outcomes as they apply to fisheries management in practical terms. Although here we have focused on improving the communication on the science of genetics (Section 8.3.3 and Section 8.4), communication is a generic issue in all fields of applied science, so these strategies are likely to be applicable to many disciplines in order to achieve effective outcomes. This report contains some examples of tools that could be used to address major communication issues identified by stakeholders. The tools are: a comprehensive review of available genetic tools (Section 8.1); a 'look-up' table that provides clear links between specific genetic tools and specific management issues (Section 8.5); and a comprehensive, concise and plain-English summary of genetic tools and how they can inform fisheries management (Appendix H).

As identified by many stakeholders, the communication responsibility must be shared so that the needs of fisheries managers, geneticists and fisheries scientists are better understood. That means communication needs to be two-way (see Sections 8.3.3 and 8.4). However, there is still a need for better integration of geneticists, fisheries managers and fisheries scientists through various mechanisms such as project involvement (Table 1), formal committees, workshops and conferences. One of the key mechanisms identified during the project stakeholder workshop to achieve this outcome was through the use of existing formal processes (such as Management Advisory Groups). In Australia, it is fisheries scientists and not

geneticists who usually sit on these committees and therefore the most effective partnership development is likely to be between fisheries scientists and geneticists, with scientists acting as a conduit to managers for relevant genetic information via the advisory groups.

Other ways to improve the integration between key fisheries and genetics personnel is for a team approach to genetic research projects. The skills and experience of fisheries managers and scientists are just as essential for successful experimental design, implementation, analysis and extension as population and molecular geneticists, statisticians, mathematicians, software engineers, bioinformatics and database managers (Table 1). Another key integration strategy identified was science-based and stakeholder-orientated workshops (Section 8.4). At a higher level, further development and extension of the 'field guide' tool developed during this project (Appendix H) into a customisable electronic platform, such as a web-based application ("app"), would enhance and optimise any future role of genetics in Australian fisheries management. This development may require further funding from FRDC, although all funding models should be considered.

To address the lack of awareness of the capability of genetics to address fisheries management issues, this review explicitly links genetic tools to management themes (Section 8.5). Stakeholders were consulted about key management issues in Australia and their relative importance (Section 8.3.4). Grouping issues into high level management themes and ranking their relative importance (by stakeholders) provides a unique, cross-jurisdictional 'big picture' view of fisheries management needs in Australia. It was an essential starting point for assessing the role that genetics can play, but can also be used for determining future research directions in other contexts. Section 8.5 explains the link between the different genetic and management themes and provides a simple look-up table (Table 6) for stakeholders, including research funding agencies, to make quick assessments of the potential for management issues to be addressed using the available genetic tools. However, the ranking of management themes was a function of who we interviewed despite efforts to be as representative as possible. For example, few freshwater fisheries managers were interviewed. Therefore, genetic tools linked to management themes with lower relative rankings should not be dismissed since all tools will have their role depending on the specific issue considered being a priority. For example, elements of some of the management themes, such as biosecurity issues, product provenance and stock enhancement, can only be effectively addressed using genetic tools.

The identification and ranking of management themes, and the tools linking them to genetics, provide a clear basis for future investment decisions involving the use of genetics to address fisheries issues. Although genetics cannot address all management themes (some are non-biological), the highest priority management themes identified for future investment in Australia are in *Fishery status and dynamics*, *Population ecology/life history/stock structure*, *Climate change and adaptation*, and *Impacts of fishing*. Genetic technology is well positioned to inform management issues from these themes. The theme *Climate change and adaptation*, in particular, is considered to be an increasingly important management issue and deserves future research investment into projects on evolutionary processes and adaptation. The ability to understand the genetic basis of adaptation to environmental heterogeneity and change (natural or anthropogenic) is a result being able to assay for genes under selection (see section 8.1.7). This is propelled by the development of genomic resources (Appendix C) for fisheries species. It may also bring with it challenges in the interpretation of genetic data for defining fisheries stocks (see section 8.1.2).

While this report has focused on the utility of genetics in fisheries management there are several other tools available (e.g. parasites, tagging, otolith chemistry) to inform fisheries management. The use of a particular method, or methods, to most effectively address management issues would need to be assessed on a case-by-case basis and depending on the specific question. We have not compared different genetic tools with other tools however a cost-benefit analysis comparing different tools in addressing management themes would be a useful resource for researchers and managers.

Clearly, the capability of genetic tools to address fisheries management issues in Australia is diverse and continually developing. In saying this, we recognise the limitations in some tools at their current stage of development. Examples of these include genetic mark-recapture, DNA as a biomarker for age, and fisheries induced and natural selection. Although further development may be required for these and other genetic tools, the rewards are high as they are tools that can help address some of the highest ranked future

management issues. **Taking on innovative approaches that adapt existing high-end genetic technologies; for example, from the medical and pharmaceutical industry, will rely on fisheries geneticists working in new collaborative contexts. The risk of doing this is not necessarily high.** As with existing technologies that have been widely applied in other fields, the risk will not be in the methodology itself but in the adaptation of that technology to a fisheries management context.

Overall, four pathways were identified that were considered to be the key areas with which to move forward. They were the lack of effective communication between geneticists, other scientists, managers and other stakeholders, the need for enhancement of information about fisheries stocks, the provision of estimates of population parameters, without relying on the process of stock assessment modelling and providing support for Ecosystem Based Fisheries Management, particularly where genetics can provide information that is unobtainable (or excessively resource intensive) elsewhere.

9   Benefits and Adoption

9.1   Benefits

1. In this project, an extensive interview process was undertaken of geneticists, other scientists and managers to obtain their perspective on the use of genetics in management. This process highlighted points of commonality, difference and critical gaps. These results were presented to a workshop of stakeholders, which allowed further discussion, comment and ground truthing of the interview findings. The benefits of this process were that it provided a more balanced, inclusive and broader perspective of the project topic. Views expressed therefore are more general and by inference, have more credibility.

2. The project team developed a list of management themes. Managers and others were asked which of these management themes (irrespective of their link to genetics) were priorities in Australian fisheries currently and in the foreseeable future. This list should be of general interest beyond the project.

3. The project also developed genetic themes by which to classify genetic methods for ease of use to those not within the field – in itself useful. However, managers and other scientists will particularly benefit from the table that links both the management and genetic themes and rates each combination in term of readiness, utility, maturity, and cost (Table 6). This means that a stakeholder can enter the Table (and therefore the rest of the report) by either asking "What genetic tool can help (if at all) with this specific management question" or equally asking "What management question can this genetic tool be applied to?" This table is likely to be the most useful product of the report.

4. A thorough review of genetic techniques was undertaken in this project. However, a user-friendly non-technical and shortened version of the different genetic themes is also provided (Field Guide). This is also likely to be an extremely useful output from the report that will benefit a range of stakeholders.

9.2   Adoption

The key area 'Lack of effective communication between geneticists, other scientists, managers and other stakeholders' should be addressed immediately (see Appendix I). Two strategies relate directly to the outputs of this report ('Communication to stakeholders, particularly industry and the community' and 'Communication to a technical audience especially scientists and managers'). The review has shown this area to be an essential gap whereas questions arise about the allocation of resources to achieve them. The other strategy ('Build effective partnerships') in this key area is more long term, but also requires negotiation for resources. Other than the issue of resources, there are no real blockages to solving the long-standing issue of communication, which would have a significant effect at many levels on the role that genetics could play in wild fisheries management.

Another key area ('Enhancement of information about fisheries stocks') was recognised as the most feasible and most attractive area to implement immediately (see Appendix I). Within this area, genetic tools could be immediately used to collect valuable information about the genetic stock structure of fisheries species, assist with the management of mixed-stock fisheries and validate the source of harvested product at all levels in the supply chain. Although some assumptions are necessary to activate strategies in this area, they are minimal. This relative lack of threats means that research in these areas should proceed in a cost-effective and efficient manner. **However, there is considerable further research to be done to implement these strategies and a clear pathway to management implementation is necessary first.**

10   Further Development

10.1   Development and implementation of quantitative survey of stakeholders

The interview data collected for this report provided a highly informative, qualitative survey of the knowledge and attitudes of fisheries stakeholders in Australia and overseas. We used interview questions to encourage interviewees to talk generally about the issues surrounding the use of genetics in fisheries management. This conversational approach provided relatively unrestrained answers, and this is reflected in the diversity of responses we recorded. Yet, this format was limited as it was time-consuming to transcribe responses, the inconsistency of responses amongst stakeholders made quantitative assessments of them difficult, and sometimes these types of responses require subjective interpretation.

In our view, consideration should be given to taking the results of our interviews and using relevant expertise to develop a structured and targeted survey that permits quantitative analysis of the attitudes of stakeholders towards genetics (and other disciplines) in fisheries. A revised survey of stakeholder perceptions of key high level management issues would also be a useful inclusion in a more structured survey process. Many online survey tools are available (e.g. www.surveymonkey.com) that are widely used. With informed survey design, we feel that this could comprehensively and accurately address expanded objectives as part of a project similar to this one.

10.2   Electronic knowledge brokerage via an app

As identified elsewhere in this report (e.g. Section 8.3), scientists and managers often have inadequate knowledge of the availability and appropriateness of different genetic analysis techniques to address management issues that concern them. One of the reasons for this is the lack of accessibility of the relevant information. Developing strategies that educate fisheries managers and scientists about the availability of genetic analysis tools and enhancing channels of communication amongst fisheries stakeholders is a central recommendation of this report. Table 1, Table 6, Section 8.5 and Appendix H represent our efforts to summarise, in an easily understood format, the nature of the available genetic tools, and how each can deliver knowledge that is relevant to fisheries management. In our view, the usefulness and accessibility of this information could be enhanced by a more interactive and customisable electronic platform, such as a web, phone, or tablet-based application ("app"). Such a tool could take Table 1 and Table 6 as a foundation and through clickable links provide instant access to greater depth of explanation either through custom documents, diagrams, scientific publications, or contact details for geneticists working in the relevant field. In doing so, such an app would effectively become a portable knowledge broker for fisheries managers, scientists and geneticists. A useful feature of an electronic platform is that it may be easily adjusted to take account of feedback from users and where new knowledge or techniques are developed.

10.3   Dissemination of the findings of this report

This report represents one of the first joint assessments of the attitudes, requirements and capabilities of fisheries geneticists, scientists and managers in Australia, and its findings are likely to be of interest to a range of interest groups. It is hoped that the findings will contribute to meeting one of the main recommendations of this study, which is to seek ways to improve communication between fisheries geneticists, scientists and managers. There may be opportunities to present the findings in professional forums, such as the Australian Society for Fish Biology and Oceania Chondrichthyan Society Joint Conference and Symposium in July 2012, and elsewhere. We believe that a communication and

dissemination plan for this material should be developed in conjunction with FRDC and stakeholder groups for implementation over the next 12 months. This will ensure maximum benefit from the resources expended on this project and work towards the establishment of new collaborative groups to propel the field into the future. We also believe that such a process would maximise the effectiveness of future R&D investments into fisheries and genetics.

10.4   Implementation of remaining 'key areas'

There were four key areas identified, and two of them were recommended for immediate implementation (see Section 9.2). Although no less important, the remaining key areas ('Provide estimates of population parameters, without relying on the process of stock assessment modelling' and 'Ecosystem Based Fisheries Management support; particularly where genetics can provide information that is unobtainable or cost prohibitive by other means.') received lower priority scores and require considerable investigation of threats potentially blocking implementation plans (see Appendix I). In these key areas, a staged implementation plan is recommended so as to highlight for which species these methods are most likely to be feasible, attractive and address a key management risk.

11   Planned Outcomes

11.1   That FRDC will be better informed about current and future applications of genetics tools

The project has delivered multiple outputs that will directly contribute to this outcome. An extensive literature review and interviews with Australian and international geneticists, fisheries scientists, fisheries managers, and industry have highlighted the current usage of genetics in a fisheries context and also the likely future direction of the use of genetic tools. We have grouped the multitude of genetic applications into logical themes and presented these in different output formats to cater for different audiences depending on their level of technical expertise and interest. These formats include: i) a technical review of each genetic theme with detailed descriptions of the respective genetic tools available (Section 8.1); ii) a simple language 'field guide' describing each genetic theme (Appendix H) a summary or 'look-up' table of genetic tools and how they link to management issues (Table 6). The report also documents key personnel and research groups involved in the use of genetic tools, and their locations within Australia.

Each of these outputs represents useful tools with significant potential to better inform not only FRDC, but all interested stakeholders of the current and future application of genetic tools. They also represent tools with great educational value.

11.2   That FRDC will be in a better position to develop an investment strategy in the area of applying genetics to wild fisheries management

The tools developed and described above also contribute to achieving this planned outcome. From the stakeholder interviews, stakeholder consultation, and the major project workshop, other key project outputs documented in this report also contribute to achieving this outcome. These include an understanding of stakeholder perceptions and understanding of genetic tools and their utility in fisheries, as well as a greater knowledge of the perceived barriers to the use of genetics in fisheries management in Australia. These were identified as issues primarily around communication and in this report we have identified strategies to better overcome this and other issues (Section 8.3.3 and Section 8.4). Further, the project has identified what stakeholders perceive as current and future fisheries management priorities (grouped as management themes) and the tools described above summarise and detail where and how genetics can address each management theme (and specific management issues).

The report combines a full appraisal of current and prospective genetic tools, how they can be applied to fisheries management issues, as well as stakeholder perceptions of priority areas for future management. Further, the report identifies barriers to the uptake of genetic research and documents ways to overcome these barriers so that the effectiveness of future investment strategies into applied genetic research in fisheries in Australia can be maximised.

The information provided here underscores the importance of genetic tools in the management of wild fisheries and provides a basis for investing in the discipline depending on the management need and the capability of genetic tools to respond to that need.

In this report, the pathway analysis (Appendix I) evaluated the relative priorities of four key areas based on their current feasibility and attractiveness. Overall, this has provided clear advice about which areas to target for development and investment.

12 Conclusion

This report analyses the role that fisheries genetics has played in the management of Australian fisheries and provides advice to strengthen outcomes in the future. The report provides a comprehensive description of existing and emerging genetic technologies, a summary of the most important Australia-wide management issues (ranked by stakeholders) and a critical evaluation of the linkages between management issues and genetic technologies. It also presents the attitudes of fisheries stakeholders, geneticists and other scientists to the utility of genetics in fisheries management and incorporates their advice for the future of the discipline. Importantly, the report has integrated across this information to identify four key areas, which have potential significant and immediate value to the Australian fishing industry and analysed ways in which these areas should be implemented. As such, the report provides guidance that will maximise the development, use and uptake of genetic technologies to maintain productive and sustainable harvests for Australian fishing industries. The major conclusions from this project are:

- Genetics represent a diverse collection of versatile and useful tools for informing fisheries managers about all issues that have a biological basis. Genetics cannot address all types of management issues: for example, those with a social or economic basis.
- There is great potential in adapting genetic technologies from other disciplines to fisheries management questions – but the adoption of these technologies relies on fisheries stakeholders, especially geneticists, staying abreast of breakthroughs in these other disciplines and funding agencies supporting the required adaptation.
- Genetic technologies and advances are not well understood by stakeholders in fisheries thereby compromising the effective and optimal use of available tools. Overwhelmingly however, stakeholders feel positive about the role genetics can play in fisheries.
- Communication using non-technical language together with clear input to the management process is the single key issue that is needed to improve the utility and uptake of genetic tools in addressing fisheries management issues in Australia.
- This report includes examples of some of the key communication strategies that could be used (e.g. fisheries managers' genetics 'field guide'). Other strategies that could be developed are: science and stakeholder based workshops, better integration of disciplines in research project teams, and building stronger relationships between fisheries scientists and geneticists as a conduit to and from fisheries managers via Management Advisory Committees.
- Australia possesses a wealth of expertise and experience in the use and application of all available genetic tools that can be applied to fisheries management.
- The genetic tools and technologies most likely to deliver significant advances in Australian fisheries management in the future are:
    - Short term: Continued research in the genetic themes *Product provenance and fisheries surveillance using genetics* (genetic theme 3), *Genetic analysis for the identification of fisheries stock structure* (genetic theme 1) and *Mixed stock analysis using genetics* (genetic theme 10)*. Spatial information on fisheries resources form a basis for management and the genetic methods are well developed, robust and low cost. Many Australian fisheries resources lack this basic information. This method works well when used together with other stock discrimination methods (e.g. parasite distribution and abundance).
    - Medium term: New methodologies such as *Genetic mark-recapture* (i.e. close-kin and genetag) (genetic theme 3) and *Genetic effective population size* (genetic theme 2) estimation already show great promise for measuring spawning biomass, catchability and harvest rates independently to the process of stock assessment modelling. This links directly to the management theme rated the most important in the next decade – *Fisheries status and dynamics* (management theme 2).

- Long term: Detecting and ameliorating the effects of climate change and fishing on fisheries resources [*Fisheries-induced and natural selection* (genetic theme 6) and *Genetics for environmental monitoring and food-web analysis* (genetic theme 11)] will become increasingly important for management. Both of these genetic themes encompass a large range of genetic tools and diverse methodologies and have the potential to provide information that is unique and cannot be obtained in other ways, but further development is still needed.
- The four key areas which have the most potential for the future
  - the lack of effective communication between geneticists, other scientists, managers and other stakeholders,
  - the enhancement of information about fisheries stocks, and
  - the provision of estimates of population parameters, without relying on the process of stock assessment modelling and providing support for harvest strategies, particularly where genetics can provide information that is unobtainable (or excessively resource intensive) elsewhere.

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14   Appendices

Appendix A Intellectual Property

This report reviews genetic methods for application to the sustainable management of wild fisheries in Australia, and provides advice for maximising the outcomes. There is no intellectual property generated as a result of this work that requires protection or acknowledgement.

This work has been performed for the public good.

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Appendix C Glossary of Terms

Allozymes: Proteins used to infer genotypes.

Allele: Refers to a genetic variant that occurs at a location in the genome (locus). Individuals have two allele copies at each locus. The alleles can be identical (individual is homozygous) or they can differ (individual is heterozygous).

AFLP (Amplified Fragment Length Polymorphism): An analysis tool that is used to detect large numbers of DNA sequence variants by means of restriction enzyme digests followed by PCR amplification.

Candidate gene: Gene that is suspected to have a direct functional relationship to a given trait.

Common garden experiment: Experimental procedure to test the genetic basis of traits by studying individuals from different environments under the same controlled conditions (in a 'common garden').

Conspecifics: Two or more individuals belonging to the same species.

Cryptic species: A pair or more of closely related species that are difficult to identify using morphometric characteristics.

Fitness: A measure of the relative reproductive success of an individual, normally measured as the number of adult offspring produced.

F_{ST}: The variance in allele frequences; a measure of genetic population sub-division or structure. Generally, $F_{ST} < 0.03$ indicates little genetic sub-division whereas $F_{ST} > 0.15$ indicate large genetic sub-division.

Genetic diversity: A description of the type and amount of allelic variation at nuclear and mitochondrial loci in a population or a species.

Genetic drift: A basic mechanism of evolution. Genetic drift describes chance changes in the frequencies of different genetic variants within a population. Genetic drift has little effect in large populations, but large effect in small populations.

Genomic resources: Refers to the availability of DNA sequences for a particular species in the public domain, from single gene regions to entire nuclear or mitochondrial genomes. (see also 'next generation sequencing').

Genomics: The study of genetic variation of individuals, populations, and species using whole or large components of the genome.

Genotyping: Process used to identify the genetic variants present at specific parts (loci) or all of an organisms genome.

Inbreeding: Loss of fitness or survival as a result of breeding amongst related individuals.

Locus (plural loci): Refers to the specific genomic location where alternate DNA sequence variants (alleles) are found.

Microarray: An apparatus used to assay genetic variation. Short synthetic DNA sequences (probes) that correspond to genetic variants of interest are attached to a substrate (usually a slide or chip). Probes are interrogated by washing a sample of interest over the slide. Where the sample contains the target genetic variants a signal is emitted and its presence and intensity recorded.

Microsatellites: A type of genetic variation that consists of repeated nucleotide motifs (e.g. CACACA etc.). Genetic variants (alleles) at microsatellite loci differ in the number of repeats. Alleles are assumed to be selectively neutral.

mtDNA (mitochondrial DNA): A circular genome present in multiple copies within mitochondrion organelles in all living cells of the body. MtDNA is maternally inherited and haploid.

Mutation rate: The instantaneous rate at which nucleotide changes occur in the genome. When measured over known number of generations, some authors call it 'pedigree rate'.

Next generation DNA sequencing: Multiple novel technologies for generating large volumes (hundreds of thousands of nucleotides) of DNA sequence. May be applied to sequencing entire genomes of individual organisms, or to sequencing parts of the genome of multiple organisms in environmental samples.

Non-model organism: Typically, these species are not models for biomedical research and have few genetic resources.

Nuclear DNA (nDNA): DNA occurring in the cell nucleus in the form of chromosomes, as opposed to mtDNA, which that occurs outside the nucleus in the mitochondrion.

Nucleotide: Basic building block of DNA molecules that exists as A, T, G or C (Adenine, Thymine, Guanine, Cytosine).

Parentage analysis: The process of assigning offspring to parents based on genetic matches that are consistent with Mendelian segregation.

PCR-RFLP: A method of detecting DNA sequence variation among samples. It involves initial amplification of DNA with PCR, then cutting the DNA with enzymes that recognise specific short sequence motifs (e.g. AAGCTT). Subjecting a sample to one or more restriction enzymes creates fragments of varying size depending on the DNA sequence. Restriction enzymes can be selected that will produce diagnostic DNA fragments for species. The characteristic patterns of DNA fragments may be visualised via gel electrophoresis.

Phenotype: Refers to the physical characteristics of an animal, which are a determined by both its genotype and the environment.

Philopatry (reproductive): Tendency of an individual to remain at, or return to, particular locations to mate and give birth.

Phylogenetic analysis: Process of estimating the evolutionary history of groups of populations, species or higher taxa. DNA sequence data and morphological characters are commonly used.

PCR (polymerase chain reaction): Technique that uses a polymerase enzyme to copy a target DNA sequence from one or a few starting copies.

Population genetics: The study of the distribution of genetic among organisms in time and space.

qPCR (quantitative PCR): fluorescence detection is used to measure the progress of a PCR reaction as the targeted DNA molecule increases in abundance.

Real-time PCR: see qPCR.

Siblings: Animals that share the same mother and father (full-sibs). Half-sibs share either the same mother or same father, but not both.

SNP (single nucleotide polymorphism): Variation in DNA sequence occurring at a single nucleotide position.

Appendix D Interview Questions

Questions for Fisheries Geneticists (national, international)

1. What taxa and what fisheries do you work with?
2. What genetic tools do you use?
3. What management questions does your genetic work address and what management actions resulted from the work?
4. How do you communicate with managers and other stakeholders?
5. What is the attitude of managers towards genetics advice?
6. How will genetic tools be used for management in the future?

Questions for Fisheries Managers/Scientists (national, international)

1. What taxa, fisheries and geographical regions do you work with?
2. Are you aware that genetic analyses of fisheries populations can provide information about the spatial extent of stocks? Have you used this type of information for management? How was it/is it used?
3. Are you aware that other fisheries management questions that genetics can help address? Do you have examples from the work you have been involved with?
4. Some fisheries managers have the view that genetic research plays little role in the science underpinning fisheries management.
   a. Would you agree or not?
   b. Why?
   c. What can be improved?
   d. Could or has this changed over time?
5. Do you think communication between scientists (including geneticists) and managers could be improved? If so, how?
6. What are the most important management questions, now and in the future, which need to be addressed? Which of these do you think may be addressed using genetics?

Questions for Fisheries Industry representatives (national)

1. What species, fisheries and geographical regions do you work with?
2. Are you aware that genetic analyses of fisheries populations can provide information about the spatial extent of stocks? Do you know any examples from the fisheries you have been involved with?
3. Are you aware that other fisheries management questions that genetics can help address? Do you know any examples from the fisheries you have been involved with?
4. Do you think that genetic research has a role to play in the science underpinning fisheries management?
   a. Why?
   b. Can genetics play a more effective role?
   c. How?
5. Do you think communication between fisheries scientists and managers, and the fishing industry could be improved? If so, how?
6. What are the most critical issues affecting fisheries, now and in the future, which need to be addressed?

Appendix E Interviewees

CATEGORY	REGION	NAME	AFFILIATION
Geneticists	International	Paulo Prodohl	Queens University (Ireland)
Geneticists	International	Tom Cross	University College Cork (Ireland)
Geneticists	International	Gary Carvalho	University of Wales (Wales)
Geneticists	International	Per Erik Jorde	Institute of Marine Research (Norway)
Geneticists	International	Robin Waples	National Oceanic and Atmospheric Administration (USA)
Geneticists	International	Serge Planes	Université de Perpignan (France)
Geneticists	International	Peter Ritchie	Victoria University (New Zealand)
Geneticists	International	Sophie Von Der Heyden	University of Stellenbosch (South Africa)
Geneticists	International	Daniel Ruzzante	Dalhousie (Argentina)
Geneticists	International	Fred Allendorf	University of Montana (USA)
Geneticists	International	Michael Hansen	Institute of Fisheries Research (Denmark)
Geneticists	International	Jeff Hard	National Oceanic and Atmospheric Administration (USA)
Geneticists	Australia	Meagan Rourke	Department of Primary Industries (NSW)
Geneticists	Australia	Cathy Nock	Southern Cross University
Geneticists	Australia	Cynthia Riginos	University of Queensland
Geneticists	Australia	Jane Hughes	Griffith University
Geneticists	Australia	Dean Jerry	James Cook University
Geneticists	Australia	Simon Goldsworthy	South Australian Research and Development Institute
Geneticists	Australia	Mark Adams	South Australian Museum
Geneticists	Australia	Luciano Beheregaray	Flinders University
Geneticists	Australia	Phillip England	CSIRO
Geneticists	Australia	Robert Ward	CSIRO
Geneticists	Australia	Sharon Appleyard	CSIRO
Geneticists	Australia	Simon Jarman	Australian Antarctic Division
Geneticists	Australia	Chris Burridge	University of Tasmania
Geneticists	Australia	Jason Kennington	University of Western Australia
Fisheries Managers	International	Magele Etuati Rapeti	Secretariat of the Pacific Community (New Caledonia)
Fisheries Managers	Australia	Steve Matthews	Northern Territory Department of Resources
Fisheries Managers	Australia	Shane O'Donoghue	Western Australian Fisheries

CATEGORY	REGION	NAME	AFFILIATION
Fisheries Managers	Australia	Kevin Donohue	Western Australian Fisheries
Fisheries Managers	Australia	Nathan Harrison	Western Australian Fisheries
Fisheries Managers	Australia	Dallas D'Silva	Department of Primary Industries (Victoria)
Fisheries Managers	Australia	Andrew Goulstone	Department of Primary Industries (NSW)
Fisheries Managers	Australia	Peter Gallagher	Department of Primary Industries (NSW)
Fisheries Managers	Australia	Mark Lightowler	Department of Employment, Economic Development and Innovation (QLD)
Fisheries Managers	Australia	Brigid Kerrigan	Department of Employment, Economic Development and Innovation (QLD)
Fisheries Managers	Australia	Malcolm Dunning	Department of Employment, Economic Development and Innovation (QLD)
Fisheries Managers	Australia	Anthony Roelofs	Department of Employment, Economic Development and Innovation (QLD)
Fisheries Managers	Australia	Eddie Jebreen	Department of Employment, Economic Development and Innovation (QLD)
Fisheries Managers	Australia	Mehdi Doroudi	Primary Industries and Resources (SA)
Fisheries Managers	Australia	Alice Fistr	Department of Primary Industries and Resources (South Australia)
Fisheries Managers	Australia	Craig Noell	Department of Primary Industries and Resources (South Australia)
Fisheries Managers	Australia	Grant Pullen	Department of Primary Industries (Tasmania)
Fisheries Managers	Australia	Andrew Sullivan	Department of Primary Industries (Tasmania)
Fisheries Managers	Australia	Bryan McDonald	Northern Territory Department of Resources
Fisheries Managers	Australia	Jim Prescott	Australian Fisheries Management Authority
Fisheries Managers	Australia	Heather Brayford	Department of Fisheries (WA)
Fisheries Managers	Australia	Steve Auld AFMA	Australian Fisheries Management Authority
Fisheries Managers	Australia	Anthony Forster	Department of Primary Industries (Victoria)
Fisheries Managers	Australia	Randall Owens	Great Barrier Reef Marine Park Authority
Stock Assessment Scientists	International	Rick Officer	Galway-Mayo Institute of Technology (Ireland)
Stock Assessment Scientists	International	Hege Overbo Hansen	Institute for Marine Research (Norway)
Stock Assessment Scientists	International	Oliver Tully	Marine Institute (Ireland)
Stock Assessment Scientists	International	Carl Walters	University of British Columbia (Canada)
Stock Assessment Scientists	International	Ray Hilborn	University of Washington (USA)
Stock Assessment Scientists	Australia	Malcolm Haddon	CSIRO

CATEGORY	REGION	NAME	AFFILIATION
Fisheries Scientists	International	Jann Martinsohn	European Commission Joint Research Centre (Belgium)
Fisheries Scientists	International	Nigel Milner	UK Environment Agency (Wales)
Fisheries Scientists	International	Odd Aksel Bergstad	Institute for Marine Science (Norway)
Fisheries Scientists	International	Richard FitzGerald	National University of Ireland (Ireland)
Fisheries Scientists	International	Johann Bell	Secretariat of the Pacific Community (New Caledonia)
Fisheries Scientists	International	John Hampton	Secretariat of the Pacific Community (New Caledonia)
Fisheries Scientists	International	Andre Punt	University of Washington (USA)/CSIRO
Fisheries Scientists	Australia	Steve Newman	Western Australian Fisheries
Fisheries Scientists	Australia	Daryl McPhee	Bond University
Fisheries Scientists	Australia	Thor Saunders	Northern Territory Fisheries
Fisheries Scientists	Australia	Tim Ward	South Australian Research and Development Institute
Fisheries Scientists	Australia	Steve Kennelly	NSW Fisheries
Fisheries Scientists	Australia	Campbell Davies	CSIRO
Fisheries Scientists	Australia	Colin Buxton	University of Tasmania
Fisheries Scientists	Australia	Chris Barlow	Australian Centre for International Agricultural Research
Fisheries Scientists	Australia	Ian Knuckey	Fishwell Consulting
Fisheries Scientists	Australia	Nic Bax	CSIRO
Fisheries Scientists	Australia	Hugh Possingham	University of Queensland
Fisheries Scientists	Australia	Ilona Stobutzki	Australian Bureau of Agricultural and Resource Economics and Sciences
Fisheries Scientists	Australia	Patrick Hone	Fisheries Research and Development Corporation
Industry	Australia	Michael O'Brien	Raptis
Industry	Australia	Martin Exel	Austral Fisheries
Industry	Australia	Rob Lowden	Seafresh Australia
Industry	Australia	Brian Jeffries	SBT Industry Association of Australia
Industry	Australia	Grant Leeworthy	Tas Seafoods
Industry	Australia	Eric Perez	Queensland Seafood Industry Association
Industry	Australia	Nick Moore	Gold Coast Marine Hatchery
Industry	Australia	Bill Sawynok	RecFishing Research
Industry	Australia	David Carter	Austral Fisheries
Industry	Australia	George Kailis	MG Kailis Group
Industry	Australia	Dave Mills	Paspaley Pearling Co. Pty Ltd
Industry	Australia	Stuart Richey	Richie Fisheries

Appendix F Workshop Agenda

Scoping current and future genetic tools, their limitations and their applications for wild fisheries management – a workshop

Ecosciences Precinct, Brisbane

November 7, 2011

TIME	ITEM
09:00 – 9:10	**Introduction and Welcome** *Cathy Dichmont*
09:10 – 10:10	**Genetics Review** *Jennifer Ovenden, Olly Berry*
10:10 – 10:45	**Morning Tea**
10:45 – 11:45	**Interview Results and Gap Analysis** *David Welch, Rik Buckworth*
11:45 – 12:00	**Setting scene on Communication Workshop** *Cathy Dichmont*
12:00 – 13:00	**Lunch**
13:00 – 15:00	**Communication Workshop** *Group discussion*
15:00 – 15:30	**Afternoon Tea**
15:30 – 16:00	**Management challenges linked to genetics** *Cathy Dichmont, Rik Buckworth*
16:00 – 16:30	**Discussion** *Cathy Dichmont*
16:30	**Workshop end** *Cathy Dichmont*

Appendix G Workshop Participants

NAME	ORGANISATION
Cathy Dichmont	CSIRO
Olly Berry	CSIRO
Rik Buckworth	CSIRO
Dave Welch	C2O Fisheries
Jenny Ovenden	Department of Employment, Economic Development and Innovation (QLD)
Wayne Sumpton	Department of Employment, Economic Development and Innovation (QLD)
Trent Timmiss	Australian Fisheries Management Authority
James Andrews	Fisheries Victoria
Thuy Nguyen	Fisheries Victoria
Mark Bravington	CSIRO
Matt Barwick	Recfishing Research
Steve Kennelly	Cronulla Fisheries Research Centre, NSW Primary Industries
Thor Saunders	Department of Resources, NT
Andy Moore	Australian Bureau of Agricultural and Resource Economics and Sciences
Phillip England	Tasmanian Department of Primary Industries, Parks, Water and Environment
Charles Gray	Cronulla Fisheries Research Centre, NSW Primary Industries
Campbell Davies	CSIRO
Brigid Kerrigan	Department of Employment, Economic Development and Innovation (QLD)
Randall Owens	Great Barrier Reef Marine Park Authority
Petra Lundgren	Great Barrier Reef Marine Park Authority

Appendix H Field Guide

Theme 1: The identification of fisheries stock structure

How does it work and why is it important?

- Stocks are the fundamental units of fisheries management.
- Each stock may respond differently to fishing pressure.
- Population genetics is widely used to determine the spatial extent of fisheries stocks.
- Genetics detects enduring patterns of stock structure, in contrast with other methods that use characteristics acquired during the lifetime of an individual (e.g. parasite load, chemical composition of otoliths).

How is it used for fisheries management?

- Genetic assays of population samples are used to divide the range of a species into stocks.
- Managers use stock assessments to model alternate harvesting scenarios and to design monitoring programs.

Skill set required

- Collaborations are needed between genetic and fisheries scientists and fisheries managers.

Case studies (Australian and International)

- Genetic stock structure was used to determine if separate or co-management was necessary for shark and snapper with continuous distributions in northern Australia and Indonesia.
- Sustainable use of salmonid species in the USA relies on spatial and temporal genetic stock structure analyses.

Technical Challenges

- There is a mismatch in the degree of connectivity between stocks as measured by genetics, demography and ecology.
- Comparison between genetic and ecological data can test for
  - type I errors- genetic structure detected but it has no biological meaning, and
  - type II errors - genetic structure is present but analyses fail to detect it).

Barriers to uptake for fisheries management

- Genetically defined stocks are widely used in management.
- One major challenge is whether management can be applied at the appropriate spatial scale revealed by genetic tests.

Future

- Connectivity between genetic stocks will be understood in the context of population dynamics, allowing seamless update for stock assessment modeling.
- Genomic resources for fisheries species will identify genetic markers under the influence of natural selection. This will address type I errors and highlight stocks with unique adaptive capability.

Theme 2: Genetic effective population size

How does it work and why is it important?

- Genetic effective population size is
  - part of a suite to tools for monitoring populations, and
  - a measure of the resilience of the population to environmental change.
- There are two types; contemporary (short-term) and historical (long-term).
- Estimates are independent of catch-per-unit-effort.

How is it used for fisheries management?

- Genetic effective population size
  - can track changes in absolute abundance,
  - is relevant to time-scales over which harvesting has occurred,
  - has potential for indexing virgin biomass that predates harvesting, and
  - plays a key role in monitoring changes in genetic diversity associated with fisheries enhancement via re-stocking (genetic theme 7).

Case studies (Australian and International)

- The short compared to long-term genetic effective population size of tiger prawns in south-east Queensland was similar, implying harvest rates have been sustainable.
- Genetic effective population size and the spawning population size of sandbar sharks on east coast of US were similar.
- Long-term genetic effective population size estimates for Pacific gray whales suggested that the current target for population recovery is too low.

Technical Challenges

- Short-term effective population size is typically smaller than the number of breeders and the total population size.
- Understanding this ratio is a major challenge.

Skill set required

- This theme requires multi-disciplinary skills in biology, genetics, statistical analysis and management.

Barriers to uptake for fisheries management

- While the concept is simple, its estimation and interpretation is complex, making it challenging to explain to fisheries managers and other stakeholders.

Future

- Close comparisons between estimates of effective size from genetic and demographic data will help to understand how they are related.
- Comparisons between genetic effective population size and estimates of spawner numbers from other systems where genetic markers are used (e.g. mark-recapture studies, genetic theme 3) will assist both fields.

Theme 3: Genetic mark-recapture for estimating mortality and abundance

How does it work and why is it important?

- Individuals are genetically tagged from a small tissue sample that doesn't necessarily require capture of the animal.
- Individuals are tagged using their unique DNA fingerprint.
- Tag loss and under-reporting does not occur with genetic tags.
- Genetic tagging program needs to be designed so each individual has a unique tag and is free of errors when read.

How is it used for fisheries management?

- Genetic tags function in the same manner as conventional tags.
- Abundance and other population parameters can be estimated from the recapture of individuals identified with genetic tags.
- Genetic tagging can be used for routine monitoring of fisheries.

Case studies (Australian and International)

- Genetic tagging was first applied to humpback whales in the North Atlantic. Estimates of abundance based on photo records were shown to be underestimates.
- The 'genetag' project used a unique hook design to take tissue samples from Spanish mackerel in NT for a genetic mark-recapture assessment of mortality.
- A 'close-kin' approach is being taken with southern bluefin tuna, where parent-offspring pairs are detected through parentage analysis and analysed as recaptures, and is being incorporated into the assessment of the fishery.

Technical Challenges

- Challenges such as lack of power to identify individuals and genotyping errors need to be anticipated and addressed in advance.

Barriers to uptake for fisheries management

- Costs per tag are higher than conventional tagging methods, but other costs (such as deployment, resampling and analysis) are similar.
- Higher costs must be traded off against the advantages of genetic tagging.

Skill set required

- Genetic tagging requires integrated team skills including population genetics and fisheries mark-recapture.

Future

- Genetic tagging is a relatively new and active field of research in the marine environment, but has been widely adopted for monitoring terrestrial fauna.

Theme 4: Product provenance and fisheries surveillance using genetics.

How does it work and why is it important?

- Samples can be tested to see if they come from individuals, families, populations, or species of interest.
- Accurate identification in this way provides a powerful and unique enforcement and surveillance tool.

How is it used for fisheries management?

- The technology is typically used for post-harvest analyses, such as the detection of product substitution and checking accuracy of labeling.
- Individuals can be assigned to biological or jurisdictional stocks as an enforcement tool.

Skill set required

- Team members should be skilled in population genetics, fisheries sciences and fisheries management.
- Legal expertise is useful if the data is to be presented as evidence in court.

Case studies (Australian and International)

- In 2011, 10 - 30% of Atlantic cod products were mislabeled in UK (Wales). In Australia in 2003, mislabeling was running at an average of 25%.
- A fisher was fined for possessing female mud crabs allegedly caught in the Northern Territory, but were genetically assigned to a Queensland population where females are protected.
- The species and population of origin was determined for pelagic seabirds that were part of fisheries bycatch.

Technical Challenges

- Appropriate reference samples are required for most applications.
- Genetic distinction between reference samples is essential. For example, individuals can be assigned to populations only when the populations are genetically different.

Barriers to uptake for fisheries management

- Establishing reference samples requires a coordinated effort ahead of application of the technology, which may involve significant cost.
- There is no coordinated, quality-assured network of laboratories across Australia to perform this type of work.

Future

- Seafood producers may use genetic provenance testing to accredit their product and protect their commercial interest and reputation.
- Customized genetic marking may be incorporated into cultured products to facilitate identification of genuine products.

Theme 5: Species recognition using genetics

How does it work and why is it important?

- DNA sequences retain evidence of their evolutionary history, thus can be used to recognize species.
- Accurate taxonomic knowledge forms the foundation for species recognition using genetics. Molecular systematics often forms the foundation for taxonomic descriptions and revisions.
- Barcoding uses standardised DNA sequences to assign specimens to species using known reference data.
- Species recognition using genetics is a special case of Genetic Theme 4 (above).

How is it used for fisheries management?

- Species recognition using genetics is useful if the specimen (eg fish fillet) cannot be identified in other ways.
- It has application in research, monitoring and marketing.
- DNA is essential for the recognition, and hence management of cryptic species.

Skill set required

- Expertise is needed in DNA extraction, sequencing and phylogenetic analysis.
- Although species recognition is not reliant on taxonomic expertise, it is required to set up reference data.
- Legal expertise is useful if the results are to be presented as evidence in court.

Case studies (Australian and International)

- 90% of 752 freshwater fish species in North America could be recognised using genetics.
- DNA species recognition showed that a black-tip shark species in northern Australia was more abundant (compared to another related species) than expected.

Technical Challenges

- Species recognition using DNA is accurate in the majority of cases, but is susceptible to reference data problems (lack of data, database errors) and issues with the type of DNA used (mtDNA; nuclear transfer, hybridization).
- Reference data per species should consist of DNA sequences from many genes, if possible.

Barriers to uptake for fisheries management

- There are no significant technical barriers to uptake by fisheries management, but it is not a tool that can be used in the field.
- Other barriers are similar to Genetic Theme 4 (above).

Future

- Species descriptions will increasingly include DNA sequences as diagnostic characters.
- DNA barcodes will soon be available for most commercial and bycatch species in Australia.

Theme 6: Fisheries-induced and natural selection

How does it work and why is it important?

- Harvesting can change the genetic characteristics of populations by removing individuals with specific traits (eg large body size, which may have faster growth rates). Over generations, these changes may reduce the productivity or resilience of fisheries.
- Natural selection results in genetic adaptation to local environments.
- Adaptive genes can
    - reveal genetic stock structure where conventional DNA markers do not, and
    - explain the genetic basis for survival in a changing environment.

How is it used for fisheries management?

- Build-up of undesirable genetic characteristics in a fisheries population may threaten productivity and sustainability.
- Management should strive to preserve original genetic diversity to maximise population resilience.

Case studies (Australian and International)

- Due to fisheries-induced selection North Atlantic cod and plaice populations now reproduce at smaller sizes and earlier life-stages.
- It is not clear whether fisheries-induced selection or increasing water temperature has been responsible for smaller body sizes in wild harvested Western rock lobster.
- Separate populations of Atlantic cod and European flounder were not detected with conventional genetic methods, but were identified by assaying genes linked to local adaptation.

Skill set required

- Expertise is needed in population genetics, genomics and translocation experiments in the wild and in captivity.

Technical Challenges

- Detection of fisheries-induced selection is difficult and may require experimental manipulations.
- Studying genes under selection is challenging as only a few fisheries species have genomic resources.

Barriers to uptake for fisheries management

- Managers are unlikely to act without clear evidence of detrimental evolutionary change associated with fishing.

Future

- Fisheries-induced selection is likely to become more recognised in Australia.
- Genomic resources are increasingly becoming available for fisheries species and will provide a means to understanding adaptive traits, including those associated with environmental (climate) change.

Theme 7: Genetic effect of captive-bred fishes on wild conspecifics

How does it work and why is it important?

- Captive-bred and wild individuals of a species interbreed when individuals escape from aquaculture or are deliberately released (e.g. restocking).
- Resulting offspring may be poorly adapted to natural environments, which can reduce the overall fitness and genetic diversity of wild populations.

How is it used for fisheries management?

- Managers are alert to the effect of aquaculture escapees on wild populations. This underlies management strategies as deleterious effects on wild fisheries populations are difficult, if not impossible, to undo.
- Re-stocking may fail if captive-bred recruits are poorly adapted to the local environment.
- Many agencies have clear policies and guidelines for restocking, and genetics typically provides an integral basis to these.

Case studies (Australian and International)

- Genetic diversity of eastern Australian freshwater cod populations decreased by over 20% due to swamping of local population with captive-bred fingerlings.
- The reproductive success of offspring of captive-bred steelhead trout in North America was 40% below wild conspecifics.

Technical Challenges

- Detecting the genetic effect of captive-bred fish when they interbreed with wild populations is challenging and requires considerable resources and time.

Barriers to uptake for fisheries management

- A balance is needed between the requirement for re-stocking or aquaculture and the possible consequences on natural fisheries populations.

Skill set required

- To investigate cases of genetic leakage, population geneticists need to work with field biologists and fisheries scientists as well as fisheries managers.

Future

- The likelihood of deleterious effects in Australian fisheries resources is increasing as aquaculture and re-stocking becomes more common.

Theme 8: DNA as a biomarker for age

How does it work and why is it important?

- The age of individuals from some valuable wild fisheries (eg crustaceans) can't be measured by sectioning hard parts (like otoliths in finfish).
- Telomeric DNA occurs at the end of chromosomes. As the animal gets older it decreases in length and has been suggested as a surrogate for age.

How is it used for fisheries management?

- If the rate of decrease of telomeric DNA was known, age (and hence growth) could be inferred from its length.
- Age is essential for estimating individual growth rates. Growth data would be valuable in stock assessment modeling.

Skill set required

- This type of research requires advanced molecular genetics skills, along with fisheries science and statistical expertise.

Case studies (Australian and International)

- A relationship was demonstrated between telomere length and shell size in abalone from Tasmania (r^2 = 0.833, P < 0.001), but it has not been extended to telomere length and age in this species.
- In North America, it has been applied to a non-fisheries species (small mammals harvested from the wild for fur). The accuracy of telomeric DNA to assign age improved when other biological information was available (e.g. body size or sex).

Technical Challenges

- As well as age, telomere length may also be correlated with cumulative biological stress (eg thermal or food stress).
- Calibrating the rate of telomere attrition is challenging if the species cannot be maintained in captivity or aged in other ways.
- Less expensive assays for telomere length are needed.
- Assays for telomere length may need to be developed *de novo* for each species and calibrated per population.

Barriers to uptake for fisheries management

- The main barrier is that not enough is known about DNA as a biomarker for age in fisheries species.

Future

- There are other DNA-based biomarkers, for age, but little is known about them.
- Knowledge about telomeric DNA will rapidly increase as genomic resources become available for fisheries species.

Theme 9: Genetics for disease detection in wild fisheries

How does it work and why is it important?

- Genetic assays can diagnose and quantify the incidence of diseases in wild and aquaculture fisheries.
- Rapid diagnosis of disease enables a targeted response, which is likely to increase its effectiveness.

How is it used for fisheries management?

- The assessment of the likely outcomes of the disease outbreak is essential for management action.

Skill set required

- The key areas are appropriate facilities and expertise for containment of biosecurity risks, and integration of molecular genetics with other aspects of disease diagnoses.

Case studies (Australian and International)

- Genetic assay for a viral disease of farmed and wild abalone was developed and deployed in southern Australia.
- In North America, genetic assays have been used to study the complex life cycle of a cellular parasite of Atlantic Salmon and Sea Bream.

Technical Challenges

- Novel tests need to be developed when new pathogens are encountered.
- Genetic assays face similar technical challenges as non-genetic tests, such as incidence of false positive and false negative results.

Barriers to uptake for fisheries management

- Monitoring wild populations throughout their range is expensive.

Future

- The potential for the spread of disease into wild populations will rise as more Australian species are farmed within their natural ranges.
- Environmental change (e.g. increasing water temperature) may change the range of a pathogen and the way in which pathogen and hosts interact.

Theme 10: Mixed stock analysis using genetics

How does it work and why is it important?

- Some fisheries resources consist of multiple stocks at the time and place of harvest.
- Mixed stocks can occur when breeding stocks disperse for feeding.
- Mixed stock analysis determines the proportion of the harvested aggregation belonging to each breeding stock.

How is it used for fisheries management?

- It allows mixed aggregations to be exploited whilst enabling independent management of breeding stocks.
- Few harvested species in Australia exhibit life histories suited to mixed stock analysis.

Skill set required

- A standard collaboration is needed for this theme, involving fisheries scientists and population geneticists, with assistance from statistician for data analyses.

Case studies (Australian and International)

- Harvested Atlantic cod from the eastern Canadian coast was shown to represent several breeding populations, in proportions ranging from 8 to 71%.
- If fishing were to recommence, some breeding populations would thus be more affected than others.

Technical Challenges

- Mixed stock analysis
  - relies on pre-existing baseline (reference) genetic data on breeding stocks,
  - requires genetic differences between breeding stocks.

Barriers to uptake for fisheries management

- Mixed stock analysis is widely used for management outside Australia, so could be readily taken up by Australian fisheries managers.

Future

- Australian species where mixed stock analysis may be needed in future include
  - sharks that have inshore breeding locations (e.g. bull and white sharks), and
  - species whose life cycles alternate between freshwater, estuarine and marine feeding and breeding stages (e.g. mullet).

Theme 11: Genetics for environmental monitoring

How does it work and why is it important?

- Genetic tools may assist ecosystem-based management.
- Genetic tools enable food web analysis, the detection of invasive species and monitoring environmental quality.

How is it used for fisheries management?

- DNA studies can reveal the diets of organisms. Dietary studies and food web analysis can be used to understand the indirect effects of fishing on ecosystems.
- Traces of DNA in the environment can reveal the presence of invasive species.
- Gene expression profiles can reveal the presence of pollutants.

Skill set required

- To implement these analyses, molecular genetics expertise and fisheries science expertise is needed with input from bioinformaticians.

Case studies (Australian and International)

- Whole genome sequencing validated the diet of fur seals.
- DNA sampled from the environment detected carp in advance of an invasive front in north-east USA.
- Environmental contaminants (e.g. copper) in north American environments were detected by assaying for gene expression in minnows.

Technical Challenges

- Analysis of whole genomes using next generation DNA sequencing is computationally intensive, but this is the case for all applications of this type of data.
- The detection of invasive species is best suited to confined water bodies.

Barriers to uptake for fisheries management

- DNA-based food-web information needs to be incorporated into ecosystem models prior to uptake by managers.

Future

- All three methods are likely to benefit from genomic resources being available for fisheries species.

Appendix I Pathways for adoption of genetic technology in Australian wild fisheries management

I.1 Purpose

This section describes the adoption and further development of pathways to address the bottlenecks that stand in the way of the use of genetic technologies in the management of wild fisheries. A ranking process is used to generate suggested options for staged investment strategies that maximise the benefits of applying genetic technologies to the management of wild fisheries.

Section 8.4 of this report highlighted that a lack of shared understanding between geneticists, fisheries scientists, fisheries managers and other stakeholders was a major bottleneck to the wider adoption of genetics in wild fisheries management.

The other bottlenecks identified relate to the technical improvements needed for genetics to better meet the needs of fisheries management. The probable R & D timeframes differ among applications. Applications most likely to yield results in the short-term were *Product provenance and fisheries surveillance using genetics* (genetic theme 3), *Genetic analysis for the identification of fisheries stock structure* (genetic theme 1) and *Mixed stock analysis using genetics* (genetic theme 10). In the medium term, they were *Genetic mark-recapture for estimating mortality and abundance* (theme 3) and *Genetic effective population size* (genetic theme 2). In the longer term, they were *Genetics for environmental monitoring* (genetic theme 11) and *Fisheries-induced and natural selection* (genetic theme 6).

I.2 Methods

I.2.1 KEY AREAS

Pathways were divided into the following key areas (A to D), with associated strategies (1, 2, 3 etc). These are based on the outputs from the review (especially key issues highlighted in the Further Development section). The Key Areas start mainly with short term implementation requirements and then to medium and long term strategies:

- A. Lack of effective communication between geneticists, other scientists, managers and other stakeholders.
  1. Communication to stakeholders, particularly industry and the community.
  2. Communication to a technical audience especially scientists and managers.
  3. Build effective partnerships.
- B. Enhancement of information about fisheries stocks.
  1. Evaluate the need for stock structure information and undertake research, if required.
  2. Provide breakdown of catch by stock in multi-stock fisheries.
  3. Validation of catch and supply chain data.
- C. Provide estimates of population parameters, independent of stock assessment modelling.
  1. Estimates of spawning biomass.
  2. Estimates of catchability and harvest rates.
- D. Ecosystem Based Fisheries Management support; particularly where genetics can provide information that is unobtainable or cost prohibitive by other means.
  1. Species recognition for diet matrices for use in ecosystem-based analyses.
  2. Managing the effects of fishing on a species such as selectivity (size, age, sex etc.).

3. Addressing the scale of conservation management and how it interacts with fisheries management e.g. gene, stock, population, species. Strategically addressing how this will change when genetic techniques mature to monitor adaptive genes (aka genes under selection).

I.2.2 IMPLEMENTATION PLAN

An Implementation Plan is presented for each Key Area. These are broken down into Strategies to achieve outcomes for that Key Area. Actions for the implementation of strategies are presented in Table 9, Table 10, Table 11 and Table 12.

Strategies are subjectively ranked by Feasibility and Attractiveness to give a priority ranking within the key areas. Ranking in this way addresses a major motivation for the commissioning of the overall report (whether, when, and after what research and development could genetic techniques provide a cheaper and better way to support fishery management than the current ways).

Feasibility is defined as

1. Readiness (availability of expertise at multiple sites in Australia).
2. Maturity (availability of practical and theoretical tools).

Attractiveness is defined as

1. Costs (based on estimate of consumable costs without infrastructure or salary costs).
2. Utility (likelihood that a genetic tool will directly address the management issue).

The feasibility and attractiveness rankings across strategies are based on those used to link issues in fisheries management to genetic themes (Table 6).

The feasibility and attractiveness rankings for each strategy are combined into five priority rankings (A – E, Table 7).

Table 7. Conversion of attractiveness and feasibility rankings into a priority score (A to E).

Attractiveness	High#	C	B	A
	Medium#	D	C	B
	Low#	E	D	C
		Low#	Medium#	High#
			Feasibility	

I.3   Results

A summary of the overall results is provided in Table 8. These are drawn from Table 9 to Table 12, which details different Implementation Strategies for each Key Area.

Table 8. Summary of the priorities assigned to key genetics in fisheries needs.

KEY AREA	STRATEGY	PRIORITY (BASED ON FEASIBILITY AND ATTRACTIVENESS)
Lack of effective communication between geneticists, other scientists, managers and other stakeholders.	Communication to stakeholders, particularly industry and the community.	A
	Communication to a technical audience especially scientists and managers.	A
	Build effective partnerships.	A
Enhancement of information about fisheries stocks	Evaluate the need for stock structure information and undertake research, if required.	A
	Provide breakdown of catch by stock in multi-stock fisheries	A
	Validation of catch and supply chain data	A
Provide estimates of population parameters, without relying on the process of stock assessment modeling	Estimates of spawning biomass	C
	Estimates of catchability and harvest rates	B
Ecosystem Based Fisheries Management support; particularly where genetics can provide information that is unobtainable or cost prohibitive by other means.	Species recognition for diet matrices for use in ecosystem-based analyses	B
	Managing the deleterious effects of fishing as a selective force, including the significant loss of productivity that this could ultimately involve.	D
	Addressing the scale of conservation management and how it interacts with fisheries management e.g. gene, stock, population, species. Strategically addressing how this will change when genetic techniques mature to monitor adaptive genes (aka genes under selection).	D

I.3.1 KEY AREA A: LACK OF EFFECTIVE COMMUNICATION BETWEEN GENETICISTS, OTHER SCIENTISTS, MANAGERS AND OTHER STAKEHOLDERS

All of the three strategies for this key area were given a high priority based on feasibility and attractiveness (Table 9). All these strategies are given a high priority in light of the stakeholder review which highlighted this as a major issue.

The establishment of a "Genetics in Fisheries Advisory Board" was considered critical to the implementation of actions across all key areas examined here (A, B, C and D). Further consideration of how such a body would operate and be funded is required.

Table 9. Implementation Plan (Key Area: Lack of effective communication between geneticists, other scientists, managers and other stakeholders).

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
1. Communication to stakeholders, particularly industry and the community.	Publication of this final report will initiate the process of communication between geneticists and stakeholders, which is advocated here. It will capitalise on the effort and expertise invested in report production.	H	H	A	1. A press release campaign led and promoted by CSIRO in conjunction with other agencies.	Report team members	X		
					2. A 'roadshow', where report authors present outcomes of the report to stakeholders around the country. Key components of the roadshow will be to (a) disseminate findings presented here, (b) hand-out brochures (and demonstrate if web-based) of key elements of the report (for example, the 'look-up' table - section 8.5, table 6 - and the 'field-guide' - appendix H) and to (c) canvas support for other communication action items (workshops, advisory boards). A funding request would need to be developed for a 'roadshow' to support items such as travel, production costs for the hard-copies, support for web-development tools, venue hire, administration support and team member participation. A TRF to FRDC may be the most appropriate route.	Report team members	X		
2. Communication to a technical audience especially scientists and managers	Publication of components of the report will communicate report to a wide audience and make it more freely available. Publications will be aimed at audience sectors such as industry, fisheries managers and fisheries scientists.	H	H	A	1. Articles for FRDC's publication FISH. The audience for this will be members of the fishing industry, representatives of peak-bodies and researchers involved in fisheries. The team will take advantage of the science-journalists who are contracted to FISH to distill elements of the report for the target audience. At least one article will be prepared, but there may be opportunity for follow-up articles on the genetics in fisheries 'roadshow',	Report team members, FISH team	X		

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
					workshops and advisory boards.				
					2. Articles into other industry and stakeholder newsletters. Effort needs to be put into scoping these out in conjunction with agency media offices and in consultation with experts (e.g. from FISH). Depending on extent of overlap and following negotiation with the FISH team, material prepared for FISH could be revised for these publications.	Report team members.	X		
					3. Submission of selected parts of the report to journals (e.g. *ICES Journal of Marine Science, PLOS Biology, Trends in Ecology and Evolution* or *Marine Policy*) read by fisheries managers.	Team members (Cathy Dichmont, Rik Buckworth and David Welch)	X		
					4. Submission of selected parts of the report to journals read by fisheries geneticists and fisheries scientists (e.g. *Fish and Fisheries*).	Team members (Jenny Ovenden and Oliver Berry).	X		
3. Build effective partnerships	The objectives of communication workshops are (a) for learning: for example, managers, industry representatives and scientists about the field of fisheries genetics, fisheries geneticists and scientists about the field of fisheries management, and scientists and managers about the challenges of operating a fisheries business, (b) to establish open, jargon-free channels of communication, (c) to facilitate development of, and engagement in, research projects aimed at current issues in fisheries management, (d) for discussion of uncertainties, limitations and implications of fields of endeavor, and (e) to establish effective partnerships between fisheries scientists and geneticists, where scientists	H	H	A	1. Facilitate workshops focused on science, such as what genetics can offer fisheries science and management. Workshops could be part of fisheries and modeling conferences (e.g. Australian Society for Fish Biology, or Australian Marine Sciences Association) and they should be regular and on-going. Request external funding support (e.g. TRF from FRDC).	Fisheries geneticists.	X		

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
	act as a conduit for genetics via advisory groups (e.g. RAGs, MAC's) to managers.								
X					2. Facilitate stakeholder-oriented workshops, involving a wide participant list (e.g. including fishers and industry). An example of a possible workshop could be 'Latest techniques in fisheries science, including new questions' and genetics would be a major part of this. The most important aspect to include is the management questions, and managers information needs. Communication should focus more on the best method of communicating complex methods (including genetics) so inclusion of science communicators in the planning would be essential. Request external funding support (e.g. TRF from FRDC).	Fisheries geneticists, fisheries scientists, fisheries managers, fishing industry representatives.			X
					3. Scope out a Genetics in Fisheries Advisory Board (GIFAB). Consult with key stakeholders about how the advisory board would operate, communicate to stakeholders and how it would be supported. This should be done as part of the 'roadshow' (above). Prepare business plan to cover these aspects and financial requirements and sources of income.	Fisheries geneticists, fisheries scientists, fisheries managers, fishing industry representatives.	X		
					4. Establish GIFAB. The goals of a GIFAB would be to (a) conduct strategic studies to anticipate major shifts in genetic science for the benefit of the fishing industry, (b) to facilitate reviews and surveys to provide advice on cost-effective and focused applications of genetics in wild fisheries, and (c) provide advice on genetics at national level (e.g. AFMF, FRDC, ARC). Examples of the operation of GIFAB are given in implementation plans for other key areas.	Fisheries geneticists, fisheries scientists, fisheries managers, fishing industry representatives.		X	

I.3.2 KEY AREA B: ENHANCEMENT OF INFORMATION ABOUT FISHERIES STOCKS

The three strategies for this key area were given a high priority based on feasibility and attractiveness (Table 10).

Despite this high ranking, assumptions made in the 'stock structure' strategy need further assessment. A sensitivity analysis is recommended on the capacity of resource managers of a particular stock to use new stock structure information. For example, if stock structure was found to exist on a fine-spatial scale, what is the range of options available to managers to implement harvest strategies on this scale? Likewise, further analysis is recommended on 'migration window' where genetics is unable to detect demographically separate stocks but where insufficient migration is occurring to demographically correlate stocks. This phenomenon has been recognised in the literature {Lowe, 2010 #80;Ovenden, In preparation #203;Waples, 2006 #93} and is important to the further development of the application of genetics to the analysis of stock structure in fisheries.

Likewise, one assumption made for the 'provide breakdown of catch by stock in multi-stock fisheries' needs further risk assessment. The assumption is made that, if information were available on the origin by stock of individuals in the harvest, then the harvest strategy would be able to encompass this information and provide guidelines for the most appropriate response. This assumption is similar to that addressed above: that managers would be able to manage on fine spatial scales, if genetic analysis showed the presence of multiple stocks.

Table 10. Implementation Plan (Key Area: Enhancement of information about fisheries stocks).

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
1. Evaluate the need for stock structure information and undertake research, if required.	Population genetic structure is a useful proxy for stock structure because genetic differences between regions imply a limitation to dispersal. The technology to apply genetics to the assessment of stock structure is widely available, rapid and cost effective. See genetic theme 1	H	H	A	1. Survey Australian fisheries resources for data on genetic stock structure	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					2. Determine the capacity of managers to make use of new stock structure data	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					3. Determine need for research based on 1, 2 and value of the fishery	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
X					4. Collect and interpret new data on genetic fisheries stock structure for Australian fisheries species.	Fisheries geneticists, fisheries managers, fisheries scientists, industry			X
X					5. Theoretical studies on the interpretation of population genetic patterns (e.g. Genetic isolation-by-distance, metapopulations) in marine species, and their implication for harvest strategies.	Fisheries geneticists, theoretical geneticists, fisheries population modelers.			X
					6. Ensure two-way communication of outcomes.	Fisheries geneticists, fisheries		X	

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
						managers, fisheries scientists, industry			
2. Provide breakdown of catch by stock in multi-stock fisheries	Mixed stock analysis is relevant to species that breed in one location and move to another location to feed, and where exploitation occurs in the feeding phase. It allows management of the feeding population to protect breeding populations. See genetic theme 10	H	H	A	1. Survey Australian fisheries resources for evidence of multi-stock fisheries	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					2. Determine the capacity of managers to make use of new data on multi-stock fisheries.	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					3. Determine need for research based on 1, 2 and value of the fishery	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					3. For multi-stock fisheries, identify spatial and temporal characteristics of spawning stocks, collect genetic reference data and ensure sufficient statistical power for assignment testing	Fisheries geneticists, fisheries managers, fisheries scientists, industry			X
					4. Apply to individuals from mixed stocks.	Fisheries geneticists			X
					5. Ensure two-way communication of outcomes.	Fisheries geneticists, fisheries managers, fisheries scientists, industry		X	

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
3. Validation of catch and supply chain data	The technology can trace a single individual (e.g. whale, dugong, turtle, sawfish) through the supply chain, can trace harvested individuals back to population of origin and recognise the species identity of fisheries products along the marketing chain. These methods can be used by processors to validate the source and species of product to satisfy consumer demand for quality and traceability and by public organisations for surveillance of illegal and inappropriate harvest practices. See genetic theme 4.	H	H	A	1. Conduct a survey of stakeholders (public and private organisations) to determine the need for this genetic technology in Australia.	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					2. Determine if method development should be funded by private sector (i.e. for in-house quality control) or public sector (i.e. for surveillance and enforcement).	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
X					3. Provide support for in-house development of tools, if required.	Genetics in Fisheries Advisory Board (GIFAB)			X
					4. Collect reference data from individuals, populations or species (as needed) and ensure sufficient power for assignment testing using the genetic reference data.	Fisheries geneticists, fisheries scientists			X
X					5. Apply to individuals sampled from multi-stock harvest.	Fisheries geneticists			X
					6. Ensure two-way communication of outcomes.	Fisheries geneticists, fisheries managers, fisheries scientists		X	

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
					7. Scope out the establishment of a national database to contain genetic data and the establishment of a 'virtual network' of qualified personnel lab to perform identification work, when required.	Genetics in Fisheries Advisory Board (GIFAB)		X	

I.3.3 KEY AREA C: PROVIDE ESTIMATES OF POPULATION PARAMETERS, WITHOUT RELYING ON THE PROCESS OF STOCK ASSESSMENT MODELLING

The two strategies for this key area were given different priorities based on feasibility and attractiveness (Table 11). Although many wild fisheries would benefit from information about spawning biomass (strategy one), this area was given a 'medium' score for attractiveness and feasibility (leading to a priority score of 'C') because of the development that needs to be done in this area to bring it into mainstream use. Strategy two (Estimates of catchability and harvest rates) was given the priority ('B') as much of the groundwork for the implementation of the methodology has been completed, but many fisheries may not require this analysis. However, for some key species these methods are essential, for example when a resource is high value and classic stock assessment methods are not robust.

Table 11. Implementation Plan (Key Area: Provide estimates of population parameters, without relying on the process of stock assessment modelling.).

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
1. Estimates of spawning biomass	Estimates of spawning biomass for a fisheries stock can be inferred from genetic estimates of effective population size (Ne) and from close-kin analyses. See Genetic Theme 2 (Genetic effective population size) and Genetic Theme 3 (Genetic mark-recapture for estimating mortality and abundance).	M	M	C	1. More fully understand the conditions (e.g. species life-histories, exploitation histories, population structure, sampling regimes) under which Ne and close-kin provide robust estimates of spawning biomass; for example by using (a) theoretical studies to understand the effect of declining spawning biomass (i.e. over the course of fishery) on Ne and close-kin estimates, and where mixed age cohort samples are used to estimate Ne, (b) theoretical studies to understand the effect of models of population structure on spatially explicit estimates of Ne, (c) cross-referencing Ne and close-kin estimates for the same genetic datasets and (d) ground-truth Ne and close-kin estimates of spawning biomass by comparison with independent estimates of spawning biomass, for example by using capture-mark-recapture methods.	Fisheries geneticists, theoretical geneticists			X
					2. Survey Australian fisheries resources (by value) where genetic estimates of spawning biomass (Ne, close-kin) would have (a) significant value (economic or conservation) for supporting harvest strategies and (b) could be feasibly implemented. Develop case on how to differentiate between the different methods to estimate spawning biomass, including genetics.	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					3. Integration of genetic estimates of spawning biomass with stock assessment models or operating models within Management Strategy Evaluations.	Fisheries geneticists, fisheries stock assessment modelers.			X

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
					4. Design, implement and interpret Ne and close-kin studies on high-value fisheries species.	Fisheries geneticists, fisheries scientists.			X
					5. Ensure two-way communication of outcomes to all stakeholders.	Fisheries geneticists, fisheries managers, fisheries scientists, FRABs, RAGs and MACs (or their equivalent)		X	
2. Estimates of catchability and harvest rates	Using genotypes as a surrogate for physical tags (i.e. gene tagging) overcomes many of the problems associated with conventional capture-mark-recapture studies. See Genetic Theme 3 (Genetic mark-recapture for estimating mortality and abundance)	H	M	B	1. Survey Australian fisheries resources (by value) where gene tagging would have (a) significant value for supporting harvest strategies and (b) could be feasibly implemented (i.e. species from which tissue can be sampled non-lethally in the field, large body-size species to minimise number of individuals in harvests).	Genetics in Fisheries Advisory Board (GIFAB)	X	X	
					2. Design, implement and interpret gene tagging studies on high-value fisheries species, taking into account previous studies (e.g. Buckworth *et al.*, 2012. FRDC 2002/011).	Fisheries geneticists, fisheries scientists.			X
					3. Ensure two-way communication of outcomes.	Fisheries geneticists, fisheries managers, fisheries scientists		X	

I.3.4 KEY AREA D: ECOSYSTEM BASED FISHERIES MANAGEMENT SUPPORT; PARTICULARLY WHERE GENETICS CAN PROVIDE INFORMATION THAT IS UNOBTAINABLE OR COST PROHIBITIVE BY OTHER MEANS

The three strategies for this key area were given priorities of 'B', 'D' and 'D' based on feasibility and attractiveness (Table 12). This key area has the potential to provide valuable information to support the long-term, profitable future of Australia's wild fisheries, and this information can only be gained by the application of genetics methodology. However, strategies in this area are challenging and expensive to implement, and require a great deal of groundwork and further development. There is an important role for the proposed Genetics in Fisheries Advisory Board to facilitate and advocate this type of research.

Table 12. Implementation Plan (Key Area: Ecosystem Based Fisheries Management support; particularly where genetics can provide information that is unobtainable or cost prohibitive by other means).

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
1. Species recognition for diet matrices for use in ecosystem-based analyses	Ecosystem-based analyses need reliable food-web knowledge to predict the effect of changes in the species abundance across the ecosystem. Genetic species recognition on gut-contents or faeces is a reliable and rapid alternative to microscopic examinations. See genetic theme 5 (Species recognition using genetics).	H	M	B	1. Develop a web-based portal to databases containing microbial, animal and plant sequences that can be used for species recognition, along with clear information about methods to amplify and sequence the gene regions containing the target sequences.	Genetics in Fisheries Advisory Board (GIFAB)			X
					2. An indexed collection of web-based methods to collect, preserve, extract and analyse tissue samples from all levels of marine consumers.	Genetics in Fisheries Advisory Board (GIFAB)		X	
					3. Sponsorship for biodiversity discovery, taxonomic description and sequence collection from Australian marine habitats.	Genetics in Fisheries Advisory Board (GIFAB)			X
2. Managing the deleterious effects of fishing as a selective force, including the significant loss of productivity that this could ultimately involve.	Harvesting of fisheries species often systematically removes individuals with specific characteristics (e.g. large body-size, slow swimming speed). If these traits are able to be inherited by offspring, the traits are controlled in part by one or a number of genes. Removal of these animals from the population by harvesting also removes these genes. In the case of genes for large body size, the result will be individuals that have smaller body size. These animals may produce fewer offspring than larger individuals, in which case recruitment into the population will decline and fisheries productivity will be affected. See genetic	L	M	D	1. Perform fishery surveys (from fishers to consumers, and by value of fishery) to determine the range of fishing methods used for harvesting, and key product characteristics that contribute to profitability. If fishing methods could be varied on a regional or temporal basis, determine if this would affect profitability. If effect of profitability was low, systematic variation of harvest methods may reduce the intensity of selective pressure on particular segments of the population.	Genetics in Fisheries Advisory Board (GIFAB)		X	X

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
	theme 6 (Fisheries-induced and natural selection)								
X					2. Demonstrate a selective effect on at least one trait in an Australian fished species. For example, select a trait with high heritability (i.e. determined by genetic not environmental factors) that may be affected by selective harvesting. Genes controlling muscular contraction in prawns may determine swimming speed, which may be selectively removed from a population if slow-swimmers cannot avoid trawl nets. A genomic approach may be needed to achieve this. Monitor the abundance of this gene across populations experiencing differing harvest levels and over the course of a fishery.	Fisheries geneticists, fisheries scientists.			X
3. 3. Addressing the scale of conservation management and how it interacts with fisheries management e.g. gene, stock, population, species. Strategically addressing how this will change when genetic technique mature to monitor adaptive genes (aka genes under selection).	The EPBC Act 1999 requires fisheries to be managed to protect species of conservation importance (i.e. TEP species). Genetics is commonly applied to a TEP species to determine its species status, but in addition to theoretical problems with the definition of a species, genetics can uncover various levels of diversity that could be seen to require conservation in their own right. A related issue is the use of genes under selection for the definition of population segments. Genes under selection may uncover different stock structures to conventional genetic analysis. It's highly likely that cogent arguments will be proposed for the conservation of these newly discovered elements, particularly if the species is TEP. See genetic theme 6	L	M	D	1. Australia may be the only first-world country with well-conserved and naturally high levels of marine biodiversity and endemism. Thus, it is in an ideal position to demonstrate leadership in maintaining fisheries profitability and marine biodiversity. To do this, taxa-specific thresholds of genetic diversity need to be established, where genetic diversity above the threshold should be protected (or managed, in the case of fisheries stocks), and below the threshold genetic diversity will reach an equilibrium driven by evolutionary forces on one hand and a reduction in population size due to exploitation on the other. Although likely to be highly contentious, if these thresholds were incorporated into the EPBC Act, they would provide clear guidelines for the continuation of the fishing industry and conservation of marine biodiversity.	Genetics in Fisheries Advisory Board (GIFAB)			X

STRATEGY	OBJECTIVES/REQUIREMENTS	FEASIBILITY	ATTRACTIVENESS	PRIORITY (FXA)	METHODS AND ACTION PLAN	RESPONSIBILITY	POSSIBLE DURATION: 6 MONTHS	POSSIBLE DURATION: 1 YEAR	POSSIBLE DURATION: 3 YEARS
	(Fisheries-induced and natural selection) and 5 (Species recognition using genetics).								