Enhancement of the Pacific oyster selective breeding program

FRDC and Seafood CRC Final Report
Project No. 2006/227

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ASI Thoroughbred Oysters

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Summary

2006/227 Enhancement of the Pacific oyster selective breeding program

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Objectives

1. To identify the traits which are economically important to the Australian Pacific oyster industry and calculate their relative importance to ensure the breeding program delivers maximum economic gains for industry.
2. To produce a computer tool, in the form of a spreadsheet, that can calculate economic values of traits for Pacific oyster industry and be used to provide regular updates of breeding objectives and customisation to individual regions.
3. To identify a new breeding strategy that delivers the best genetic gains for the Pacific oyster industry in a sustainable way and fits within the resources available to ASI.
4. To determine the genetic gains possible with different oyster selective breeding strategies and the relative economic benefits of these different strategies.
5. To develop specifications for a hatchery facility to produce the required number of families.
6. To develop specifications for computer systems to support the breeding program (such as genetic evaluation systems and a best mate allocation system).
7. To update the ASI database to accommodate the needs of the revised breeding program.
8. To develop a model for electronic data capture and processing.

NON TECHNICAL SUMMARY:

Outcomes achieved to date

This project has resulted in significant changes to the ASI Pacific oyster breeding strategy. The breeding objective has changed and is now firmly focused on an economic outcome, which is to reduce the cost of production. The size and structure of the breeding population has changed to allow greater genetic gains on a sustainable basis. The goal is to produce 50 families per year and 42 families were produced for the 2009 year class, an increase from 24 families in the previous strategy. A new nursery system has been implemented to produce the expanded population. Data collection and storage systems have been completely revised to allow more efficient data collection, more efficient storage, and safeguards against data loss. A new genetic evaluation system has been implemented which will provide more accurate selections. And a revised commercial deployment strategy has been implemented which will increase the supply of selectively bred spat to industry.

The Australian national Pacific oyster selective breeding program commenced in 1998. In 2005, after 6 generations of breeding, it was apparent that there were limitations to the breeding strategy. The first was a lack of understanding of which genetic traits to select. Whilst the program was achieving genetic improvements in growth, little was known about which traits influenced grower profitability. The second was a need to develop a breeding strategy that increased genetic gains and maintained inbreeding at safe levels. And the third was a need for systems and tools to enable the breeding strategy to be efficiently implemented. The purpose of this project was to address these limitations.

The genetic traits that influence profitability for the oyster grower were identified. This was done by developing a computer model of the Pacific oyster production system. This model included all sources of income and expense, and predicted changes in income and expense resulting from changes in genetic traits. The model was validated by actual farm data and scientific trials. Economically important traits were growth rate, shell width index, time to reach market condition, mortality and uniformity. All were of approximately the same economic importance, meaning a breeding strategy needs to consider all to maximise profitability.

Computer simulations were used to evaluate 17 different breeding strategies, each with different population sizes, population structures, and selection strategies. The strategy that provided the best balance of genetic gains and inbreeding was selected. That strategy was based on producing 50 families per year, using both between and within family selection, and managing the breeding population as a single population rather than discrete year classes. This strategy was estimated to deliver genetic gains in the breeding population of 8.5% per generation, or 4.25% per year whilst maintaining inbreeding at acceptable levels.

A practical breeding plan was developed to allow the breeding company (ASI) to implement this strategy without increasing the resources required to operate the program. Concerns of commercial hatcheries were addressed and solutions incorporated into the strategy. The strategy is now able to provide two year old commercial broodstock rather than four year old stock. This allows supply of better quality broodstock in much higher numbers. The strategy also provides far more commercial selection options, allowing hatcheries to combine desirable traits with far more flexibility. The four year time lag between the breeding population and commercial population has been eliminated, which will increase the genetic gains to growers. A Hatchery Reference Group has been formed giving the major industry partners, Shellfish Culture and Cameron of Tasmania, more input into all aspects of the

program. The aim is to provide them with confidence to use higher numbers of breeding program derived spat, which are marketed as Thoroughbred Oysters.

New systems and tools were developed to assist the implementation of the new strategy. Improved statistical methods are now used to evaluate family performance (provided as Estimated Breeding Values). This gives more accurate selections and greater flexibility with decision making. A new hatchery system (Cawthron Ultra Density Larval rearing system) has been adopted to enable an increase in annual family production. A purpose built database is being developed. The database, together with the new electronic data capture system, will provide greater efficiency, accuracy and safety of data storage.

All outcomes of this study have been incorporated into the Australian Pacific oyster breeding program. Five traits that affect grower profitability have been identified. Three of these are now used as part of routine breeding decisions and research is underway to develop knowledge and methodologies for the others. The number of families produced each year has increased to 42, with a target of 50. This will accelerate genetic gains and ensure the breeding population is sustainable with regard to inbreeding. Systems developed as part of this project have been adopted and have allowed the expanded breeding program to operate with current resources. These changes have allowed the breeding program to improve the quality of commercial families produced and hence increase the profitability of oyster growers.

KEYWORDS: Pacific oyster, *Crassostrea gigas*, selective breeding, economic weights, breeding strategy

Chapter 1

Introduction

Peter Kube and Matthew Cunningham

1.1 BACKGROUND

Pacific oyster (*Crassostrea gigas*) selective breeding commenced in Australia in 1997 (Thompson and Maguire 2007, Ward *et al.* 2005). At the outset this included both mass selection lines and pedigreed families, but the program is now exclusively based on the production and performance testing of families. Initial work demonstrated genetic variation in commercially important traits and concluded that commercial benefits were possible. A focus was to develop an operational breeding program. Provision of selected families to commercial hatcheries has been an essential part of the breeding program since its inception.

The breeding strategy has been comparatively simple and the breeding population small. It has been based on selection for family performance, followed by within family selection of favoured families. The number of families produced annually has varied from 17 to 40, and the generation time is nominally two years. Progeny testing is usually done on four sites (in Tasmanian and South Australia) and a single population is used for all regions. Initially, the breeding objective concentrated on growth rate, but in later years additional traits such as shape and condition were added. To date, 11 year classes have been produced.

Australian Seafood Industries Pty Ltd (ASI) is a grower-owned company formed in November 2000 to carry forward the oyster breeding program and, importantly, ensure the benefits of genetics research and development were realised by the Australian Pacific oyster industry. ASI makes broodstock available to commercial hatcheries who then produce genetically improved spat for sale to growers. ASI receives a royalty based on the amount of spat sold and it is this royalty that funds the operation of the breeding program. The ASI business plan is to achieve sufficient sales to fully fund the routine operations of the breeding program. The model of an industry cooperative to develop breeding technology was unique in Australian aquaculture, although this approach has been successful in other primary industries in Australia.

1.2 NEED

In 2005, after six generations of breeding, it was apparent that there were shortcomings to the breeding strategy. The uptake by industry had been slow. Some growers were expressing concern about the traits that were being selected and were unconvinced about the economic benefits of the breeding strategy. In addition, there was uncertainty about the priorities for genetics research. Different genetic technologies were being proposed, such as inbreeding, double haploidy and marker aided selection, and funding bodies were unclear where priorities lay. As a consequence, a review team examined future research directions (Ryan *et al.* 2006). This review recommended that future research focus on addressing the shortcomings of the selective breeding program. Three major issues were identified.

Firstly, there was a need to design a program that maximised profit. Selection for traits in the existing ASI breeding program could not be based on economic criteria because the economic values of Pacific oyster traits were unknown. There was a need to know the dollar value of

current traits (growth rate, shape and uniformity) as well as the value of new traits. The program was unable to objectively select multiple traits without knowledge of economic weights. This current project used techniques used routinely in other industries to address this problem.

Secondly, there was a need to design a breeding program that increased the rate of genetic gain, maintained genetic diversity at levels that avoided deleterious effects from inbreeding, and allowed genetic improvement long into the future. Genetic theory was suggesting there was considerable scope for increasing the rate of genetic gain in this breeding program (Ryan *et al.* 2006).

Thirdly, there was a need to begin the specification and development of systems to support operational breeding. The most immediate needs were for upgraded hatchery facilities able to accommodate the needs of a selective breeding program, a data management system to safely manage the data that underpins a selective breeding program, and a genetic evaluation system to allow better genetic selections.

This project addresses these issues. It involves research and development of concepts which are entirely new to breeding programs for the Pacific oyster and other Australian aquaculture industries. However, they are concepts that are well established in many terrestrial livestock industries. Experience in these industries has demonstrated that these concepts can provide a strong foundation for operational selective breeding and, consequently, a firm foundation for a viable and sustainable Pacific oyster industry.

1.3 OBJECTIVES

The objectives of this project were to:

1. To identify the traits which are economically important to the Australian Pacific oyster industry and calculate their relative importance to ensure the breeding program delivers maximum economic gains for industry.
2. To produce a computer tool, in the form of a spreadsheet, that can calculate economic values of traits for the Pacific oyster industry and be used to provide regular updates of breeding objectives and customisation to individual regions.
3. To identify a new breeding strategy that delivers the best genetic gains for the Pacific oyster industry in a sustainable way and fits within the resources available to ASI.
4. To determine the genetic gains possible with different oyster selective breeding strategies and the relative economic benefits of these different strategies.
5. To develop specifications for a hatchery facility to produce the required number of families.
6. To develop specifications for computer systems to support the breeding program (such as genetic evaluation systems and a best mate allocation system).
7. To update the ASI database to accommodate the requirements of the revised breeding program.
8. To develop a model for electronic data capture and processing.

1.4 SCOPE OF THIS REPORT

This report presents the work undertaken to address the above objectives as separate and stand alone chapters. It represents as extension of the earlier work described in Ward *et al.* (2005) and addresses the needs articulated in Ryan *et al.* (2006).

Chapter 2 describes the study to identify the economically important traits and their economic values, or economic weights (objective 1). It introduces the spreadsheet tool that has been

developed to allow regular updating and customisation of the trait economic values (objective 2). Chapter 2 also presents estimations of expected genetic gains in the breeding population when selecting using the economic weights. This is done for the combined index, which expresses gains in terms of changes in the cost of production, and for each trait in the selection index (objective 4).

Chapter 3 describes studies done to validate the assumptions in the economic weights model and to fill in gaps where information was deficient (part of objective 1). There were two main components to this work. The first was to measure the time required to 'grow' a long and narrow oyster to an acceptable shape. The second was to gather data from a farm on some of the main production variables. A third aim was to gather data on the relationship between growth rate and condition time, however, it was decided that this was beyond the capacity of this current project.

Chapter 4 evaluates options for different breeding strategies (objectives 3 and 4). This is done by computer simulations, and potential genetic gains and inbreeding from 17 different strategy options are presented. This chapter also provides guidelines regarding the future implementation of the ASI breeding strategy.

Chapter 5 presents the specific details of both the revised ASI breeding strategy and the commercial deployment strategy (objective 3). This includes a description of the limitations of the previous strategy and the ways in which the new strategy differs from the old.

Chapter 6 describes the changes made to the hatchery procedures that were necessary to accommodate the needs of the revised breeding strategy (objective 5). The system adopted is an ultra high density larval rearing system that was developed at the Cawthron Institute in New Zealand. The equipment is described, the protocols detailed, and experiences and issues in moving to this new system are outlined.

Chapter 7 describes the development and implementation of the genetic evaluation process used as part of the revised breeding strategy (objective 6). This includes the collation of the existing data, the evaluation of the genetic parameters, and the procedures used to estimate genetic merit.

Chapters 8 and 9 address data systems needed to support the new breeding strategy and the genetic evaluation process (objectives 7 and 8). The conceptual design for the database is presented, as well as the database design in the form of a database schema. The electronic data capture systems for the collection of field data are also described.

Chapter 2

An economic breeding objective for the Australian Pacific oyster industry

Peter Kube, Scott Parkinson and Matthew Cunningham

2.1 INTRODUCTION

2.1.1 Background

Most selective breeding programs involve selecting for multiple genetic traits. One of the most important and, at times, the most difficult issue in developing a breeding strategy is to apply the correct weightings to each trait. It is important because selecting for multiple traits invariably requires making complex trade-offs. The ideal mix of commercial traits rarely occurs within a single animal and, therefore, the breeder must make a decision about what combinations of traits are best suited for the required purpose. It is difficult because there is usually a vast continuum of combinations and many possible individuals to select between. The task becomes more difficult as more traits are added. Experience has shown that intuitive decisions are often poor decisions that can have serious economic consequences. It is possible for selective breeding programs to make genetic gains, and even large genetic gains, but fail to make economic gains.

A successful approach to the problem of finding the best mix of traits is that of bio-economic modelling and the calculation of economic weights. A bio-economic model is a synthesis of biology and economics. In these applications it involves developing a model of the animal production system that includes the biological components that influence production, costs of all major inputs, and predicted returns both in terms of biological output and income. An economic weight is the expected change in profit with a unit change in the biological trait. This approach was developed for livestock industries by Ponzoni and Newman (1989), and has since been applied to other industries such as forestry (e.g. Borralho *et al.* 1993, Ivkovic *et al.* 2006). It has proven to be a sound system and is routinely applied to many advanced breeding programs. It is fundamentally simple in its approach. The many applications of this methodology always involve some variation around four key steps which are:

(1) Describe the production system, which is the process used for animal production

(2) Identify the sources of income and expense

(3) Identify the biological traits that influence income and expense

(4) Calculate the economic weights for each biological trait

2.1.2 Need

Finding the best mix of traits for the ASI Pacific oyster breeding program has been problematic. At the commencement of the breeding program (in 1998), a survey of growers (31 respondents) was used as a means of rating the importance of traits. That survey, which is summarised in Ward *et al.* (2005), identified 18 traits of interest. Meat yield (akin to condition in this report) and growth rate were clearly the most important. Shell shape and disease resistance were also considered important, but were rated with lower importance.

Other traits rated as moderately important included various aspects of the meat quality (such as glycogen content, meat and mantle colour) and non-spawning.

Growth rate and meat yield became the main focus of selection. Shell shape was, at times, a secondary trait but it is unclear how selection effort was divided between all traits. It appears that the majority of selection emphasis was placed on growth rate. After four generations of selection there were large responses in growth rate. However, and unfortunately, this was accompanied by a significant decline in the width index (the ratio of shell width to shell length). This resulted in long and skinny oysters that were, at times, unsuitable for market. The options for growers were to either grow them back into shape, or to cull them. Either way, it was a significant cost to growers. It was also a severe set back in the grower's confidence of the breeding program. Anecdotally, there is evidence that there was a favourable response to meat yield but these benefits were largely lost, and overlooked, by the strong and adverse response of shell shape.

The problem with the ASI breeding program was not that shell width had been overlooked as an important trait. The survey by Ward *et al.* (2005) correctly identified shell shape as one of the most important traits (ranked third out of 18) and some priority was place on assessing this trait. Rather, the problem was that inappropriate selection emphasis had been placed on this trait. The issue was compounded by two additional factors. Firstly, there was an adverse genetic correlation between growth rate and width index (Chapter 7, Table 7.13) resulting in a negative response to width index. And secondly, there was a lack of understanding of the severer economic consequences of an adverse change in shell width to market acceptability.

2.1.3 Objectives

The aim of this part of the project was to apply the economic weights methodology to the Pacific oyster breeding program. The main objective was to define an economic breeding objective or, in this case, a breeding objective that minimises the cost of production (COP).

Specifically, the objectives were to:

1. Produce a bio-economic model of the Australian Pacific oyster production system.
2. Determine the traits that are economically important to the Australian Pacific oyster production system and determine the relative importance of those traits by calculating economic weights.
3. Determine how the economic weights differ on different sites and assess the need for regionalised breeding objectives.
4. Produce a spreadsheet system that allows regular updating and checking of the economic weights by ASI staff.
5. Estimate potential genetic gains when selecting using an index based on true economic weights, both in terms of overall economic benefit and individual changes in each breeding objective trait.

2.2 PACIFIC OYSTER PRODUCTION SYSTEM

The Australian Pacific oyster industry produces for the live half shell market. The main farming systems used, and the systems modelled in this study, are the intertidal rack and basket systems and the intertidal long-line systems. These farming systems are explained in greater detail in Treadwell *et al.* (1991), Love and Langenkamp (2003), PIRSA (2003), and Cox (2004). The subtidal long-line system has not been included in this analysis.

This analysis covers the on-farm production system. The starting point is the arrival of oyster spat at the farm, and the end point is the sale of product at the farm gate. Therefore, this analysis does not include the hatchery phase of the production, post harvest processing, or consideration of consumer preferences.

The framework for the bio-economic model was based on the production system description of Cox (2004). This was progressively developed through discussions with key industry personnel, the project team, and the project Technical Committee. Farm data from Bolduans Bay Oysters (Smithton, Tasmania) was used to validate data used in the model. Specifically, data on growth times in each unit, mortality in units, and grade percentage was sought. Bolduans Bay Oysters has a comprehensive batch tracking system which is supported by a database. Chapter 3 describes the analysis and results of this component of the work.

2.2.1 Defining the production system

There are 7 main features of this production system which are explained below, and are diagrammatically represented in Figure 2.1.

1. Spat input: The starting point is the arrival of a batch of hatchery produced spat.

2. Grow-out equipment: Oysters are grown in mesh baskets, or mesh cylindrical bags which are referred to as units. As the oyster grows, it is progressively graded into a unit with a bigger mesh size. Generally, up to four different types of units are used.

3. Stocking densities: The number of oysters stocked varies from farm to farm according to site conditions and management preferences. Stocking rates are defined by number of oysters per unit and number of units per hectare.

4. Grading: An ongoing and regular management activity is grading. At defined intervals, stock is brought ashore and size graded to ensure oysters of a similar size remain together. Oysters meeting a size threshold will be placed in a unit with a larger mesh size whilst others will be returned to the water in the same sized unit. Generally, an oyster gets no more than three chances to progress to the next sized unit before it is culled.

5. Growth and conditioning: The grow-out usually involves a growth phase and a conditioning, or fattening, phase. The growth phase is focussed on producing a shell to a suitable size, shape and uniformity. The conditioning phase is the final phase of the grow-out and is focussed on producing suitable meat quality rather than shell growth. In practice, there is usually overlap of these phases.

6. Losses: Oysters are lost from the production system through mortalities and culls. Mortalities occur throughout the grow-out and are identified and removed at the gradings. Culls are oysters that deemed unlikely to be saleable and may be runts, or have severely misshapen shells.

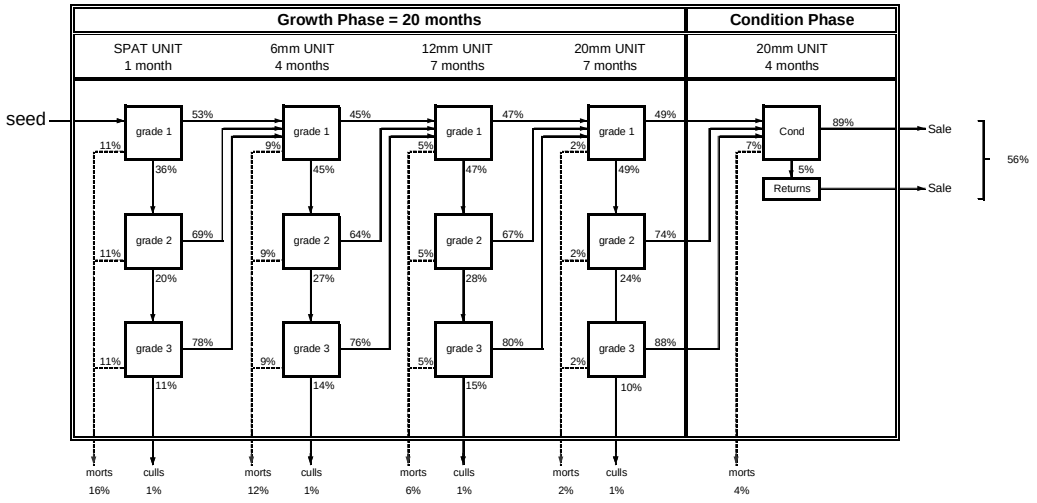


Figure 2.1. Diagrammatic representation of the intertidal Pacific oyster production system.

7. Harvest and sale: The endpoint of the modelled system is the harvest and on-farm packing of the oysters; that is, the farm-gate. Oysters are sold in different size grades which have different prices. Generally, a grower will produce for a particular market specification and the farming system (such as growth and condition times) will be adapted to meet those market requirements. Oysters from a given input leave the farm at different times. This is due to the grading events, and the fact that some oysters take longer than others to progress to larger size grades.

2.2.2 Sources of income and expense

Sources of income and expense have been grouped into five main categories. These are explained below and indicative values are given in Table 2.1.

1. Spat costs: Farms purchase spat from hatcheries. There is an established market price for spat and that was used in this analysis. Spat production is a complex and specialised process and has been deliberately excluded from this analysis.

2. Fixed costs: Fixed costs are costs that do not change with the level of production. They include annual operating costs and capital items. Examples of annual operating costs are permanent labour, licences, fuel, and electricity. Examples of capital items, all of which have a defined life, are racks, baskets, punts, motors, sheds, and tractors. An excellent and still relevant analysis of fixed costs is given by Treadwell *et al.* (1991) and these have been used for this analysis. They were adjusted to present day values using Consumer Price Index (CPI) figures (ABS 2010). Appendix 2.1 provides details of the categories defined by Treadwell *et al.* (1991) and the CPI adjustments made for this analysis.

3. Grading costs: Grading costs are the main variable costs in this production system. They vary at different stages of the grow-out and different oysters will have different numbers of gradings. The total grading cost for a particular oyster is a function of the number of grading events at each stage of the grow-out process. Grading costs used in this analysis were the averages of values provided by four key growers and include labour and operating.

4. Harvest costs: Harvest costs are the second category of variable costs. This includes the costs of sorting, packing and consumables (such as hessian bags). The endpoint for this analysis is the farm-gate and therefore the costs of transport to market are not included. These costs were also from data provided by four key growers.

5. Sale income: Income is a function of the quantity sold and the sale price. Sale prices are defined by size grade and well defined product grades exist (see PIRSA 2003, Love and Langenkamp 2003). Growers generally target a particular product grade. Table 2.1 shows product grades, shell lengths for each grade, and indicative prices.

Table 2.1 A summary of the main sources of income and expense and some indicative values

Cost item		Indicative values	Source
Spat		$22 per ‘000	Market price
Total fixed		$20,000 per ha per year	Treadwell *et al.* (1991) CPI adjusted
Grading and handling:	Spat unit	$0.02 per dozen	Industry representatives
	6 mm unit	$0.11 per dozen	Industry representatives
	12 mm unit	$0.18 per dozen	Industry representatives
	20 mm unit	$0.22 per dozen	Industry representatives
	Condition	$0.24 per dozen	Industry representatives
Harvest and packing		$0.15 per dozen	Industry representatives
Sale	bistro (50-60 mm)	$4.80 per dozen	Market price
	buffet (60-70 mm)	$5.20 per dozen	Market price
	standard (70-85 mm)	$6.00 per dozen	Market price
	large (85-100 mm)	$7.60 per dozen	Market price

2.2.3 Biological factors that influence income and expense

There are five main biological factors that influence on-farm income and expenses and these are described below.

1. Time to grow the shell, which is the number of months required to produce a shell size of the desired product grade. This is measured as the shell length at a given time point.

2. Time to condition, which is the number of months required to produce an oyster with meat quality suitable for sale. This is separate from the time to grow the shell and, therefore, is the time interval between reaching a suitable shell size and sale. The total period to produce an oyster is the sum of the time to grow the shell and the time to condition. Time to condition is measured as either the meat to shell ratio or the degree to which the meat covers the shell cavity of a freshly opened oyster (see the Tasea Pacific oyster grading system).

3. Mortality, which is the total losses that occur due to death. It does not include culls or oysters that vanish from the production system. It is likely to be an amalgamation of a number of biological factors and may include temperature tolerance, stress tolerance, salinity tolerance, shell density (influencing the ability to withstand mechanical grading), and tolerance to specific pathogens. This is measured as the number of empty shells in a unit at a given time point.

4. Uniformity, which is the variability in size classes for a particular input batch. It influences the proportion of oysters that progress to the next sized unit at grading and, consequently, influences the number of grading events for a batch of oysters. It also influences the number of culls. Batches with high variability will have a higher proportion that fail to progress to the next unit by the third grading and become culls. There are no established methods to measure uniformity, although growers are aware of the relative proportions that progress to the next sized unit.

5. Shell shape, which is a measure of the ratio of width to length, referred to as the width index. Although there are other shell shape measures, this is considered the one of prime importance. The ideal ratio of width to length is 2 to 3, or a width index of 0.67. Oysters have a tendency to grow long and narrow in this production system, particularly if grading events are delayed. A long and narrow oyster is rarely acceptable for sale. The management response to a long and narrow oyster is to extend the growing period in conditions that allow it to grow back into shape. In extreme cases it may be a cull. Width index is measured as the ratio of width to length at a time point near to harvest.

2.3 MODELLING THE PRODUCTION SYSTEM

2.3.1 An overview of the model

This model was produced from first principles. It simulates the process by which individual oysters move through a farm and is designed to measure how changes in the five main biological traits influence the cost of production and profit. Typically, a bio-economic model of a production system model can be built using other software tools or growth models produced as management tools for growers. However, there were no such models for Australian Pacific oyster production.

The model was produced as an Excel spreadsheet. All key variables can be easily changed allowing scenario testing, sensitivity testing, and continual updating with new data. The model requires biological and economic data to be input to characterise an enterprise. The majority of the input variables are entered through the front page of the model, which is illustrated in Figure 2.2. Additional variables are input on other worksheets. These are variables less likely to require regular changing and include definition of proportions of total mortality in each unit type, proportion of total growth time in each unit type, thresholds for unacceptable shell shape, and the relationship between shell growth and conditioning.

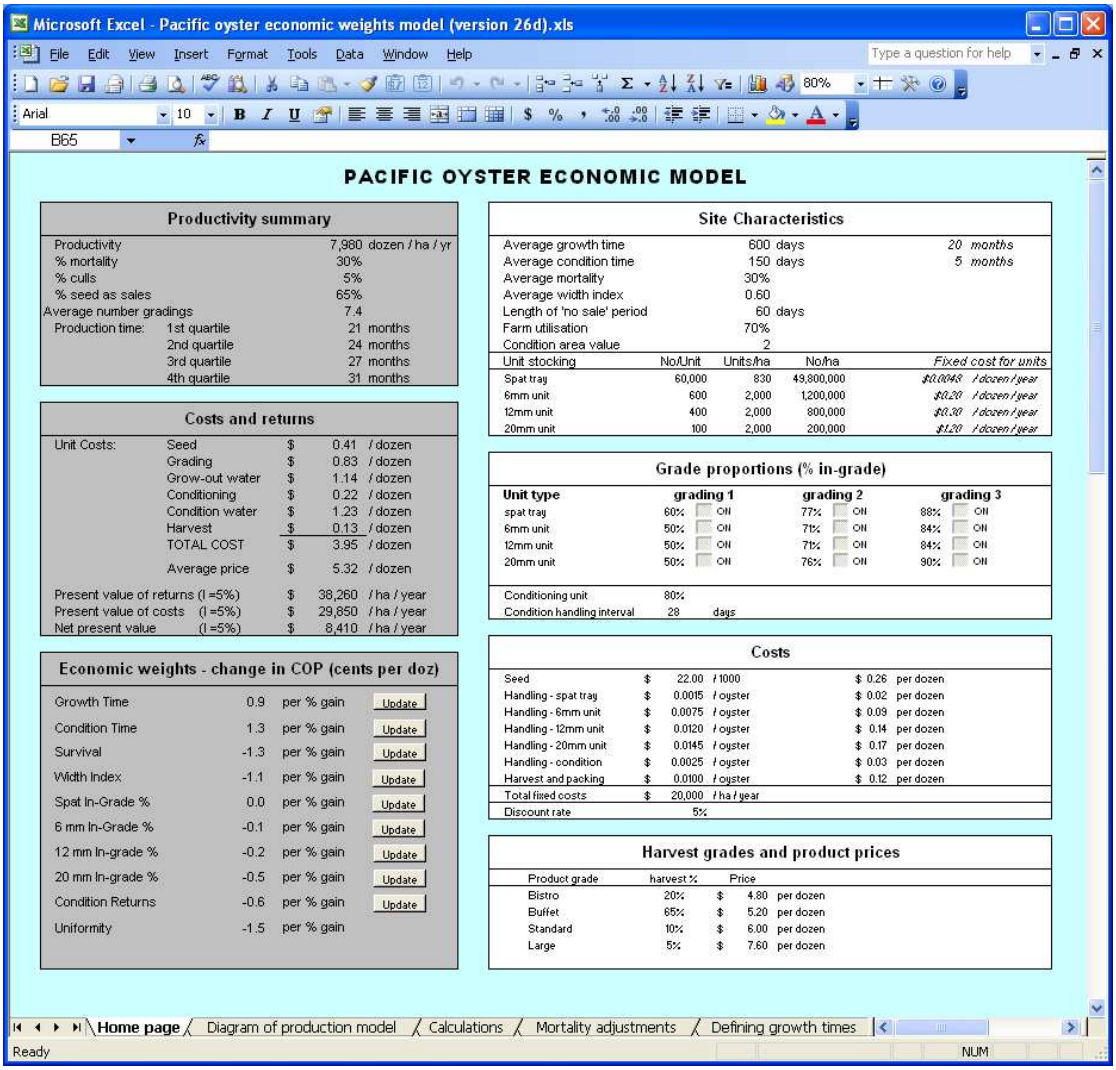


Figure 2.2 Screen shot of the front page of the economic model, showing the main outputs (in the grey boxes) and the main inputs (in white boxes).

Model inputs

Input variables (Figure 2.2, right hand side) can be grouped into four categories which are:

1. Site characteristics: These define the growth potential of a site. They include typical values of the main biological traits (growth time, condition time, mortality, and width index). They also include the stocking configuration of the farm (number of oysters per unit and number of units per hectare) and average utilisation of the farm (the average proportion of racks unstocked). There is also an option to assign those parts of the lease that are used for conditioning a greater value. This reflects the situation where growers may use the best parts of their lease (such as areas that have the best food supply) for conditioning.

2. Grade proportions: These define the proportions of oysters that move to the next sized unit. Different values can be input for each grading. There are also options to 'turn-off' particular grading events. For example, the use of spat trays can be turned-off, or the maximum number of grading events for an oyster in a unit size can be reduced (the maximum and default values are three grading events per unit type).

3. Costs: These include variable costs, which are spat and grading costs, and fixed costs, which include annual operating and capital items. There is also an option to add a

discounting rate to account for the time value of money. With this, all costs and returns are discounted to present day values where present day defined as the input of spat.

4. Product prices: These are the farm gate prices received by the grower for each product grade. The product mix produced also needs to be input. This is defined by the proportions of the crop that fall into each product grade.

Model outputs

Output variables are calculated by the model (Figure 2.2, left hand side) can be grouped into three categories, which are:

1. Productivity: This is a measure of output expressed as dozens of oysters per hectare per year. Sale dates for individual oysters from a particular input batch vary and production time for a batch essentially follows a sigmoid curve (an S-curve). This is due to the gradings and the fact that out-of-grade oysters require longer time periods to meet product specifications. The model predicts the production time for each quartile of a batch to give an indication of the variation in production time.

2. Costs and returns: Costs are expressed as both cost of production per dozen oysters, and as cost per hectare per year. Production costs per dozen are also broken down to six main components (see Figure 2.2). Profit is the difference between income and costs expressed as dollars per hectare per year. When a discounting rate is used, costs represent the present value of costs, and profit represents net present value (NPV).

3. Economic weights: This is a measure of the value of an improvement for each biological factor. These are expressed as a change in the cost of production with each one percent change in the mean value of that biological factor. (Economic weights are discussed in greater detail in section 2.4.)

2.3.2 How the model works

The model can be explained as an 8-step process. The following sections outline these steps and a diagrammatic representation of each step is shown in Appendix 2. Full details of each step can be seen on the spreadsheet model, where descriptive notes have been added to explain processes.

Step 1: Define production pathways

The key concept of this model is the production pathways. There are many pathways by which an oyster passes through the production system. A batch of seed that is input on the same date does not leave the farm at the same time. This is due to the many gradings where some individuals are at a sufficient size, and progress to the next sized unit, whilst others do not meet the size grade and are returned to the same sized unit.

Each pathway has a different number of grading events and a different production time. Consequently, each pathway has a different cost of production. Some pathways lead to a sale and others lead to a cull. For this model, there are 202 potential pathways through the production system. Of these, 162 are pathways for a sale oyster and 40 are pathways for a cull oyster. Figure A2.1 illustrates 3 of these potential pathways.

On the spreadsheet model, there is a single row for each pathway.

Step 2: Allocate oysters to pathways

The grade proportions are the ‘gates’ to the pathways. The percentage in-grade and out-of-grade determines the proportion of the batch that travels on a particular pathway. That proportion is a function of all gradings along a pathway. Pathways that have a large number of gradings have a very small proportion of the total. In reality, batches such as these get bulked with others and composite batches are formed from the same or different input

batches. The grade proportions also determine the number of culls, with those oysters that are out of grade after the third grading becoming culls. Figure A2.2 illustrates the grade proportions for three potential pathways. The grade proportions shown in this Figure are less than the actual input values because they are adjusted for mortality. This is explained in the next section.

Grade proportions for all gradings are variables and can be easily changed in the model. In addition, gradings can be 'turned-off' to allow modelling of situations where less than three gradings occur for a particular unit.

Step 3: Subtract the mortalities

Morts are subtracted at each grading. This represents removal of empty shells when grading is done. The model requires inputting two categories of mortality information. The first is the total mortality that occurs during grow-out, which is a statistic that growers would know with some accuracy. The second is the proportion of mortality that occurs at each stage of the grow-out or in each unit type. This is a statistic that appears to be known with less accuracy, but can be approximated by growers. The model then calculates and subtracts the appropriate number of mortalities from each pathway and at each grading so the input values are achieved.[1] The number of morts that need to be subtracted at each grading is also a function of the input grade proportions, and the model also adjusts for this. Figure A2.3 illustrates the removal of morts for a given set of input values.

Step 4: Define the growth phase

The length of the growth phase is different for each pathway. It is dependent on the number of grading events in that pathway. The length of the growth phase for a batch is the weighted average of all pathways, where pathways are weighted according to the proportion of total batch in that pathway.

The model requires input of two categories of growth data. The first is average growth time for the farm and the second is average time in each unit. The first is generally known with reasonable accuracy, although a distinction must be made between growth time and condition time. In reality, there is not a clear distinction between the two phases used in this model. The second input value, time in each unit, essentially represents the time between handlings and is also generally known with reasonable accuracy. The model uses the proportional times in each unit but will adjust actual time in each unit so that appropriate values are used to exactly match the average growth time. Figure A2.4 illustrates the growth times for three potential pathways.

Step 5: Define the condition phase

The length of the condition phase is different for each pathway. It is assumed the condition time for a pathway is inversely related to the growth time for that pathway. That is, a pathway with a rapid growth time requires a longer conditioning phase to be acceptable for market.

The model requires the input of the average condition time for the farm, which is generally known with reasonable accuracy. Condition times for each pathway are then calculated assuming the relationship:

$$C = a (G + 1)^{-b}$$

Where C is the predicted condition time for the pathway, G is the growth time for the same pathway (calculated in the previous step), and a and b are constants defined by input values.

[1] Since there are three grading events for each unit, this involves solving a cubic polynomial.

The constants are calculated after inputting a single value which is an estimate of how condition time is expected to change with a given change in growth time. The model uses this point value and the mean values for growth time and condition time to predict the constants. An example with the current default values is shown in Appendix 2.3 and the condition times for three potential pathways, using these default values, are illustrated in Figure A2.5.

The exact nature of the relationship between growth time and condition time is unknown and it was unable to be verified within the time span of this study. It remains an assumption that needs to be checked, and a process to do this has begun.

Step 6: Define the influence of width index

Oysters with poor shape (that is, oysters that are too narrow) are returned to the 20 mm growth unit, thereby extending their growth time. This is modelled as a lower proportion of oysters progressing to the next stage at each of the 20 mm unit grading events. The proportion of oysters that are below a width index threshold is estimated, and the grading percentages are adjusted by that factor. This process also increases the proportion of culls, which is considered realistic.

The model requires the input of two variables. The first is the average width index for that farm and the second is the threshold for the minimum acceptable width index. Both are likely to be known accurately. The proportion that have unacceptable shape is calculated from a truncated normal distribution, where the truncation point is the minimum width index value. This calculation also requires a population standard deviation for width index, which has been accurately estimated and can be readily updated. Figure A2.6 illustrates the effect of two levels of width index.

A separate trial was designed to validate the assumptions used in the model, and this is described in Chapter 3.

Step 7: Estimate the cost of production

Costs are calculated for each pathway, and the total cost is the weighted average for each pathway. Costs include variable costs and fixed costs, with each contributing approximately an equal amount to the average cost of production (see the Costs and Returns box in Figure 2.2). Variable costs can be very different for each pathway because each pathway has different numbers of grading costs. Fixed costs are a function of the total time in the water and the area occupied (they are calculated as \$ per m^2 per year). They are calculated for each pathway as the proportional share of the area occupied. They can also be different for each pathway. Figure A2.7 illustrates the cost of production for three potential pathways.

All costs are discounted to the batch input time, which is year zero. If the discounting factor is zero, then no discounting is applied. The costs of the lease area are also discounted using the gradings as the time points.

Step 8: Estimate the productivity

Productivity, which is expressed as dozen per hectare per year, is calculated for each pathway. The total productivity is the weighted average for each pathway. Productivity is calculated by segmenting each pathway into grading events and calculating the area-time required (expressed as m^2.days). The total area required for each pathway is then summed. This calculation will assume the lease is optimally configured for full occupancy. This is unlikely to occur in practice and, therefore, productivity can be adjusted using the 'area occupied' variable to account for the average amount of empty rack space (see Site Characteristics box in Figure 2.2). Figure A2.8 illustrates the productivity for three potential pathways.

2.4 ECONOMIC WEIGHTS

2.4.1 Methods

Economic weights were calculated for each of the five biological traits identified as being economically important (see section 2.2.3). Economic weights are defined as the change in economic value for a unit change in that biological trait. For this application, cost of production (COP) was used as the economic measure rather than profit. Although profit is used in most other studies, COP was the measure preferred by the industry. Economic weights are, therefore, independent of product prices.

The bio-economic model was used to calculate economic weights. This was done by calculating the COP for nine different values of each trait (a mean value, four values greater than the mean, and values four less than the mean) and plotting the change in COP against the change in trait value. The slope of the plotted values is the economic weight. This process and the range of values tested is shown in Figure 2.3 and the assumed mean values for each trait are shown in Table 2.2. Estimates are made using one trait at a time whilst keeping values for all other traits constant. These calculations are done automatically in the economic model using an inbuilt macro. The economic weight for uniformity is the sum of economic weights for gradings in each individual unit, including condition returns. This, therefore, assumes all gradings are influenced by the same biological trait.

Economic weights are expressed on two scales (Table 2.2). The first is change in COP for a percentage change in the trait mean. For example, the change in COP for a 10% decrease in growth time, which is a change from 600 to 540 days. The second is the change in COP for a unit change in the trait. For example, the change in COP for a one day change in growth time, which is a change from 600 to 599 days. Both scales have their applications, and the scale used is dependent on the scale on which data used to make selections, or estimated breeding values (EBV), are expressed. Currently, EBVs are expressed on a percentage change basis so the former scale is the one in use (see Chapter 7 for details of EBV calculation).

The bio-economic model was also used to test the degree to which economic weights change in different situations. Ten scenarios were tested and these were defined by changing site characteristics and cost structures. These scenarios could represent different regions (such as South Australia, Tasmanian and New South Wales) where it is recognised that different conditions exist. For example, South Australia generally has higher mortality, and New South Wales generally has faster growth rates. The scenarios could also represent different sites within a region. For example, different farms have differing issues with shape (due to different husbandry), different growth rates, and different cost structures. The scenarios evaluated were:

1. Industry standard: Industry averages for site characteristics and costs.
2. Slow growth: Growth and condition time are 25% greater than industry standard.
3. Fast growth: Growth and condition time are 25% less than industry standard.
4. High mortality: Mortality is 33% higher than industry standard.
5. Low mortality: Mortality is 33% lower than industry standard.
6. Late-age mortality: Higher proportion of mortality in oysters > 25 mm length
7. Poor shape: Width index is 10% less than industry standard.
8. High uniformity: Percentage in-grade are 20-50% higher than industry standard.
9. High costs: Variable and fixed costs are 25% higher than industry standard.
10. Low costs: Variable and fixed costs are 25% lower than industry standard.

Assumed industry standard values are as shown in Tables 2.1 and 2.2 (cost and site characteristics respectively) and the percentage variations for each scenario are calculated as deviations from the industry standards.

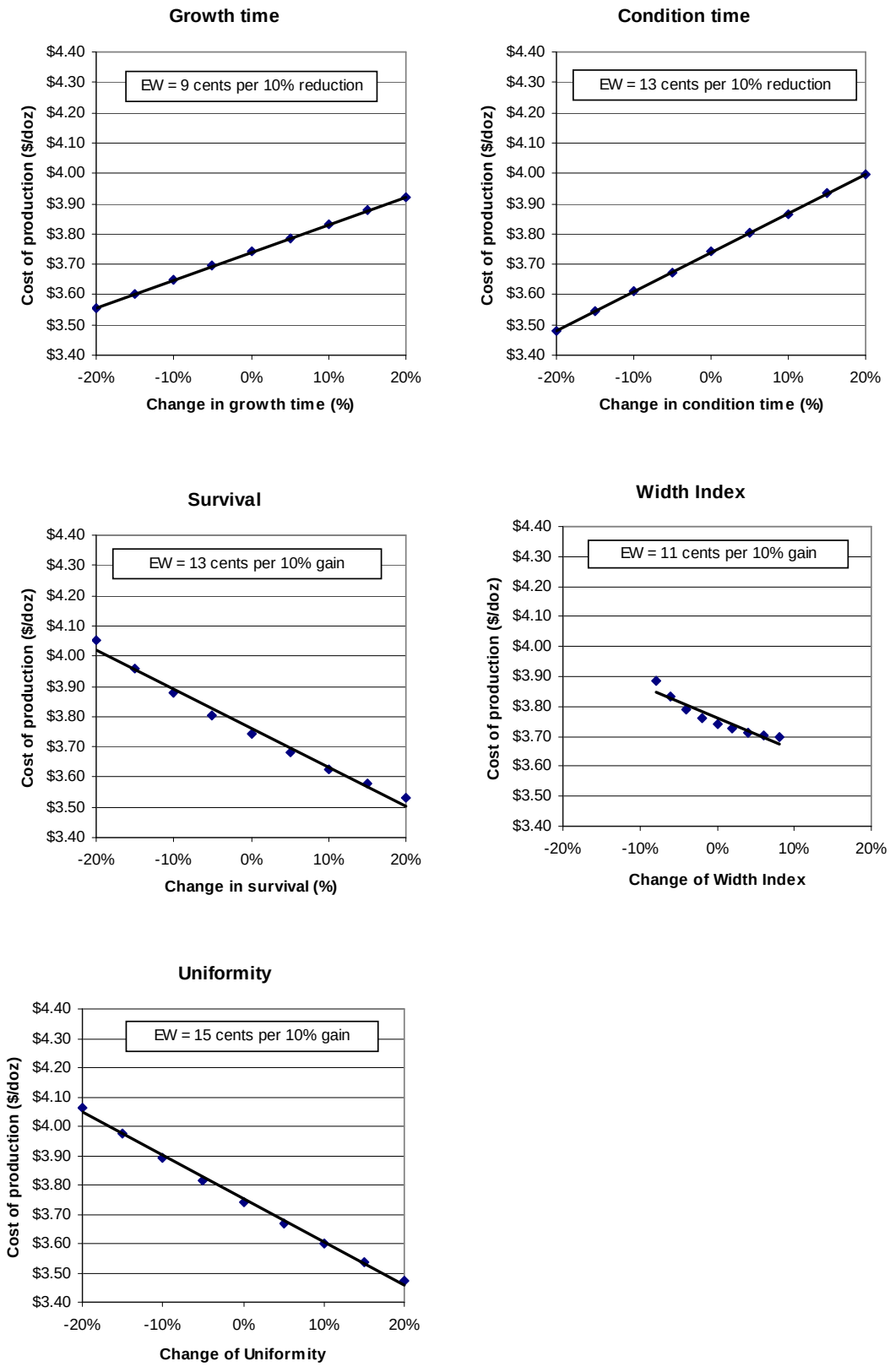


Figure 2.3 The relationship between changes in each of five biological traits and the cost of production. The slope of the line is the measure of economic weight and that value is shown in the box on each chart. Note growth time and condition time have a positive slope, meaning a reduction in value is economically advantageous, whereas other traits have a negative slope, meaning an increase is advantageous.

Table 2.2 Economic weights, expressed as a change in cost of production (COP), for a population represented by the standard industry values. The trait uniformity is the combined value of all gradings, and the separate components of this trait (uniformity in each unit type) are shown in the lower part of the table. Economic weights were calculated using a 5% discount rate.

Trait	Mean value	Economic weighs (cents per dozen)	
		COP change with 10% gain	COP change per trait unit change
Growth time	600 days	9	0.15
Condition time	150 days	13	0.86
Survival [1]	30%	13	1.83
Width index (width / length) [2]	0.6	11	1.83
Uniformity	60%	15	2.49
Spat grade proportions [3]	60%,	0	0.07
6 mm unit grade proportions [3]	50%, 71%, 84%	2	0.29
12 mm unit grade proportions [3]	50%, 71%, 84%	2	0.42
20 mm unit grade proportions [3]	50%, 71%, 84%	5	0.98
Condition grade proportions [4]	90%	6	0.73

[1] Proportion of mortalities in each unit (and oyster size class) are assumed to be: Spat tray (6 – 15 mm length) 40%; 6 mm unit (15 – 25 mm) 30%; 12 mm unit (25 – 50 mm) 15%; 20 mm unit (> 50 mm) 5%; 20 mm conditioning unit 10%.

[2] Economic weight calculations for width index assume the threshold value for unacceptable shape is width index = 0.525 and the coefficient of variation is CV=10%. Assuming a normal distribution, 11% have unacceptable shape when the mean width index = 0.6.

[3] Mean values are the percentage of oysters moving to the next unit size for the first, second and third gradings respectively.

[4] Mean value is the percentage of oysters suitable for sale at the condition grading

2.4.2 Results

Economic weights for each of the five main traits are approximately of equal value when expressed as a percentage change of the trait mean (Table 2.2 and Figure 2.3). Growth time has the lowest relative value (9 cents change in COP with a 10% change in growth time), and uniformity has the highest relative value (15 cents change in COP with a 10% change in uniformity). For uniformity, there are large differences in the values for each unit type. The individual economic weights for the spat grade, 6 mm unit grade and the 12 mm unit grade are low, indicating a change in these traits will have negligible economic outcomes (Table 2.2). As is expected, the economic value of uniformity increases as the size of oysters increases. This is a function of the higher costs of handling larger oysters (Table 2.1) and the extra lease space occupied by out of grade returns.

Economic weights for all traits are near linear except for width index. Width index is non-linear because the proportion of oysters with unacceptable shape is calculated from the truncation point of a normal distribution. Therefore as mean values change, proportions of misshapen oysters change according to a sigmoid (s-curve) function. However, a linear approximation appears valid over the range of values that are likely to be expected for this trait, which are no more than ±10% (see Figure 2.3). If changes beyond this range were considered likely then a linear assumption would underestimate economic weights and non-linear economic weights would need to be considered. That would add a greater level of complexity and would require different economic weights at a different population means.

The degree to which economic weights change in different situations is shown in Table 2.3. Changes in relative values of economic weights (values in brackets in Table 2.3) compared to those of the industry standard (scenario 1) are indicative of different economic drivers to production costs in that situation. Except for the ‘poor shape’ scenario, there is surprising consistency between the economic weights under different site conditions and cost scenarios. Economic weights change and, at times these changes are significant but the relative values do not substantially change (e.g. compare low and high cost scenarios in Table 2.3). Therefore, it is appears unnecessary to use different breeding objectives for sites that have different productivity, different survival or different cost structures. An untested assumption

in the bio-economic model is that growth time and condition time are inversely related (section 2.3.2, step 5). The sensitivity of economic weights to changes in the this relationship were tested (see Appendix 3 for details of the relationship) and, with a 50% change in the values for 'assumed changes' there were no substantial changes in economic weights.

The economic weight for width index is highly sensitive to changes in the assumed shape characteristics of a population. A 10% change in the shape characteristics resulted in a three-fold increase in the economic weight (Table 2.3). This may represent a situation where the farm site has greater issues with shape due to different husbandry or a situation where the threshold for acceptable shape is higher. This highlights the importance of, firstly, knowing the shape characteristics associated with particular grow-out sites or husbandry practices and, secondly, knowing precisely the thresholds for unacceptable shape. Additional data was collected to validate shape assumptions (see section 3.2), however, there would be value in ongoing collection of industry shape data for continual revision of economic weights.

Changes in average mortality and shifts in the age at which mortality occurs caused only minor changes to economic weights (Table 2.3, compare scenario 1 to scenarios 4, 5, and 6), and these differences appear insufficient to warrant multiple breeding objectives. This was contrary to industry expectations. It was thought that higher mortality in some regions would be the most likely reason for different breeding objectives. The range of average mortalities tested were from 20 to 40% which is representative of differences within Australian regions. Differences in mortality could be twice this range before differences were comparable to those of scenario 7 (poor shape), at which point regionalised breeding objectives may be worth considering. Shifts in the age at which mortality occurs has the potential to change relative values of economic weights. Although the range tested here did not cause large changes, a situation where, say, 60% of total mortality occurred in oyster size grades greater than 25 mm coupled with higher average mortality would warrant revision of breeding objectives. Therefore, ongoing monitoring of mortality to continually revise breeding objectives is important. Adopting a single breeding objective with respect to survival assumes mortality has a common cause across all regions and sites. In this case, the assumption is that the underlying cause is a non-specific mortality and selection for a general resistance, or a general stress tolerance, will result in improved survival in all situations. This assumption is untested and it is possible that greater knowledge of the causes of mortality may necessitate regionalised breeding objectives to address specific causes of mortality.

Table 2.3 Economic weights, expressed as a change in the cost of production with a 10% change in the means, for ten different scenarios. The relative importance of economic weights is shown in brackets. Economic weights were calculated using a 5% discount rate.

Scenario	Economic weights (relative value in brackets)				
	Growth	Condition	Survival	Width index	Uniformity
1. Industry standard	9 (15%)	13 (21%)	13 (21%)	11 (18%)	15 (25%)
2. Slow growth and slow conditioning (25% less)	11 (16%)	16 (23%)	14 (20%)	13 (19%)	16 (23%)
3. Fast growth and fast conditioning (25% greater)	7 (14%)	10 (20%)	11 (22%)	10 (20%)	13 (25%)
4. High average mortality (33% greater)	10 (15%)	13 (20%)	15 (23%)	12 (18%)	16 (24%)
5. Low average mortality (33% lower)	9 (16%)	13 (23%)	11 (19%)	10 (18%)	14 (25%)
6. High late-age mortality (20% higher for >25mm oysters) [1]	10 (15%)	13 (20%)	16 (24%)	11 (17%)	16 (24%)
7. Poor shape (width index 10% less)	10 (11%)	13 (15%)	13 (15%)	36 (41%)	15 (17%)
8. High uniformity (in-grade percent 50% higher)	9 (16%)	13 (23%)	11 (19%)	10 (18%)	14 (25%)
9. High costs (25% higher)	11 (15%)	16 (21%)	16 (21%)	14 (19%)	18 (24%)
10. Low costs (25% lower)	7 (15%)	10 (22%)	10 (22%)	8 (17%)	11 (24%)

[1] The 'Industry standard' scenario assumes 30% of total mortalities occur for sizes classes > 25 mm length. The 'High late-age mortality' scenario assumes 50% of total mortalities in this size class.

2.5 PREDICTED GENETIC GAINS

2.5.1 Methods

Estimations were made of the genetic gains in each trait when selecting on a single index. They were made using the equations of Lin and Allaire (1977) and Lin (1978) which are based on selection index theory. Simulation studies (Chapter 4) have provided an assessment of the potential gains in breeding strategies based upon the population structure and selection approach. However, those predictions were for a single trait, the selection index, and could not describe how individual traits respond due to the absence of economic weights.

Predictions of gains in individual traits require the economic weights (Table 2.2) and genetic and phenotypic variances and covariances between traits. For growth, condition and width index, estimates were available from the genetic analysis of the ASI breeding population (Chapter 7, Table 7.13). For survival, estimates were used from studies in France (Dégremont *et al.* 2007) and from a preliminary study in South Australia (Alex Safari pers. comm.). No data was available for uniformity, so values were assumed. Variances for the breeding objective traits were estimated using known means, coefficients of variation and heritabilities (Table 2.4). Covariances were estimated from correlations, which were obtained from the previously mentioned sources, and both are shown in Table 2.5.

The equations used to produce the estimations were:

$$h^2_I = \mathbf{b'\ G\ b} / \mathbf{b'\ P\ b}$$

$$\sigma^2_{a\,I} = \mathbf{b'\ G\ b}$$

$$\sigma^2_{p\,I} = \mathbf{b'\ P\ b}$$

$$\Delta Gain_i = \mathbf{G}_i\ .\ \mathbf{b}\ .\ i / \sigma_{p\,I}$$

Where h^2_I is the heritability of the index, **b** is a vector of the economic weights, **G** is the genetic variance/covariance matrix, **P** is the phenotypic variance/covariance matrix, $\sigma^2_{a\,I}$ is the additive genetic variance of the index, $\sigma^2_{p\,I}$ is the phenotypic variance of the index, $\mathbf{G}_i$ is a row vector of genetic covariances between the i th trait and each component trait incorporated in the index, $\Delta Gain_i$ is the genetic gain in the i th trait, $\sigma_{p\,I}$ is the phenotypic standard deviation of the index, and *i* is the selection intensity. The assumed selection intensity was 500 from 16,000 (*i* = 2.25).

Table 2.4 Population parameters for the objective traits.

Trait	Units	Mean $\bar{x}$	Coefficient of variation $\sigma_p / \bar{x}$	Standard deviation σ_p	Variance σ^2_p	Heritability h^2	Genetic variance σ^2_a
Growth time	days	600	15%	150	8000	0.4	3240
Condition time	days	150	15%	37.5	500	0.25	127
Survival	% points	70	20%	14	200	0.3	59
Width index	ratio x 100	60	15%	9	80	0.4	32
Uniformity	% points	60	20%	12	150	0.25	29
Index (COP)	cents / dozen	380	12%	47	2218	0.29	643

Table 2.5 The economic weights and phenotypic and genetic variances, covariances and correlations used for genetic gain estimations. Correlations are shown above the diagonal, covariances below the diagonal, and variances on the diagonal (in bold). The P and G matrices were symmetric matrices of variances and covariances.

TRAITS	Code	Units	Eco wt	Phenotypic corr/var/covar matrix (**P**)					Genetic corr/var/covar matrix (**G**)				
			b [1]	GR	CON	SUR	WI	UN	GR	CON	SUR	WI	UN
Growth time	GR	days	-0.15	**8000**	-0.03	0	0.45	0	**3200**	0.3	-0.2	0.7	-0.1
Condition time	CON	days	-0.86	-60	**500**	0	-0.01	0	170	**125**	0	-0.3	0
Survival	SUR	% points	1.83	0	0	**200**	0	0	-88	0	**60**	0	0
Width index	WI	ratio	1.83	360	-2	0	**80.0**	0	224	-17	0	**32**	0
Uniformity	UN	% points	2.49	0	0	0	0	**150**	-31	0	0	0	**38**

[1] The economic weights used in this calculation are expressed as the change in COP per trait unit change (days, ratio, and percentage points).

2.5.2 Results

Selecting on the index with the current selection traits (growth time, condition time and width index) is predicted to decrease the cost of production by $0.15 per dozen per generation, or $0.07 per dozen per year (Table 2.6). The changes mainly arise through a decrease in growth time (11 days per year) and a decrease in condition time (5 days per year). Some of this gain comes through a change in survival due to the favourable genetic correlation of survival and growth rate. This is based on the French data (Dégremont *et al.* 2007) and it is possible that different correlations may exist in the Australian population. Without this favourable correlation, the benefit would be reduced to $0.06 per dozen per year.

Selecting on the index with all traits included is predicted to decrease the cost of production by $0.31 per dozen per generation, or $0.16 per dozen per year (Table 2.6). This represents a gain of 8% per generation (4% per year) assuming COP is four dollars per dozen. Changes in growth time are similar to the current strategy, and changes in condition are slightly less. A large proportion of the benefit (70%) will be obtained by selecting for survival and uniformity. Survival is predicted to change by 3% per year (say from 70% to 73%) and uniformity by 2% (say in-grade proportions from 60% to 62%).

Under both the current and future index selection strategies, very little benefit is realised through a change in width index. This is due to the adverse relationship between this and other traits. The selection pressure applied essentially will hold this trait at current levels which is likely to be acceptable if current values for this trait are acceptable. It emphasises the need to use different economic weights when populations have poor shape or thresholds for acceptable shape change.

Table 2.6 Predicted genetic gains per year for the current selection strategy (which does not select on survival and uniformity) and a future strategy that includes all traits. Gains are shown for each individual trait (in trait units, percentage change, and their dollar value) and for the combined effect of all traits (in percentage change and dollar value). ΔCOP is the change in the cost of production per dozen oysters.

Trait	Units	Gain per year with current strategy			Gain per year with future strategy		
		Trait units (% gain)		ΔCOP [1]	Trait units (% gain)		ΔCOP [1]
Growth time	days	-10.6	(-2%)	$0.016	-11.5	(-2%)	$0.017
Condition time	days	-4.6	(-4%)	$0.004	-2.4	(-2%)	$0.021
Survival	% points	0.6	(1%)	$0.011	2.9	(4%)	$0.054
Width index	ratio x 100	0.4	(1%)	$0.007	0.2	(0%)	$0.004
Uniformity	% points	0	(0%)	$0.000	2.4	(4%)	$0.059
Index	ΔCOP [1]		(2%)	$0.074		(4%)	$0.155

[1] Estimated mean cost of production (COP) is $4 per dozen, based on 'industry standard' scenario (Figure 2.2 and Table 2.2).

2.6 FUTURE DEVELOPMENT

An inverse relationship between growth time and condition time is assumed in this analysis. The validity of this assumption remains untested and there is, therefore, a need to measure this relationship. This is necessary to provide more accurate economic weights. It will also contribute to a better understanding of the growth characteristics of Pacific oysters.

Shell width index is the trait that is most sensitive to changes in economic weights. A change in the proportion of the crop deemed unacceptable can have a large impact on the cost of production. This proportion can be altered either by a change in the mean value of the crop, or a change in the threshold value for unacceptable oysters. There is a need for greater certainty regarding the definition of acceptable shape and for a better understanding of how environmental effects and husbandry influences shape.

The index that will be used for selection is scaled in units of cost of production. The value used to measure the genetic merit of any oyster will therefore be the change in the cost of production. The economic weights will need regular updating to remain applicable. Although out-of-date economic weights are unlikely to change selection decisions, they do risk becoming meaningless numbers. The model has been designed so that this can be done easily, but there will always be a need to obtain appropriate data. The Benchmarking Project, which is currently being undertaken as part of the Seafood CRC, will be an excellent data source to update model inputs. Therefore there is a need to ensure that links are maintained between the Benchmarking Project and the ASI breeding program.

2.7 CONCLUSION

Assigning the correct mix of traits for the Pacific oyster breeding program has hindered progress and resulted in lost opportunities to add value to the industry. This problem has been addressed by developing a bio-economic model and using that model to calculate economic weights for traits. The methodology was developed for livestock breeding, and this application is the first time it has been used for a shellfish breeding program. The bio-economic model was produced as an Excel spreadsheet and was designed so that economic weights can be regularly updated.

Five traits have been identified as economically important and these are growth time, condition time, survival, shell shape, and uniformity. Economic values have been calculated for each of these traits. All traits have approximately equal value, meaning all should be included as part of the selection strategy. Four of the five traits are insensitive to variations in site characteristics and cost structures. The one exception is shell shape (or width index) and continual care is needed to ensure the selection strategy is appropriate for all site conditions and all market requirements. Given that this attention is given to shell shape (in the form of a continual watching brief) a single breeding objective for all Pacific oyster growing regions will be acceptable.

The breeding objective for Pacific oysters is relatively complex due to the number of traits involved and the adverse genetic relationships between traits. The economics weights methodology will provide a sound means of ensuring future selections optimise economic value for the Pacific oyster industry. This methodology will be supported by the economics weight calculator and the genetic evaluation system also developed as part of this project.

A breeding strategy centred upon the economic weights will benefit the industry by lowering the cost of production. Using the current suite of selection traits, the cost of production is expected to decrease by $0.07 per dozen for every year of breeding. Including the additional traits of survival and uniformity is estimated to decrease the cost of production by $0.16 per dozen per year.

APPENDIX 2.1
Estimation of fixed costs for Pacific oyster production

Table A2.1 Fixed cost categories and values for Pacific oyster production. Categories and 1990 values are those from Treadwell *et al.* (1991). The 2009 costs are 1990 costs adjusted for the CPI changes shown in Table A2.

Item	Life (y)	1990 cost ($/ha)	1990 cost ($/ha/y) [1]	2009 cost ($/ha/y)
Operating				
Electricity and fuel			$ 500	$ 1,267
Protective clothing			$ 80	$ 203
Labour - owner			$ 2,000	$ 5,067
Labour – permanent [2]			$ 3,067	
Licence and levies			$ 133	$ 338
Repairs & maintenance			$ 1,533	$ 3,884
Administration			$ 467	$ 1,182
Miscellaneous			$ 333	$ 844
Sub total			$ 8,113	$ 12,785
Capital items				
Racks (post and rails)	7	$ 3,600	$ 514	$ 1,303
Baskets	6	$ 6,000	$ 1,000	$ 2,533
Trays	3	$ 725	$ 242	$ 613
Bags	1	$ 200	$ 200	$ 507
Punts	10	$ 800	$ 80	$ 203
Outboard motors	3	$ 333	$ 111	$ 281
Trailers	10	$ 400	$ 40	$ 101
Tractor	5	$ 667	$ 133	$ 338
Truck/utility	5	$ 667	$ 133	$ 338
Grader	10	$ 667	$ 67	$ 169
Tools and equipment	3	$ 267	$ 89	$ 225
Office equipment	5	$ 133	$ 27	$ 68
Shed	10	$ 2,000	$ 200	$ 507
Sub total			$ 2,836	$ 7,185
TOTAL				$ 19,970

[1] Treadwell *et al.* 1990 costs have been expressed as $ per ha

[2] Permanent labour has not been included as a fixed cost in this analysis because these costs have been factored into the grading, handling and harvest costs.

Table A2.2 Consumer Price Index (CPI) data from 1991 to 2009, from ABS (2010) using the category 'All Groups'.

Year	CPI
1991	4.3%
1992	4.3%
1993	4.4%
1994	4.5%
1995	4.7%
1996	4.8%
1997	4.8%
1998	4.8%
1999	4.9%
2000	5.1%
2001	5.4%
2002	5.5%
2003	5.7%
2004	5.8%
2005	6.0%
2006	6.2%
2007	6.3%
2008	6.6%
2009	6.7%
Average	5.3%
Adjustment	2.53

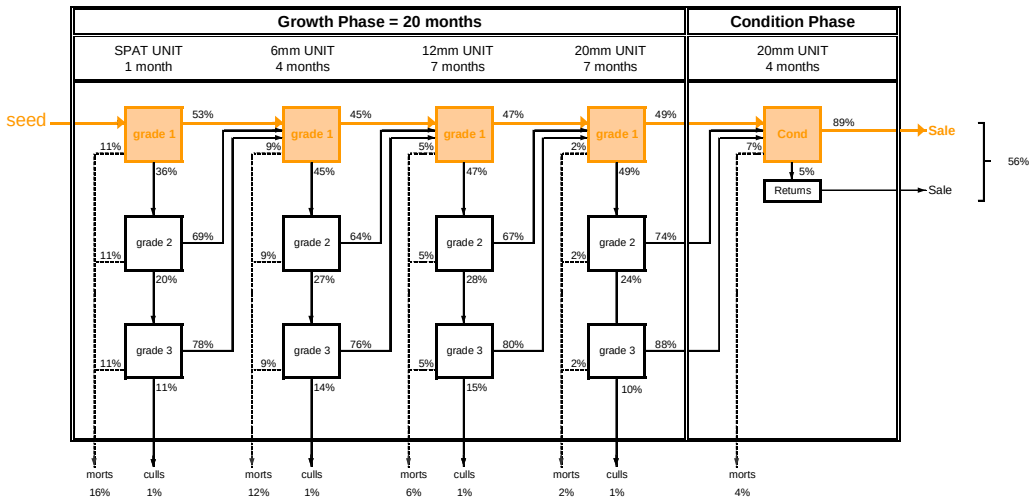
Adjustment = $(1+i)^{t}$

where i = average annual CPI
and t = years since 1991 (18 years)

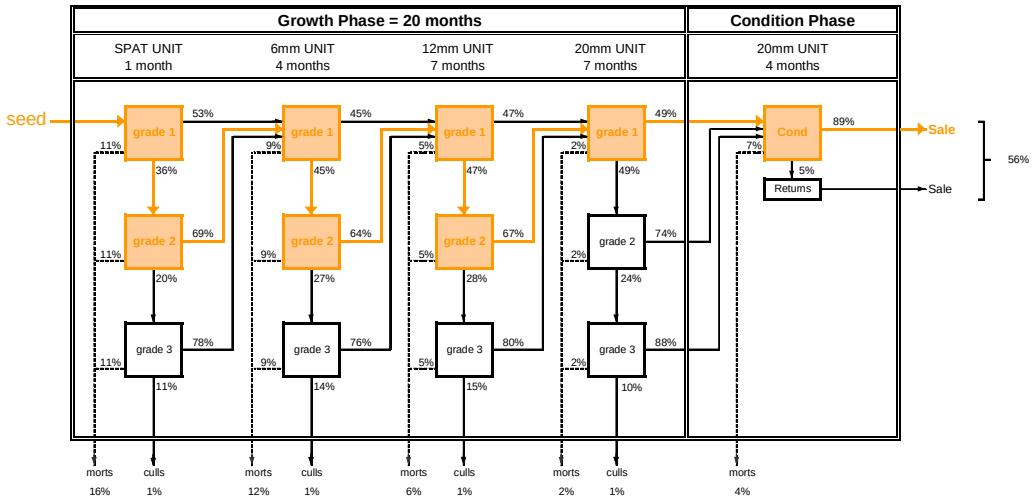
APPENDIX 2.2
Diagrammatic representation of the economic model

Figure A2.1 Step 1 – define the production pathways. There are potentially 202 pathways though the system. Examples of three possible pathways through the production system are shown.

(a) The shortest pathway



(b) A medium length pathway



(c) A long pathway

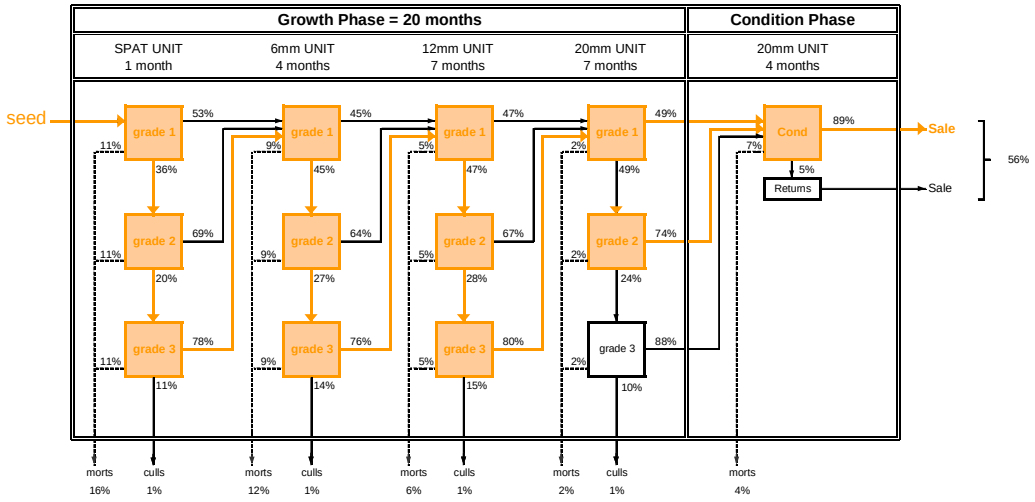
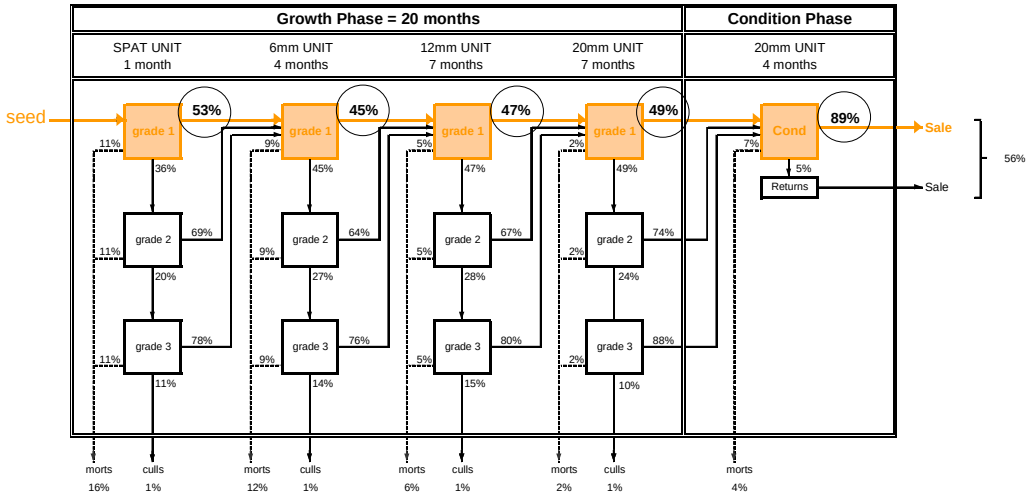
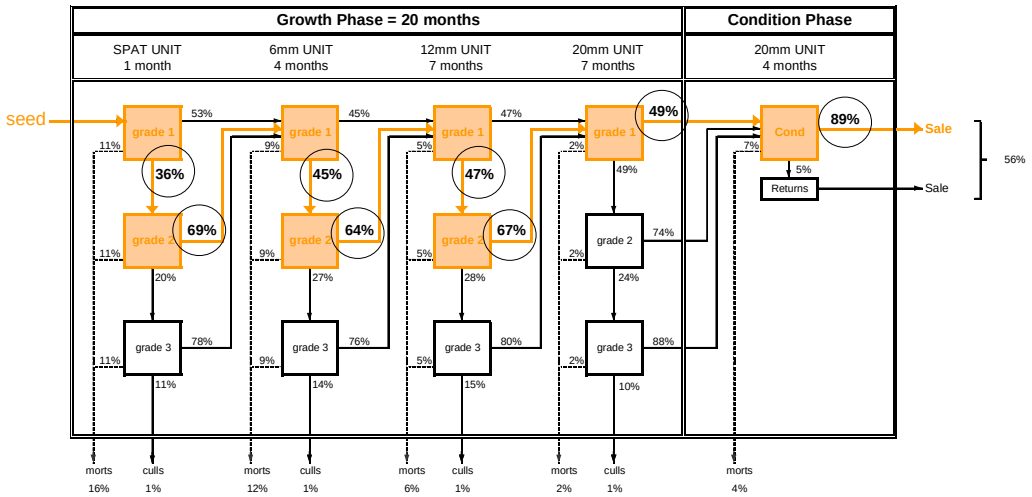


Figure A2.2 Step 2 - Allocate oysters to pathways. The grade proportions determine the percentage of total in each pathway. Grade proportions for three possible pathways through the production system and the resulting proportions in those pathways are shown.

(a) The shortest pathway = 5.9%



(b) A medium length pathway = 1.0%



(c) A long pathway = 0.02%

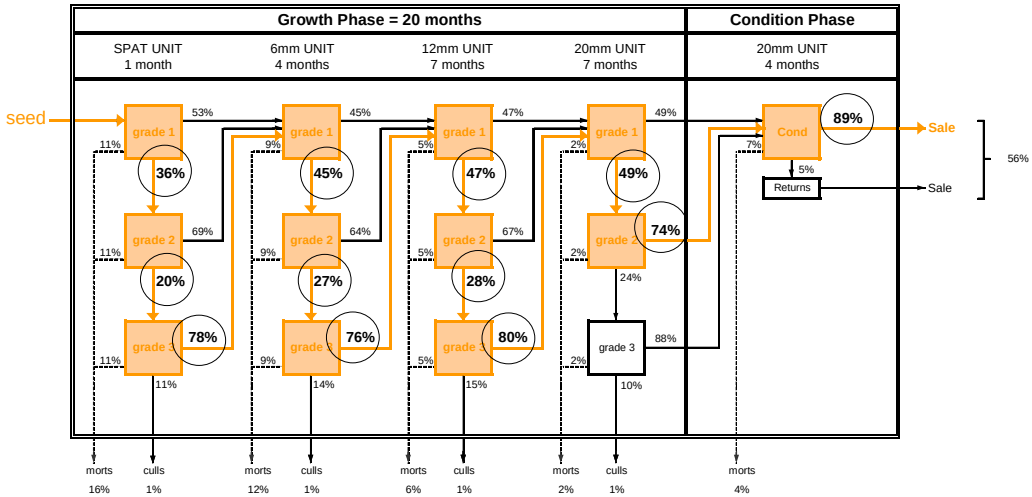
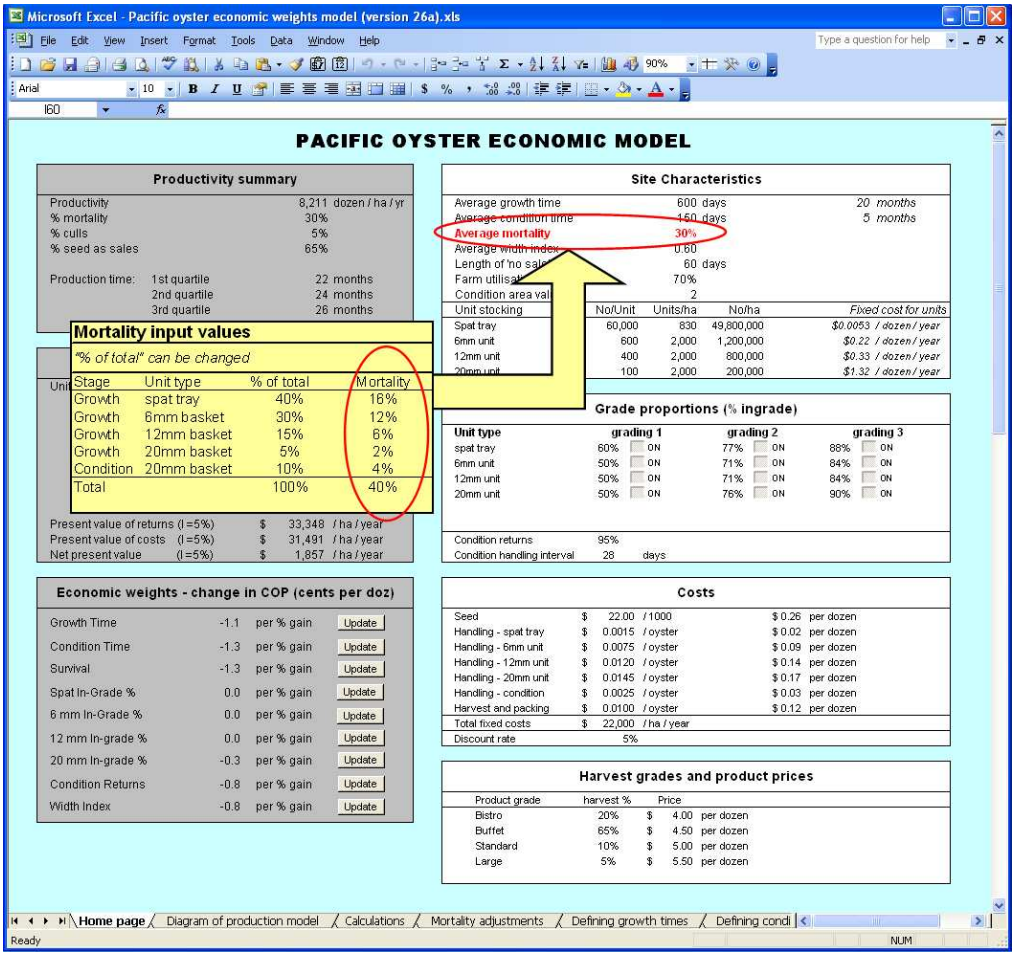


Figure A2.3 Step 3 – subtract morts. Morts are subtracted at each grading event and for each pathway. The morts subtracted at each grading are calculated to match a given set of input values, shown in the table.

(a) Average mortality is entered on the Home Page, and the proportion of morts in each unit type is entered on another worksheet (Mortality adjustments worksheet).



(b) Morts are at each grading event and in each unit to match input values.

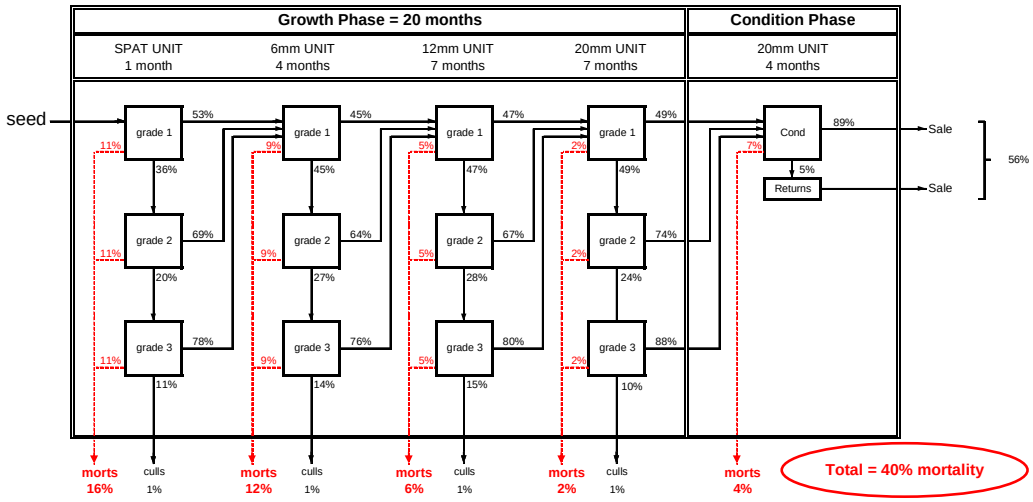
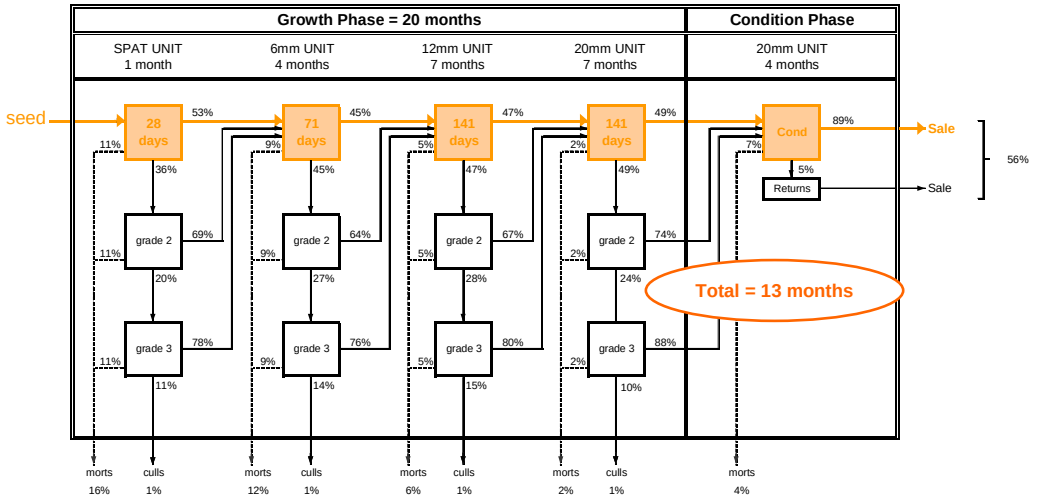
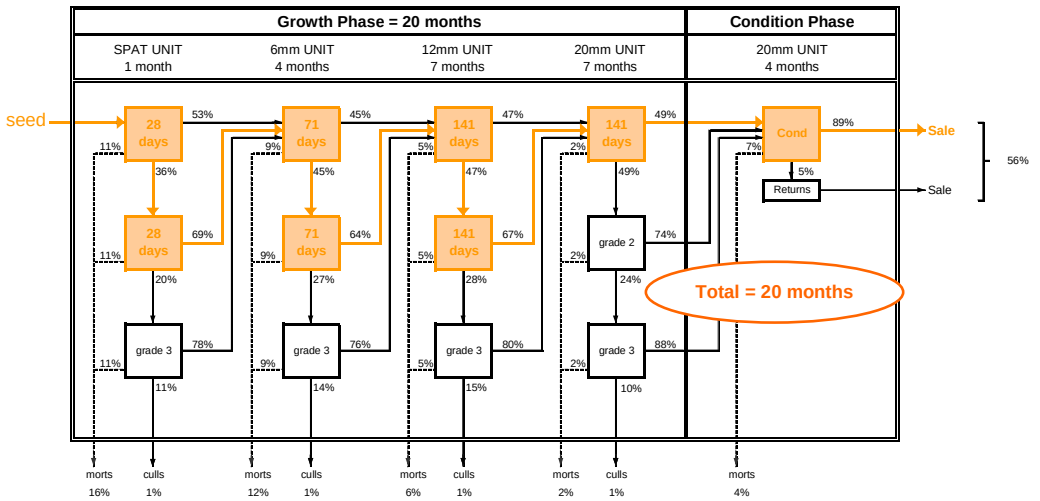


Figure A2.4 Step 4 - define the growth phase. The length of the growth phase for a particular oyster is dependent on the number of grading events which is, in turn, dependent on how quickly it progresses to the next sized unit. Growth times are shown for three possible pathways through the production system for a site that has a growth phase of 20 months.

(a) The shortest pathway = 13 months



(b) A medium length pathway = 20 months



(c) A long pathway = 33 months

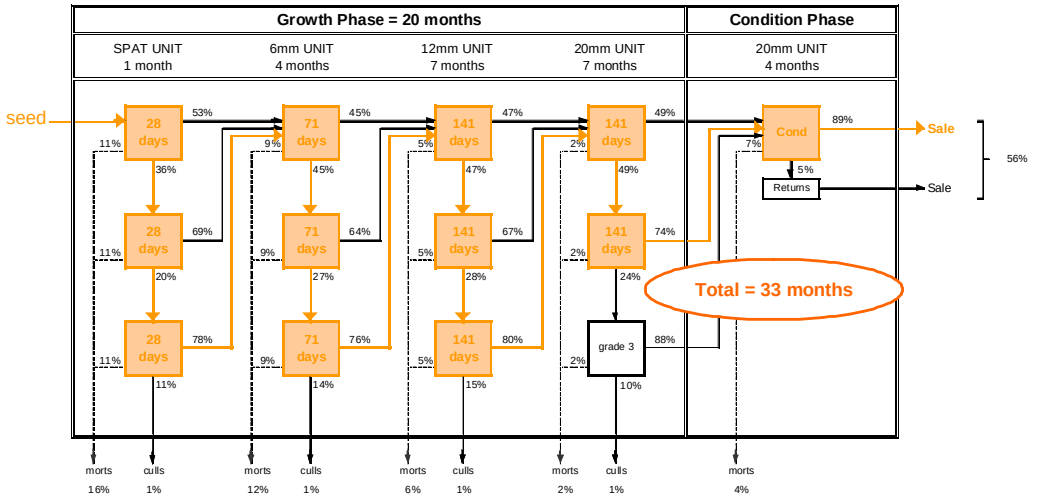
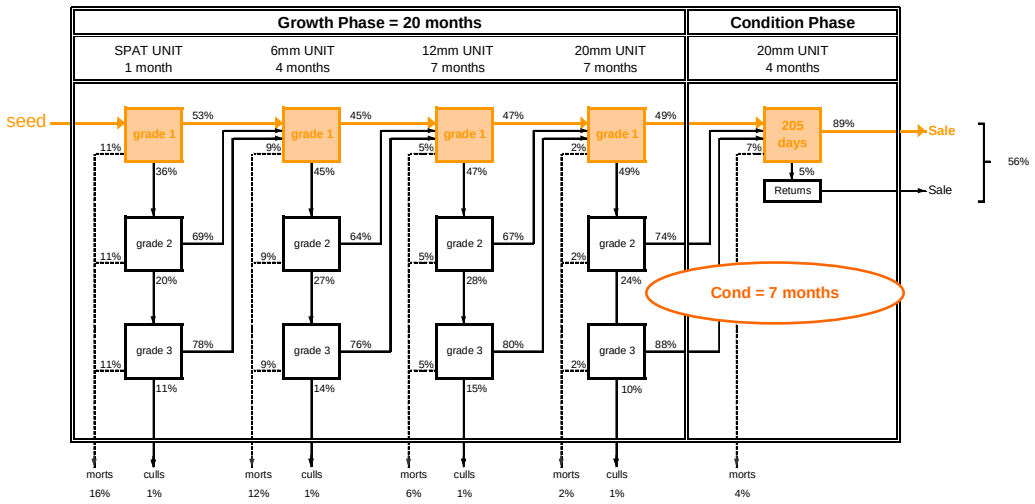
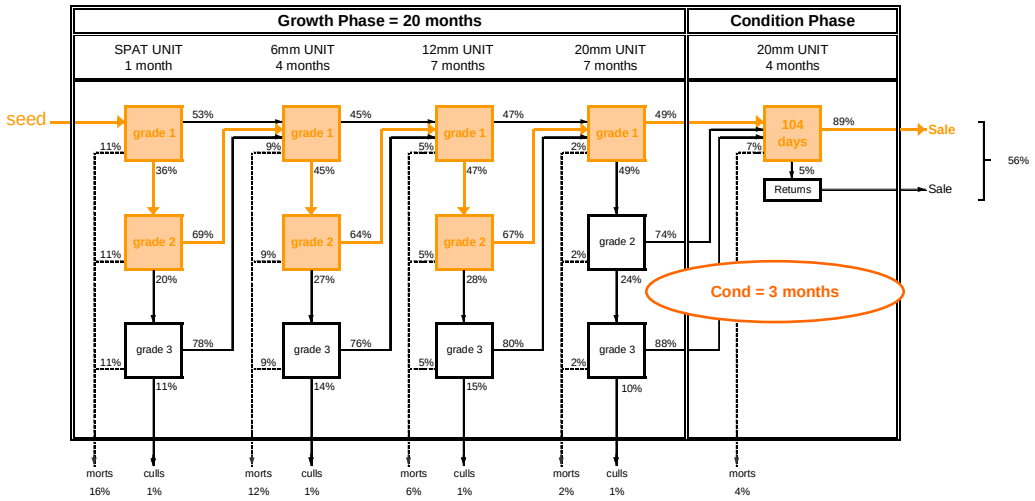


Figure A2.5 Step 5 - define the condition phase. The length of the condition phase for a particular pathway is inversely related to the growth time for that pathway. Condition times are shown for three possible pathways through the production system for a site that has a growth phase of 20 months.

(a) The shortest pathway = 7 months (growth time was 13 months)



(b) A medium length pathway = 3 months (growth time was 20 months)



(c) A long pathway = 1.5 months (growth time was 33 months)

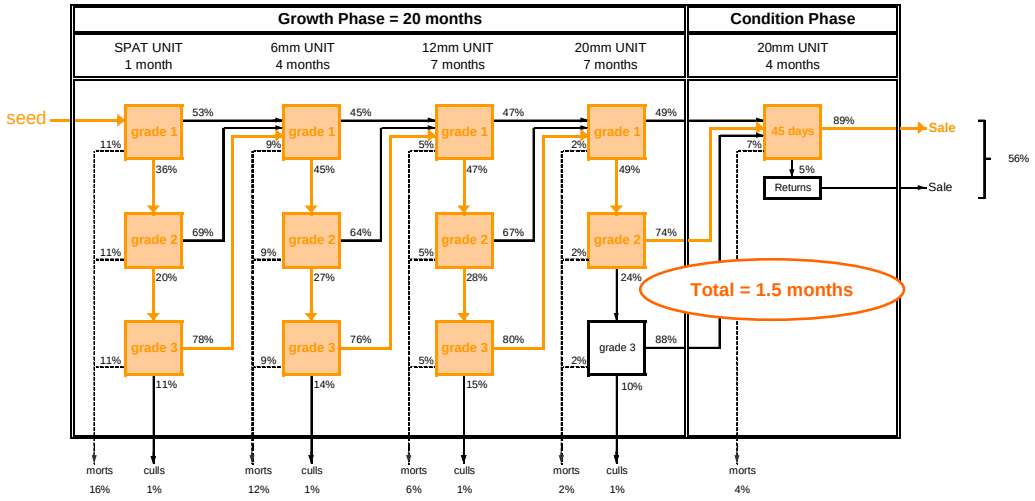
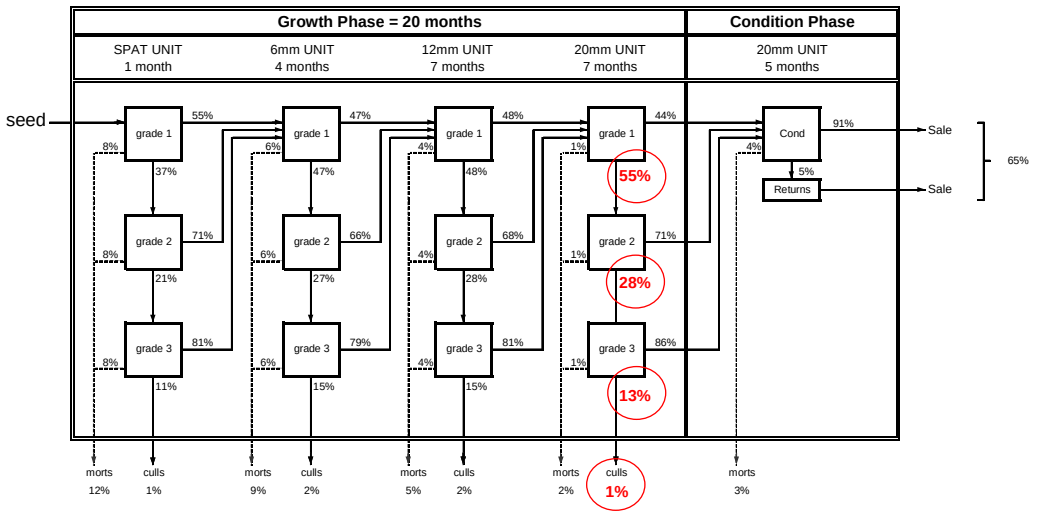
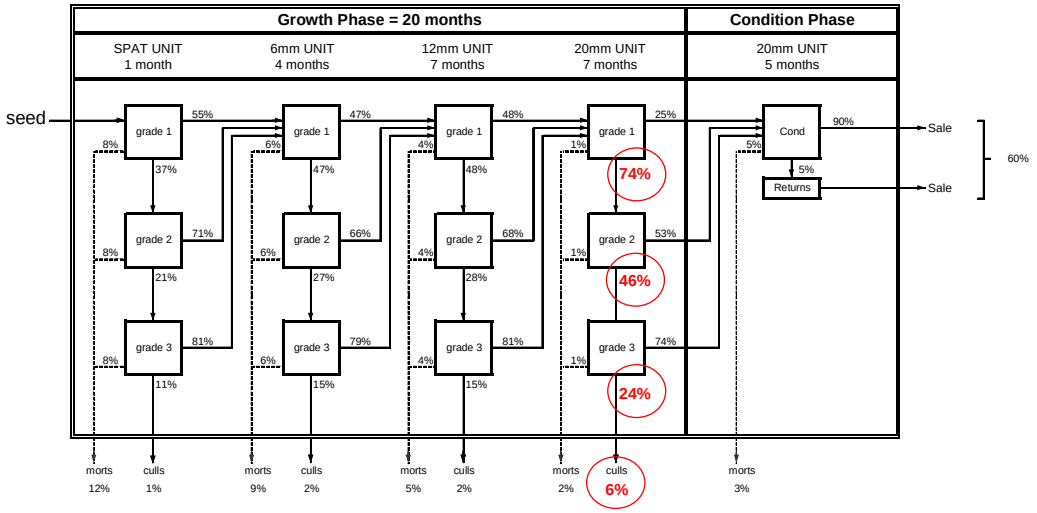


Figure A2.6 Step 6 - define the influence of width index. Oysters with poor shape are returned to the 20 mm growth unit, thereby extending the growth time. The effects of these returns are shown for three scenarios.

(a) Site with good shape (WI = 0.6) and low threshold for culling on shape (WI = 0.525).



(b) Site with good shape (WI = 0.6) and high threshold for culling on shape (WI = 0.6)



(c) Site with moderate shape (WI = 0.575) and high threshold for culling on shape (WI = 0.6)

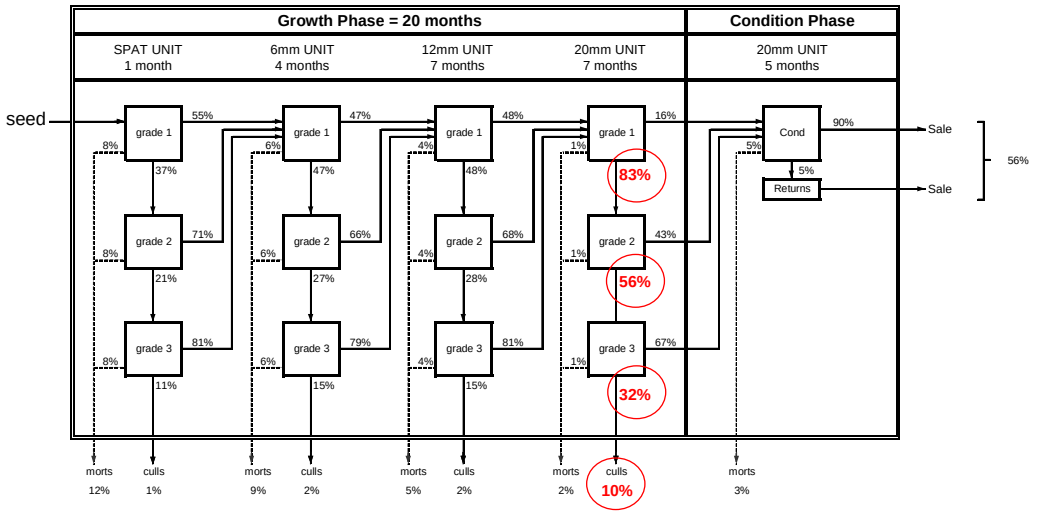
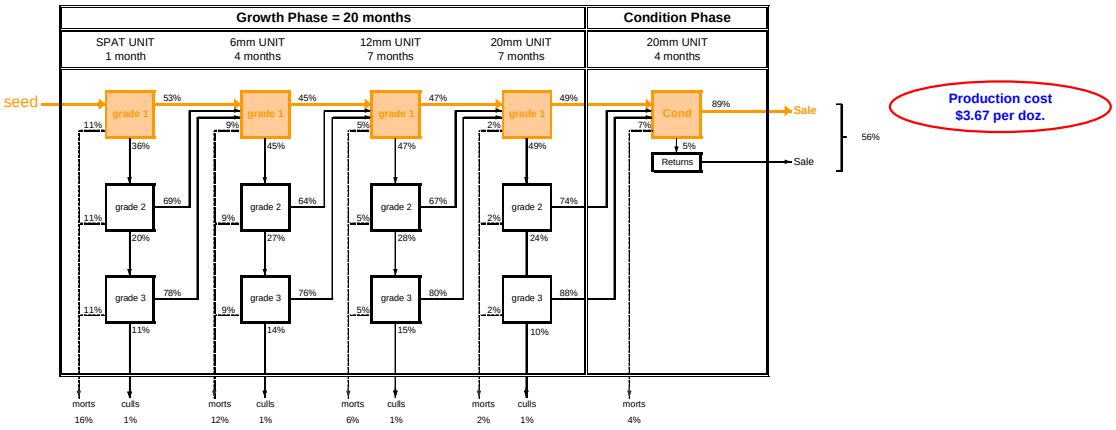
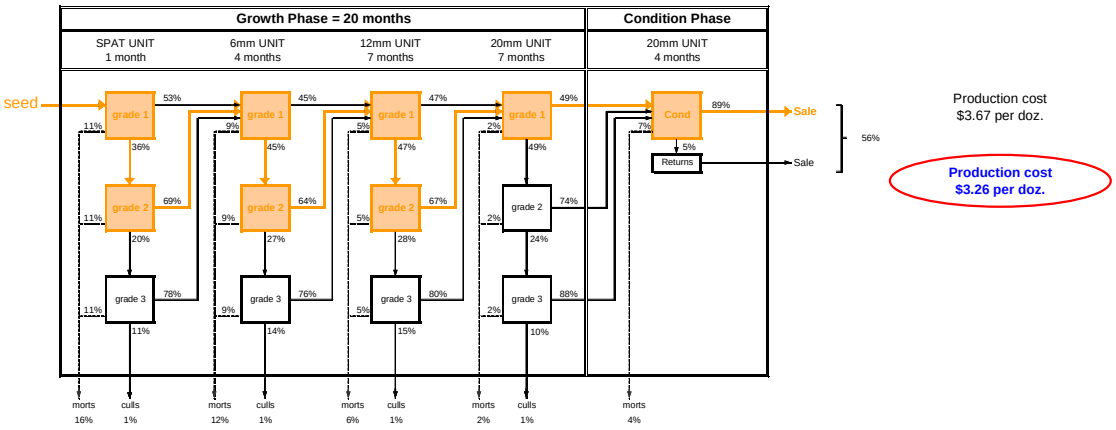


Figure A2.7 Step 7 - estimate the cost of production. Each pathway has a different production cost due to different numbers of grading events and different lengths of time in the water. Production costs are shown for three possible pathways through the production system for a site that has an average production cost of $3.71 per dozen. The medium length pathway has the lowest production cost due to the inverse relationship between growth time and condition time.

(a) The shortest pathway = $3.67 per dozen



(b) A medium length pathway = $3.26 per dozen



(b) A long pathway = $4.10 per dozen

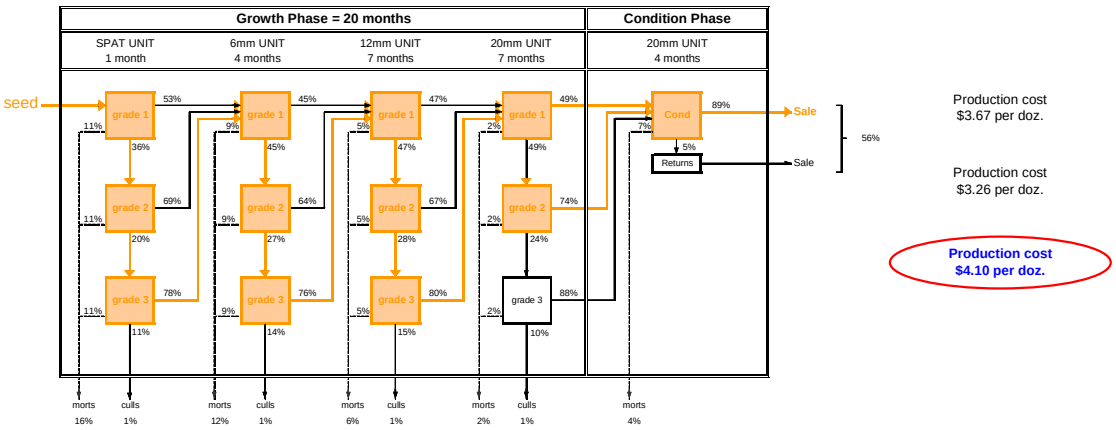
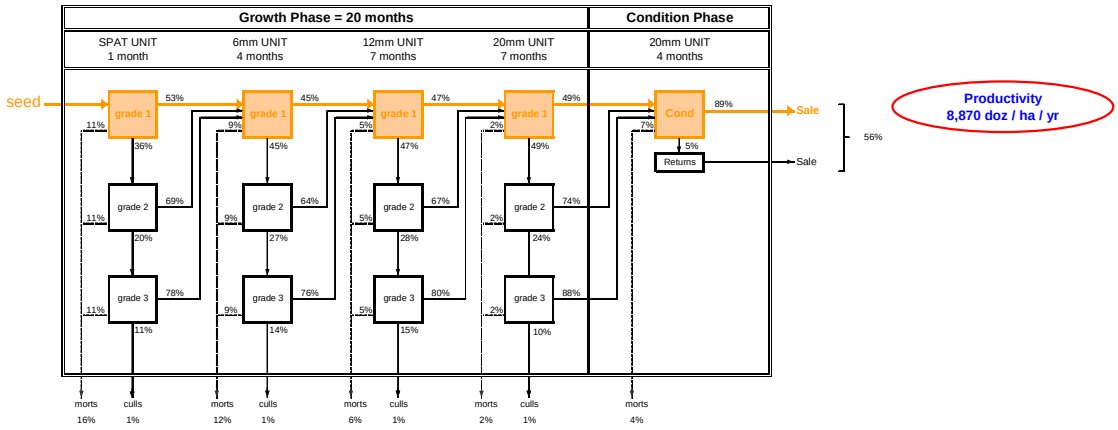
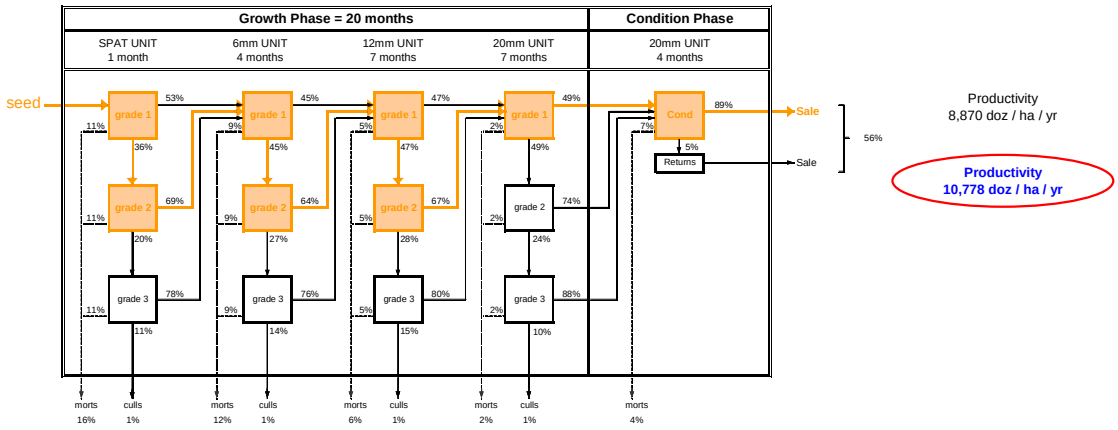


Figure A2.8 Step 8 - estimate the productivity. Productivity is expressed as dozens per hectare per year, and each pathway has a different productivity due to different lengths of time in the water. Productivity is shown for three possible pathways through the production system for a site that has an average production of 8,587dozen per hectare per year. The medium length pathway has the highest productivity due to the inverse relationship between growth time and condition time.

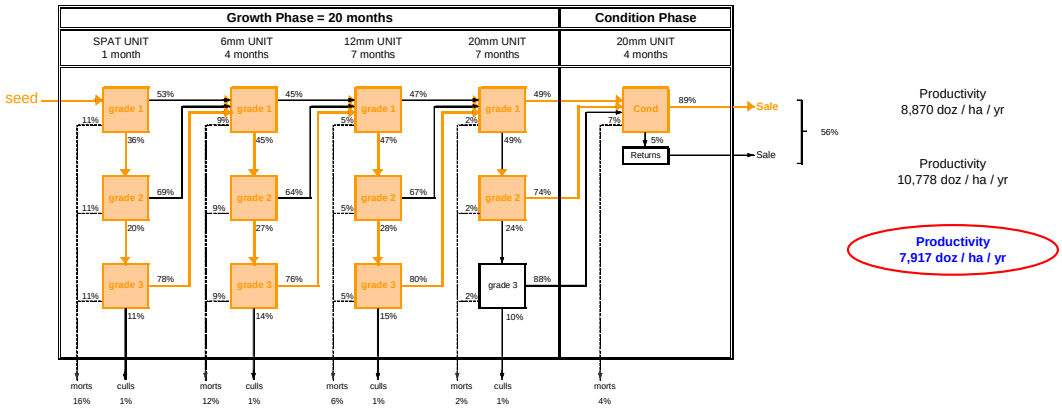
(a) The shortest pathway = $3.67 per dozen



(b) A medium length pathway = $3.26 per dozen



(b) A long pathway = $4.10 per dozen



APPENDIX 2.3
Relationship between growth time and conditioning time

Condition times for each pathway are calculated assuming the relationship:

$$C = a (G + 1)^{-b}$$

Where C is the predicted condition time for the pathway, G is the growth time for the same pathway, and a and b are constants defined by input values.

The constants are calculated after inputting a single value which is an estimate of how condition time is expected to change with a given change in growth time. The model uses this point value, and the mean values for growth time and condition time to predict the constants.

An example, and the default values in the model, is:

Mean growth time:	G_m = 600 days	
Mean condition time:	C_m = 150 days	
Assumed changes:	G' = 720 days (a 120% increase in growth time)	
	C' = 112.5 days (a 75% reduction in condition time)	
Constants:	$a = 2^b$	= 8.103
	$b = \log_{10}(C' (2 / (G' + 1)))$	= 3.018

The relationship to calculate condition time from growth time is therefore:

$$C = 8.103 (G + 1)^{-3.018}$$

This relationship is illustrated in Figure A2.9.

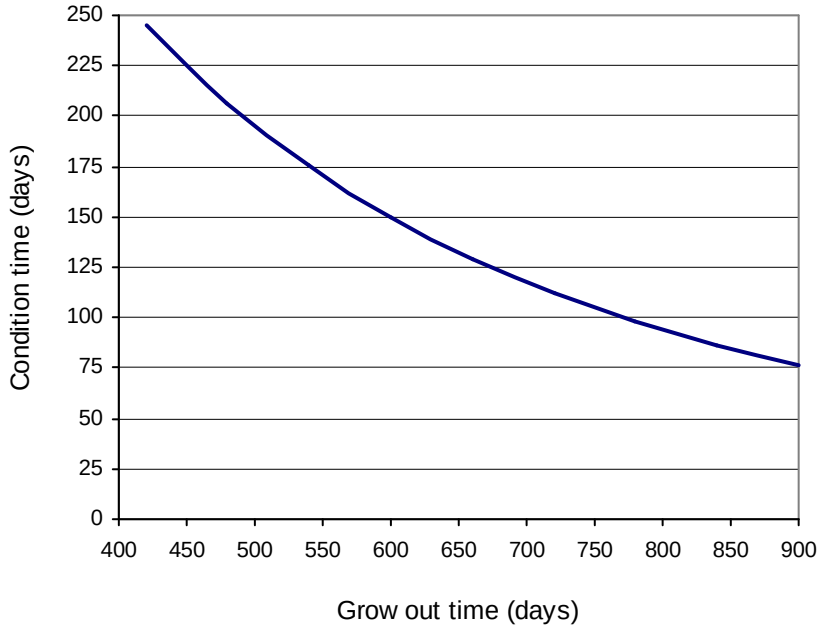


Figure A2.9 The assumed relationship between grow-out time and condition time in the default settings of the economic model.

Chapter 3

Validation of the economic weights model

Benjamin Finn, Rosie Bennett and Peter Kube

3.1 INTRODUCTION

A bio-economic model of the Pacific oyster production system has been developed (Chapter 2). The aim of that model is to calculate the economic importance of genetic traits to the selective breeding program but it does have general application beyond this. The model estimates the productivity, cost of production and profitability of an oyster growing enterprise. It is dependent on the input of values to characterise farming practices. Some of these were readily available from growers, but for others there was less certainty about actual values or the range of values. The aim of this part of the project was to collect data where information was identified as lacking, and where the bio-economic model was shown to be most sensitive to input values.

The areas identified as needing additional and detailed information were:

- The number of handlings per batch of oysters in each unit type
- The time spent in each unit type
- Percentages of oysters upgraded to the next sized unit at each handling and the percentage returned to the same unit size
- Mortality in each unit size
- Time of sales
- The time required to correct shape defects and the proportions of oysters that can be corrected
- Relationship between the shell growth rate and the time to condition

The data collection done for this part of the project are presented as two main tasks which are, firstly, a re-shaping trial established to measure the time required for a poorly shaped oyster to grow into a market acceptable shape and, secondly, an analysis of farm management data which was used to collect the data required. Measuring the relationship between growth rate and condition time requires significant resources. This research was highlighted as important, but was deemed to be outside the scope and resources of the current project. It is now planned to address this as part of a new project (Seafood CRC Project 2009/743).

3.2 TIME REQUIRED TO CORRECT SHELL SHAPE

3.2.1 Background

Australian oysters are exclusively produced for the half-shell market and therefore external appearance is important. Shell shape, and in particular the ratio of width to length, is an important component of appearance. Oysters that are long and skinny are considered unsuitable for sale. It is generally accepted that the ideal oyster has ratios of length, width, and depth of 3:2:1. Standard measures used are width index (WI = width / length) and depth index (DI = depth / length). Using the ideal shape ratio (3:2:1), optimal width index = 0.66 and optimal depth index = 0.33. Values less than these are accepted by the market, and there

are no fixed and universal standards to define minimum acceptable values for the Australian market. A study in the United States defined critical values for depth index and width index of 0.25 and 0.63 respectively (Brake *et al.* 2003). However, they found these thresholds to be less useful in predicting quality when used in combination.

Environmental conditions and husbandry are known to have pronounced effects on the shell morphology of cultured oysters (Carriker 1996). Growers have long known that the amount of wave action at a growing site has a strong influence on the shape, and other shell characteristics of oysters. Oysters often develop undesirable shape if stocking densities within individual baskets are high and space is restrictive. Bio-fouling and overcatch, which limit water movement within the culture environment, can accentuate these problems (De Nys *et al.* 2003). Genetic factors also influence shape (Chapter 7). It is possible that some oysters will always have inherently unacceptable shape, but it is more likely that a genetic predisposition to poor shape, coupled with husbandry and environmental factors is the cause of the majority of misshapen oysters in commercial grow-out.

Management practices such as vigorous rumbling and the placement of stock on intertidal leases with increased wave action are methods effectively used by farmers to manage shell morphology issues. Oysters with a tendency to poor shape can generally be controlled and oysters with poor shape can usually be recovered. But this is a cost to growers. There is additional handling which is a direct cost. There is also additional time in the water at a stage when they occupy maximum space, which represents an opportunity cost of lost production caused by reduced turnover.

A goal of the economics weights study (Chapter 2) was to put an economic value on all traits identified as being economically important. The shell shape was identified as an economically important trait but calculating an accurate value was difficult. This is because there is no information on the time required to correct unacceptable shell shape. Many attempts have been made to categorise oysters according to their shape and appearance (BIM 1996; Galtsoff 1964; Heath and Wilson 1999, Brake *et al.* 2003), but the ability for oysters to change their shape has not been investigated. Therefore the aim of this part of the study was to measure the time period in which an oyster with undesirable shell morphology takes to correct its shape given favourable culture conditions.

3.3.3 Methods

This trial was conducted at two sites in Tasmania; Pipeclay Lagoon (latitude 42.98^{o} S, longitude 147.53^{o} E) and Pittwater (latitude 42.82^{o} S, longitude 147.48^{o} E). It was done over a six month period starting in January 2009 and finishing in June 2009. Mature oysters from the same input batch were used and, at the start of the trial, average length was 94 mm and the coefficient of variation was 9%. Oysters were individually sorted into two groups, termed “acceptable” and “unacceptable” according to the suitability of their shell shape for market. This was done visually, without measurements. Measurements done after sorting were used to determine threshold values assumed by sorters, and minimum acceptable values for width index and depth index were 0.57 and 0.30 respectively.

Three replicates per site were used for the unacceptable group and a single replicate at each site for the acceptable group. Each replicate contained thirty (untagged) oysters housed in 20 mm oyster baskets. All oysters were measured for length, width and depth at the start of the trial, and at monthly intervals. Baskets were shaken vigorously once per month to mimic the machine rumbling used by growers as part of the re-shaping process.

Subjective visual assessments were done at 4, 5 and 6 months in addition to measurements. This assessment rated oysters as suitable for market based on the overall visual appearance of each individual oyster, taking into account width index, depth index, uniformity in shape, and deformities. Grading was done independently by two assessors at each site. One was the site farm manager, which was different at each site and the other was an ASI assessor which was the same at each site.

3.3.4 Results

Oysters with a low width index will re-shape with an extended grow-out. Mean values of width index increased at both sites for the group initially graded as having unacceptable shape (Figure 3.1). Different responses are evident on different sites. At Pipeclay Lagoon, average width index increased from 0.52 to 0.58 but at Pittwater the increase was from 0.52 to only 0.54. Differences appear due to different growth rates. At Pipeclay Lagoon there was a 13% increase in length compared to only 3% at Pittwater. Changes in the proportions of acceptable oysters illustrates the importance of the increases in width index. Assuming the threshold value for width index is 0.57, all of the unacceptable group were unmarketable at the start of the trial. After 6 months, the proportions with a width index greater than or equal to 0.57 and, therefore, suitable for market were 55% at Pipeclay Lagoon and 33% at Pittwater.

Changes in width index for oysters already having acceptable shape were much less and barely detectable (Figure 3.1). Length growth was comparable between the two groups at each site, however, width growth was proportionally greater for oysters with a lower width index (greater for the unacceptable group). For example, at Pipeclay Lagoon the average width increase of the unacceptable group was 22% (from 49 to 60 mm) whereas the increase for the acceptable groups was only 13% (53 to 60 mm).

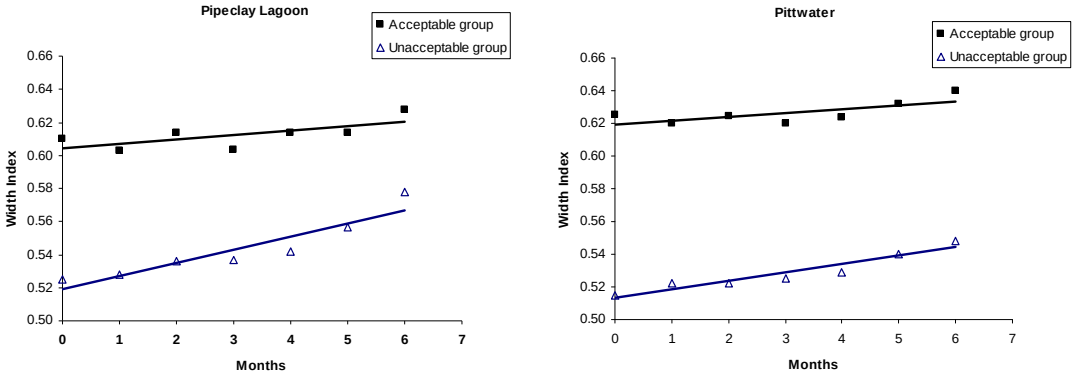


Figure 3.1 Changes in width index at the Pipeclay Lagoon and Pittwater trial sites. Market sized oysters were subjectively categorised as acceptable or unacceptable for market and then on-grown for 6 months. The minimum acceptable width index was 0.57.

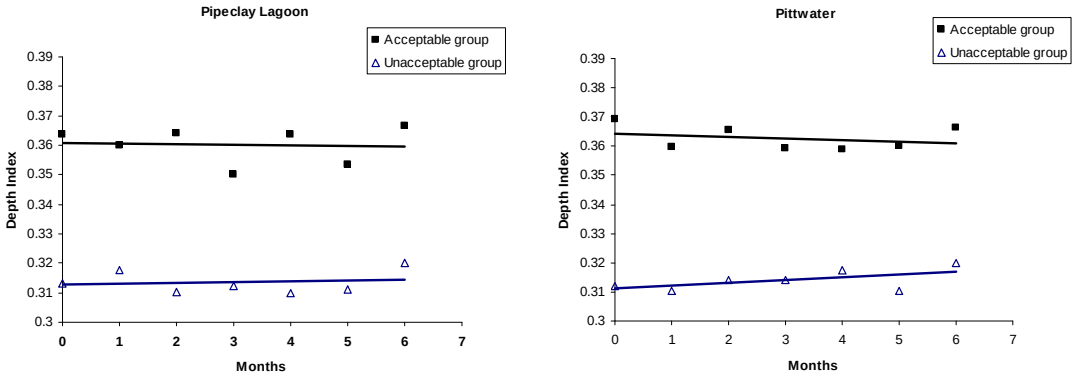


Figure 3.2 Changes in depth index at the Pipeclay Lagoon and Pittwater trial sites. Market sized oysters were subjectively categorised as acceptable or unacceptable for market and then on-grown for 6 months. The minimum acceptable depth index was 0.30.

Oysters with a low depth index did not appear to reshape with an extended grow-out, suggesting depth, or cup shape, is unresponsive to the husbandry treatments used to reshape width. The mean values of depth index did not change for both groups at both sites (Figure 3.2). The proportional increase in depth was similar to that for length. For example, at the Pipeclay Lagoon site, the average depth increase was 14% (from 29 mm to 33 mm).

A subjective visual assessment of overall shape also found shell shape to recover with an extended grow-out (Tables 3.1). At 5 months, approximately 90% of oysters were considered acceptable and at 6 months this figure was approximately 95%. There were no differences between different assessors. Assessments were also done on the acceptable group (data not shown) and all oysters at every assessment were classed as suitable. The visual assessments rated much higher proportions of oysters as suitable for market than an evaluation based on the actual measures of width and depth index of the same oysters (55% at Pipeclay Lagoon and 33% at Pittwater). This indicates that different threshold values were used in the different assessments.

Table 3.1 Changes in percentages of acceptable oysters at the Pipeclay Lagoon and Pittwater trial sites as determined by a visual assessment of overall shape by two assessors. All oysters were graded as unacceptable at the start of the trial, based on a shell shape.

Pittwater	Pipeclay		Pittwater	
	Assessor 1	Assessor 2	Assessor 1	Assessor 2
4 months	73%	84%	38%	41%
5 months	89%	89%	93%	93%
6 months	96%	97%	96%	94%

3.3.5 Discussion

Oysters that were unmarketable due to a low width index corrected at both sites over a 6 month period but there were no changes to depth index. This confirms that width index can be altered through management techniques such as artificial rumbling or exposure to greater wave action and gives an indication of the timeframe needed to reshape an oyster. However, this study suggests depth index is insensitive to these same treatments. The rate of change in width index varied between the sites, with Pipeclay Lagoon displaying a greater change than Pittwater. This is probably due to the higher growth rate at Pipeclay Lagoon. Growth rates at Pittwater were much slower, but reshaping at this site was probably assisted by greater wave action (it is a more exposed site). This wave action may also have contributed to the lower length growth, with more shell frill being constantly eroded.

There is a need to determine with more certainty the critical threshold for acceptable shape. The differences between the measured data and the visual assessments indicate that the threshold assumed for the measured data (width index of 0.57) is higher than that used for the visual assessments (which approximates that used operationally). A study in the USA suggested perceptions of the ideal oyster may be influenced by interactions of width index and depth index (Brake *et al.* 2003) and may be more complex than an independent assessment of different criteria. This may explain the large differences in this current study between the grading by a subjective visual score and grading using data measurements. Therefore determining an threshold value for width index may be complex.

Poor shape is potentially a significant cost to growers. The economic model (Chapter 2) can be used to estimate the cost of reshaping an oyster and accounts for the additional handling costs, the opportunity cost of lost production due to reduced turnover, and a slightly higher proportion of culls. If 50% of oysters require reshaping, and if the reshaping can be done in 6 months, then the cost of production will increase by 11%, or approximately $0.40 per dozen.

Assuming a 'typical' farm with production of 100,000 dozen per year (Treadwell *et al.* 1993)[2] the total cost to the grower will be approximately $40,000 per year. If 70% of oysters require reshaping, then the cost of production is increased by approximately 20%.

The time taken to correct shape may mean that when that oyster is sold it is in a different size class (e.g. Buffet may have grown to Standard). This can have both a positive and negative affect on growers. A larger oyster attracts a higher price, however, some growers only sell specific size grades and different size grades may not be readily saleable for them.

3.3.6 Conclusion

Data from this trial indicates that long and skinny oysters can be corrected, but it is difficult to correct oysters with a shallow cup. That is, width index can altered by husbandry but not depth index. In a visual assessment, approximately 95% of oysters had reshaped to a marketable shape in 6 months. In an assessment based on actual measurements, approximately 50% had reshaped in that period. Rates of reshaping vary on different sites, and it appears that reshaping is more effective when growth rates are higher. The results of this trial demonstrate that management techniques such as rumbling and re-location of stock to intertidal leases exposed to increased wave action do facilitate the re-shaping of oysters. Results from this study have been included in the economics weight model (Chapter 2) and provide a means of measuring the economic significance of poor shape.

3.3 ANALYSIS OF FARM MANAGEMENT DATA

3.3.1 Background

The development of the bio-economic has highlighted the need for general oyster practices to be quantified and validated in order to determine their economic significance, but there is a lack of definitive data to quantify oyster husbandry practices within the oyster industry. Obtaining data is made more difficult due to the diversity of farming practices for Pacific oysters in Australia. Cultivation occurs over a diversity of geographic locations, climatic conditions and water quality parameters. However, some forms of cultivation are seen as being more traditional within industry than others (i.e. 'post and rail' culture is seen as being the traditional cultivation method.).

The main body of data was provided by Bolduans Bay Oysters, located at Smithton in north-west Tasmania (latitude 40.08^{o} S, longitude 145.09^{o} E). Bolduans Bay Oysters cultivate oysters using a traditional post and rail system, where seed is initially grown in wooden trays with 3 mm plastic mesh (3 mm trays). Once large enough, oysters are then grown in a series of soft mesh bags which are adhered to a wooden frame backed with 16 mm plastic oyster mesh. There are two soft mesh bag sizes, an A015 bags which has fine nylon mesh holes and an A116 bag which has courser nylon mesh holes. Oyster baskets with varying mesh sizes (12 mm, 16 mm and 20 mm) are then used to cultivate the oysters until they are harvested.

Additional data was provided by Zippel Enterprises, located at Smokey Bay in South Australia (latitude 32.39^{o} S, longitude 133.90^{o} E). Zippel Enterprises also cultivate oysters using a traditional post and rail system, using seed bags and oyster baskets with varying mesh sizes (12 mm, 16 mm and 20 mm).

[2] The profitability analysis of Treadwell *et al.* (1993) assumed the average enterprise had a lease area of 15 ha. The production on a good site was assumed to be 123K dozen per year, and on a poorer site this was assumed to be 89K dozen per year. The value used here is an approximate midpoint.

3.3.2 Methods

Data on the management and performance of commercial batches of oysters was provided by Bolduans Bay Oysters (Tasmania). Bolduans Bay Oysters have a comprehensive stock management system which is supported by an electronic database. Data was provided from nine separate batches for which there were records of all movements and handlings from the point of purchase (from the hatcheries) until sale. Each time the oysters in these batches were brought in for grading, information such as the date, size, total number, unit type, mortality and location was recorded.

This data was used to collate the following:

- The time spent in each unit type – this was obtained by calculating the time (in days) the oysters spent in each different unit type after each grade.
- The number of handlings per batch
- Percentage of oysters 'in-grade' – this was obtained by calculating the percentage (per grade) of oysters which were upgraded into the next unit type.
- Percentage of oysters 'returned' to unit size from which they came.
- Mortality – calculated as both a total percentage for the batch and at each grading.
- Sales – the size of the oysters at point of sale, the number of oysters sold and the number of days spent in the water since purchased.

The data from each of the nine batches were pooled and averages determined. For most batches, the majority of the oysters were not sold as market ready oysters. Instead, they were predominantly sold at a young age as 'on-growers' to other oyster farms which then grew them to a marketable size. This made it difficult to validate the sales component of the model based on the information collected.

Data on the production times for batches of oysters was provided by Zippel Enterprises (south Australia). Zippel Enterprises maintain accurate farm records of batch history, and data for the sale date and product grade of every oyster sold. Data from three batches was used to measure production times. This data also provided an accurate estimate of the proportion of each batch that was sold, however, it could not provide estimates of when losses actually occurred, or attribute reasons for losses. The input dates and sizes of each batch were:

- Batch 1: input date 24/12/2002, number input 3.0 million
- Batch 2: input date 09/02/2004, number input 1.08 million
- Batch 3: input date 20/02/2004, number input 2.08 million

3.3.2 Results from Tasmania

The average time spent in each unit is shown in Table 3.2 and the grade returns are shown in Table 3.3. It was sometimes difficult to determine how many grades an individual had received. Occasionally batches were mixed, or farming practices were such that oysters were not always upgraded directly into the next unit size. Only the data that was clear, accurate and easily deciphered was included in the validation. It was also difficult to gain information on larger unit sizes. For example, the majority of 12 mm, 16 mm and 20 mm units only went through one grade. This meant obtaining data on secondary handling was difficult for these unit sizes.

Table 3.2 Average number of days spent in each unit.

Input unit size	Upgrade unit size	Time to 1st grading (days)	Time to 2nd grading (days)	Time to 3rd grading (days)
3mm	A015	47	39	37
A015	A116	141	122	30
A116	12mm	98	225	
A116	16mm	163	122	
A116	20mm	232	120	
16mm	20mm	142	109	
16mm	Sales	170	119	
20mm	Sales	143	113	

No reliable mortality estimates could be obtained. Calculating mortality within the batches was difficult and was reliant on comments attached to the data quantifying mortality events. Estimates based purely on a reduction in stock numbers were inaccurate due to the way in which the total numbers were calculated. Small sub-samples were weighed and counted and used to estimate numbers for the total batch. Mortality was relatively low (about 10%) and it was not possible to separate trends in mortality from random variation due to sampling. Therefore it appears that mortality data cannot be accurately monitored using farm data, even with a highly sophisticated farm monitoring system such as the one used by Bolduans Bay. Accurate mortality data will need to be collected as part of specially designed study.

The economic model assumes oysters are always upgraded to the next unit size (e.g. 12 mm to 16 mm). However, it appears common practice for oysters to skip a unit size (e.g. A116 bags to 20 mm unit). Table 3.3 demonstrates this best with 47% and 42% of oysters that under went their first grading in A116 bags were re-housed directly into 16 mm and 20 mm baskets respectively, by-passing the next 12 mm basket size. Whilst the handling data from this study has not altered the design of the economic weights model, it has highlighted that throughout the oyster industry there is no standard production system for culturing oysters.

Table 3.3 The average in-grade percentage at each handling for each unit size.

Unit Size	Grade number	At handling	
		% Upgrade	% returned
3mm	1	47	53
3mm	2	46	54
3mm	3	47	53
3mm	4	40	60
A015	1	97	3
A015	2	91	9
A015	3	100	0
A116	1	92	9
A116	2	80	20
12mm	1	65	35
16mm	1	85	15
16mm	2	98	2
20mm	1	100	0

Table 3.4 Average allocations at different grades and for different sized units.

Unit size	Grade number	Breakdown of handling						
		3mm	A015	A116	6mm	12mm	16mm	20mm
3mm	1	45%	55%					
3mm	2	49%	51%					
3mm	3	46%	48%	6%				
3mm	4	60%	40%					
A015	1	2%	2%	74%			19%	2%
A015	2		2%	55%		5%	30%	7%
A015	3						100%	
A116	1			8%	1%	3%	47%	42%
A116	2			12%		8%	42%	39%
12mm	1			35%			15%	50%
16mm	1					1%	16%	83%
16mm	2						2%	98%

3.3.3 Results from South Australia

The production times for three batches of oysters from a farm located at Smokey Bay in South Australia are shown in Figure 3.3. Each batch had very similar patterns of growth. The first sales began at about 24 months after input, and the final sales occurred at about 36 months. For batches 1, 2 and 3, the average time to sale (calculated as weighted averages) were 30, 29 and 30 months respectively. There was a remarkably similar mix of product grades, and therefore size grades, for every batch at every sale period. This mix was 9% bistro (50-60 mm shell length), 49% plate (60-70 mm), 40% standard (70-85 mm), and 2% large (85-100 mm). This is suggestive of a normal distribution of size grades with a constant mean and variance. The proportion of total input sold was also similar between batches. For batches 1, 2 and 3, the percentages sold were 65%, 62% and 55% respectively, and the overall average was 60%.

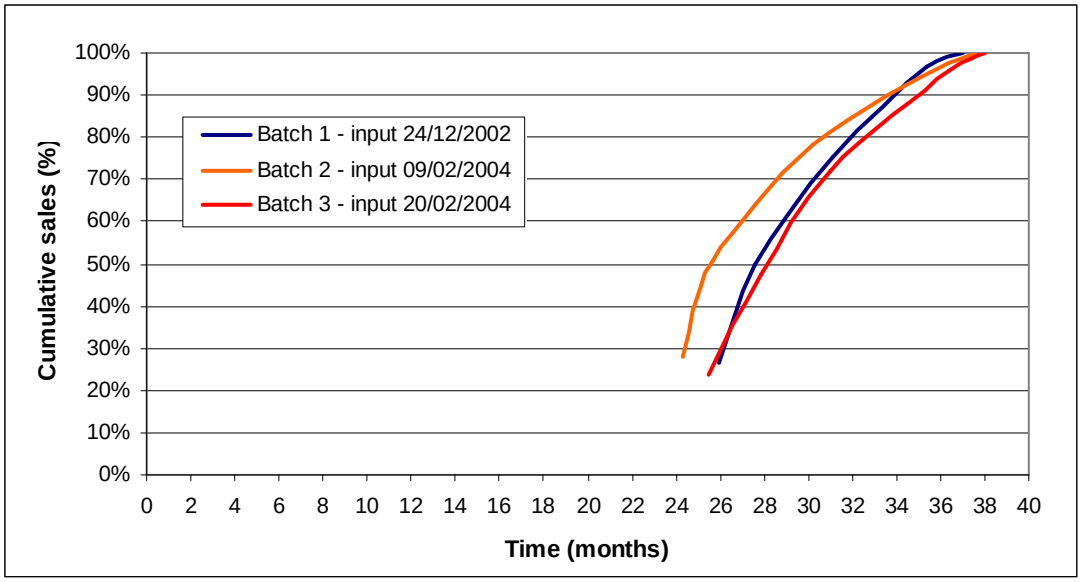


Figure 3.3. Production times for three batches of oysters from a farm at Smokey Bay in South Australia. Time is measured from spat input date. Output is expressed as a percentage of total sales for that batch.

The production times predicted by the economic weights model were very similar to those of this farm. The model input values (see Figure 2.2) were set to the averages for this data, which were a 30 month turn-out time (24 months growth time and 6 months condition time) and 60% seed making sales (consisting of 35% mortality and 5% culls). The model predictions for output at each quartile varied by no more than one month from actual values for each batch.

3.5 FUTURE DEVELOPMENT

The relationship between growth time and conditioning time needs validation. This work will be done as part of a new project (CRC Project 2009/743) and can be accommodated within that project with minimal extra effort. Further research is required to measure and amount of mortality at all stages of commercial oyster cultivation. This current study found that stock records of growers do not distinguish between dead and discarded oysters and accurate measures of the impact of mortality are not possible without this separation.

Chapter 4

Prediction of genetic gains and inbreeding rates with different breeding strategies

Sonja Dominik, Peter Kube and John Henshall

4.1 INTRODUCTION

4.1.1 Background

The aim of selective breeding is to select animals that are superior for breeding objective traits and use these as parents for the next generation, thereby genetically improving the population. As the selection intensity increases it becomes more likely that the best performing animals will originate from fewer families, which can lead to selection of related animals and consequently increase the rate of inbreeding in a population. The effects of inbreeding manifest as decreased genetic variation and inbreeding depression. Inbreeding depression has been documented in livestock, in particular for reproductive and fitness traits (Falconer and Mackay 1996). For Pacific oysters, Evans *et al.* (2004) found significant inbreeding depression in yield, individual growth rate and survival. Therefore, the challenge in designing a sustainable closed breeding program is to achieve a balance between the genetic gain and resulting level of inbreeding.

Computer simulation is an effective tool for comparing large numbers of long term breeding strategies. The alternative, running multiple breeding programs and comparing the results, is obviously impractical. Given data or assumptions on the genetic architecture of the traits of interest, breeding programs can be simulated to represent alternative breeding structures and decisions. Input parameters can be varied to investigate effects. Literature on simulations of breeding program design in oysters is rare. Dupont-Nivet *et al*. (2006) simulated breeding programs in fish, but that study had little relevance to this study. Bentsen and Olesen (2002) stochastically simulated mass selection breeding programs in aquaculture in general and provided useful comparisons for the results of this study.

Simulations can be undertaken deterministically or stochastically. In a deterministic simulation, the selection program is modelled as a set of equations, and changing the input parameters changes the results. Deterministic simulations are quick but inflexible because it can be very difficult to express anything other than simple scenarios as a set of equations. Further, the results obtained represent what would be expected on average and take no account of the uncertainty or randomness of the process. In a stochastic simulation the randomness inherent in the system is explicitly included in the model. Instead of a single estimate of the mean result, the simulation is run many times, each time producing a 'random' result representing what might happen in reality and accounting for the uncertainty associated with a true selection program. Stochastic simulations require more computing time, but can be used to model more complex breeding systems, and can provide information on the uncertainty inherent in biological systems. Both types of simulation have been very useful in animal breeding for the design and development of breeding systems (Smith 1998) and have been used for terrestrial livestock (Weigel 2001, Lstiburek *et al.* 2004) and for aquaculture (Sonnesson and Meuwissen 2009, Hayes *et al*. 2007).

4.1.2 Need

The current ASI breeding strategy is limited to producing a small number of families each year. This is due to the complexities of producing pedigreed families of Pacific oysters, limited access to hatchery resources and limited staff resources. Increasingly, there is pressure to increase the selection intensity. This is due to the need to accommodate the selection for more traits and the desire to produce greater genetic gains. There is also a recognised need to ensure that the breeding program operates within sustainable levels of inbreeding. Finding an acceptable balance between these conflicting needs and defining a suitable long term breeding strategy has been difficult.

4.1.3 Objective

This study looked at some basic questions in breeding program design, and adds to the knowledge of factors influencing rate of genetic gain (ΔG) and rate of inbreeding (ΔF) in Pacific oysters and, more generally, in aquaculture species. The objective of this simulation study was to provide ASI with an alternative suite of breeding strategies that maximise genetic gain whilst minimising inbreeding. This was done by comparing the predicted performance of breeding programs with different population sizes by varying the numbers of families, and numbers of related individuals selected, and comparing breeding programs with discrete year classes against single populations with genetic links.

4.2 METHODS

4.2.1 Computer simulation

Stochastic computer simulations were used. The software was written in Fortran and operated in a UNIX environment. The main elements to these simulations were:

1. A mechanism to represent the underlying genetic model, which determines the distribution of the genetic components of the variation between animals, including the degree of resemblance between relatives;
2. a mechanism to select animals to be parents;
3. the model of the breeding program; and
4. definition a set of scenarios that evaluate the range of possible breeding programs under consideration.

The genetic model

Here the term *phenotype* refers to the trait value that is observed and *genotype* refers to the component of the phenotype that is due to genetics. The phenotype is the sum of the genotype and a component due to random environmental effects. In real populations the genotype is unobserved. A polygenic model was assumed where the net effect of the genotype is considered to be the sum of the effects of many genes, each with a very small effect. Under this model, rather than simulating many genes, the genotype can be simulated directly because the sum of the gene effects has a normal distribution. The *genetic variance* is the variance of the genotype, the *environmental variance* is the variance of the random environmental effects, the *phenotypic variance* is the variance of the phenotype, which is equal to the sum of the genetic and environmental variances. The *heritability* is the ratio of the genetic variance to the phenotypic variance.

The simulation commenced with a number of founder animals, assumed to be unrelated, with genotypes randomly sampled from a normal distribution with a mean appropriate to the trait being simulated and variance equal to the genetic variance. These animals (and later subsequent generations) were bred, with the genotype for progeny simulated as the mean of

the parents' genotypes plus a random Mendelian sampling term drawn from a normal distribution with mean of zero. If the parents are not inbred, the variance of the Mendelian sampling term is one half of genetic variance. If the parents are inbred then the variance of the Mendelian sampling term is less than one half of the genetic variance. For all animals, founders and descendants, an environmental effect was sampled from a normal distribution with mean of zero and variance equal to the environmental variance. When simulating multiple traits, genotypes and environmental effects were sampled from multivariate normal distributions with covariance matrices describing the relationships between the traits.

A complete pedigree was maintained so that in the simulated datasets, unlike in real datasets, the coefficient of inbreeding was known in relation to the true, unrelated base population. Neither dominance effects nor effects for inbreeding depression were simulated. All effects were additive.

In the real Australian Pacific oyster population the generation identified as founders cannot be assumed to be unrelated. Accordingly, a number of generations were simulated in advance of the breeding program population simulation to produce founder animals with age and relationship structures consistent with the best guess of those from wild caught stock. For the oyster simulations, the unrelated base population was generated with year of birth 1987, and parents were chosen at random for 10 years to produce a starting population for the breeding program simulation in 1997. The actual breeding population was then simulated by selecting the actual numbers of parents used in the ASI program from 1997 to 2007, as shown in Figure 4.1. This was used as the starting point for evaluating alternate strategies.

Selecting parents

The method for selecting individuals to be parents in the simulation can be the same as that in any real breeding program. That is, it can include phenotype information, pedigree information and random elements. Phenotype information and pedigree information can be combined to produce estimated breeding values (EBV). BLUP is the optimal way to combine phenotype and genotype information when using the relationships between all of the animals. However, when there are many progeny in each family, a weighted mean of own phenotype and family mean phenotype is almost as good. When simulating many rounds of selection in many replicates for a range of scenarios an EBV based on own record and family mean is also much faster to compute, and this approach was used for the simulations reported here.

To limit inbreeding, pedigree information is used to control the distribution across families of the animals selected to be the parents of the next generation. In the simulations, the number of males and females selected from each family was capped, with a range of caps considered.

Model of the breeding program

The breeding program was modelled on the existing ASI breeding strategy. A mating ratio of 1 x 1 was assumed and 800 progeny of each mating are measured for economically important traits. However, there is annual uncertainty around the numbers of progeny that can be measured, which could not be captured in the model, but is addressed by simulating varying progeny numbers measured, ranging from 5 to 800. Animals were selected on a composite trait (or an index value) that reflects the breeding objective. In addition to the selection candidate's own phenotype records, the family mean was included in estimating the merit of the individual for the composite trait. The heritability of the trait was assumed to be $h^2 = 0.3$ and the coefficient of variation CV = 0.25.

Scenario selection

The computer simulations were run in two stages. The aim of the first stage was to identify priority breeding program strategies that would be evaluated in more detail in the second stage. Priorities were determined by a group of applied oyster breeders and geneticists, and strategies were identified from both practical and theoretical considerations.

The first stage used a version of the simulation software with a graphical user interface. In an interactive process, different combinations of input variables were tested to shortlist logistically and economically feasible strategies. The interface to the user was through an Excel spreadsheet. This provided a quick process with a user-friendly visual interface for the input and output, but limited the complexity of scenarios that can be described. Individual input variables were altered in the spreadsheet and the simulation output was displayed in a graph, which facilitated the visualisation of the interactions of the various input parameters (Appendix 4.1). The software simulated a 20 year breeding program selecting on a composite trait that reflects the breeding objective. The stage-one process assumed no particular population starting structure and did not simulate the ASI population illustrated in Figure 4.1.

Priority breeding strategies identified during stage-one were simulated in stage-two using a version of the software with a text based user interface. This allowed the description of more complex breeding programs that could not be defined in the software used for the first stage. It also allowed simulation of the past selection history of the breeding population from 1997 to 2007 to use as a starting point. From this starting point, each strategy was evaluated over 15 years of selection. Each strategy was simulated 50 times and the mean was calculated. In total, 17 breeding strategies were evaluated in the stage-two process.

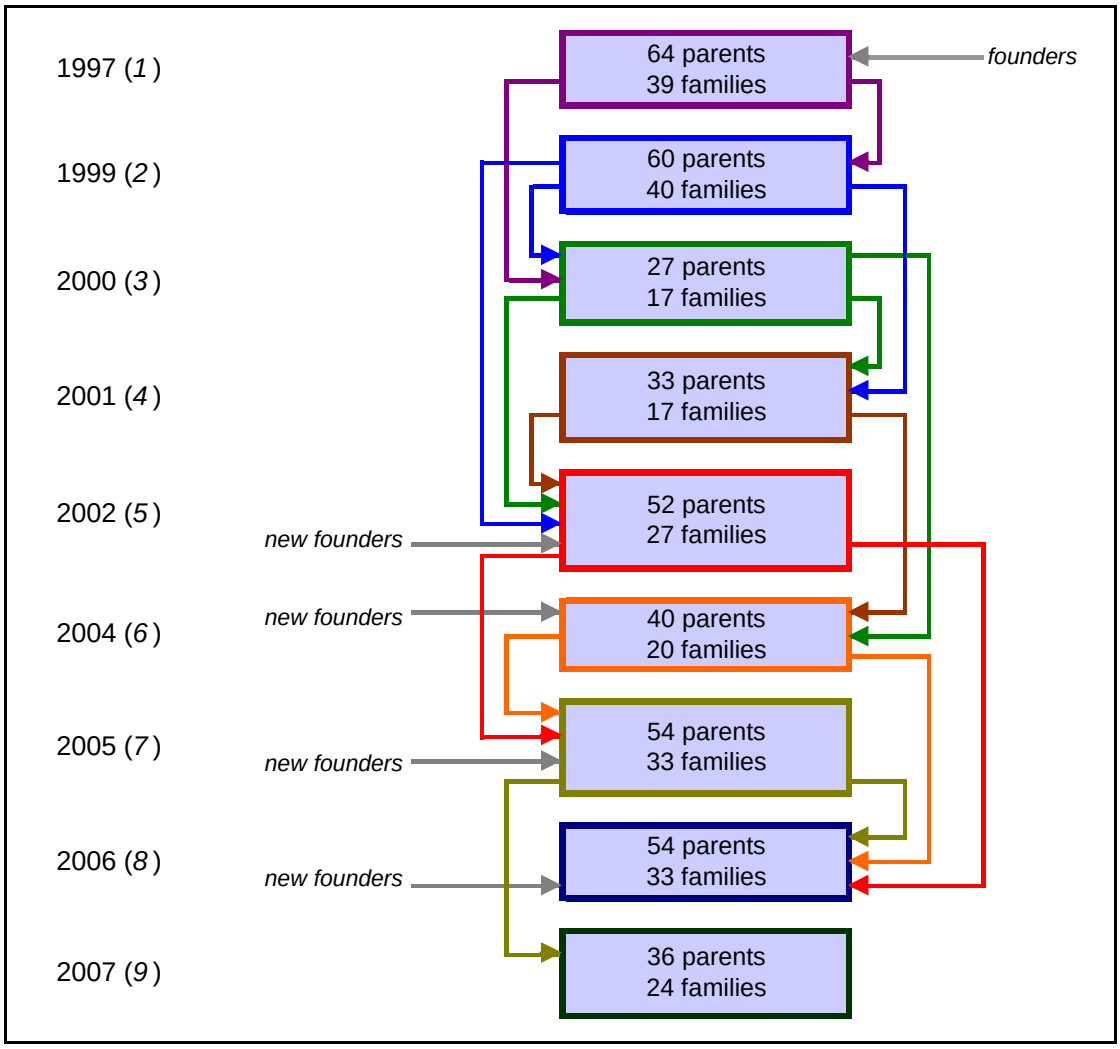


Figure 4.1 A schematic representation of the ASI breeding population from commencement in 1997 to 2007. The arrows show the sources of broodstock for each year class. This population structure was simulated and used as a starting point for simulations of alternate strategies.

Table 4.1 Description of breeding strategies simulated during the stage-two process. ΔF refers to the rate of inbreeding and ΔG to the rate of genetic gain.

Strategy code	Population size (no. families)	Maximum no. siblings selected per family	Number of genetic links (%)	General description of strategy
24-4	24	4	0	Very small population, discrete year classes, minimise ΔF
30-4	30	4	0	Small population, discrete year classes, minimise ΔF
30-6	30	6	0	Small population, discrete year classes, emphasis on ΔF
30-8	30	8	0	Small population, discrete year classes, emphasis on ΔG
30-10	30	10	0	Small population, discrete year classes, maximise ΔG
40-4	40	4	0	Medium population, discrete year classes, minimise ΔF
40-6	40	6	0	Medium population, discrete year classes, emphasis on ΔF
40-8	40	8	0	Medium population, discrete year classes, emphasis on ΔG
40-10	40	10	0	Medium population, discrete year classes, maximise ΔG
50-4	50	4	0	Large population, discrete year classes, minimise ΔF
50-6	50	6	0	Large population, discrete year classes, emphasis on ΔF
50-8	50	8	0	Large population, discrete year classes, emphasis on ΔG
50-10	50	10	0	Large population, discrete year classes, maximise ΔG
24-4-10 [1]	24	4	10	Very small population, single combined pop., minimise ΔF
24-4-15	24	4	15	Very small population, single combined pop., minimise ΔF
50-6-10	50	6	10	Large population, single combined pop., emphasis on ΔF
50-6-15	50	6	15	Large population, single combined pop., emphasis on ΔF

[1] 24-4-10 represents the ASI breeding program as at 2007

4.2.2 Breeding program strategies

The breeding strategies that were identified for detailed evaluation (the stage-two evaluation) are summarised in Table 4.1. These strategies are characterised by changes to three input variables:

1. population size, as defined by the number of families,
2. intensity of between family selection permitted, defined as the maximum number of full-sibs selected per family, and
3. discrete year classes or single populations, defined by genetic links between year classes.

The population sizes evaluated ranged from a minimum of 24 families per year (the current population) to 50 families per year, which was considered the maximum possible given the resources available to the breeding organisation (ASI). Differing intensities of between family selection represent a shifting emphasis on avoidance of inbreeding and seeking genetic gains. When selecting low numbers of individuals per family, between family selection intensity is lower and preference is given to inbreeding avoidance over genetic gains. As the number of selections per family increases, the between family selection intensity increases and the emphasis shifts from inbreeding avoidance to genetic gain. Genetic links are formed by using sibling broodstock in different year classes. Use of repeat spawners would form stronger genetic links, however, this is not possible because strip spawning, which is lethal, is the standard process. Genetic links were formed using either 10% or 15% of broodstock.

Each simulated breeding strategy is identified by a code (Table 4.1), which is a concatenation of numbers of families, numbers of siblings selected and, for some, the percentage of matings used to link year classes.

4.2.3 Within family selection

In the simulations of breeding program strategies described above it was assumed broodstock selection is perfectly aligned with the breeding objective. This is unlikely to be the case. In practice, selection is done as a two-stage process of, firstly family selection, then within family selection. Within family selection is done without data, so it is unlikely that the characteristics of the selected animal will perfectly align to the breeding objective. In addition, traits other than the breeding objective traits (such as hinge shape) are usually considered when making within family selections. This would further decrease the correlation between the true breeding objective and the characteristics of the selected individual.

To evaluate the effect of such practice, simulated selections were done in two stages. Firstly, on a trait ($h^2 = 0.30$) that might be visually assessed and has no objective data and, secondly, on the composite trait of the breeding objective. Since nothing is known about the relationship of the new trait with the composite trait, varying strengths of correlations were assumed ($r^2 = -0.2, 0, 0.2, 0.8$). This practice of within family selection was only simulated for a single strategy which was 50 families, a maximum of six full-sibs selected, and genetic links through 10% of broodstock (50-6-10).

4.2.4 Current ASI breeding strategy

The breeding strategy used by ASI has been variable (Figure 4.1). Population size has varied and parents have been opportunistically sourced from different year classes. The simulated strategy 24-4-10 (24 families per year, maximum of 4 selections per family, and a single population) best represents what has been done. However, this does not represent the strategy that was likely to be followed in the future. The strategy was moving towards discrete year classes and, in the absence of this revision project, that would have been the adopted position. The reasons for this shift included the needs of the commercial deployment plan (see Chapter 5) and difficulties in making objective selections across year classes. Therefore, the simulated strategy 24-4 (24 families per year, maximum of 4 selections per family, and a discrete year classes) represents what was becoming the future strategy.

4.3 RESULTS

4.3.1 Genetic gain

The genetic gain (G) in the composite trait was high for all breeding strategies, ranging from 7.7% to 8.9 % per generation or 58% to 67% over 15 years of selection (Table 4.2). This was due to high selection intensities for all breeding strategies. Within family selection was a large part of this with 800 animals being available per family. Between family selection was also important, especially for strategies allowing high numbers of siblings per family. The high selection intensities allow selection of the very best candidates and even families without outstanding performance could contribute superior individuals. In a more applied context, even the scenario with the smallest number of families and a conservative approach to selection of related animals (24-4), could achieve considerable genetic gains due to the high selection intensities.

If selection of siblings from the best performing families was restricted, selection intensities and consequently genetic gain dropped slightly but remained high, even if superior individuals of the next best performing family needed to be selected. Even though differences were small, genetic gain increased slightly with increasing size of the breeding population and larger numbers of siblings selected (Table 4.2). The increasing genetic gains with increasing population size demonstrates that the potential to select superior individuals is increased with higher number of families in the population even if restrictions are placed on the numbers of siblings selected per family.

Table 4.2 Genetic gain (G) for the composite trait over 15 years of selection and average rate of inbreeding (ΔF in %) per generation for each of the 17 strategies.

Breeding strategy	Gain in 15 years (%)	Gain per gen (%)	ΔF per gen (%)	General description of strategy
24-4	58	7.7	1.30	Very small population, discrete year classes, minimise ΔF
30-4	59	7.9	1.08	Small population, discrete year classes, minimise ΔF
30-6	61	8.1	1.66	Small population, discrete year classes, emphasis on ΔF
30-8	62	8.3	1.98	Small population, discrete year classes, emphasis on ΔG
30-10	62	8.3	2.38	Small population, discrete year classes, maximise ΔG
40-4	60	8.0	0.82	Medium population, discrete year classes, minimise ΔF
40-6	62	8.3	1.28	Medium population, discrete year classes, emphasis on ΔF
40-8	64	8.5	1.64	Medium population, discrete year classes, emphasis on ΔG
40-10	64	8.5	1.78	Medium population, discrete year classes, maximise ΔG
50-4	62	8.3	0.66	Large population, discrete year classes, minimise ΔF
50-6	65	8.7	1.05	Large population, discrete year classes, emphasis on ΔF
50-8	66	8.8	1.44	Large population, discrete year classes, emphasis on ΔG
50-10	67	8.9	1.55	Large population, discrete year classes, maximise ΔG
24-4-10	59	7.9	0.88	Very small population, single combined pop., minimise ΔF
24-4-15	58	7.7	0.94	Very small population, single combined pop., minimise ΔF
50-6-10	64	8.5	0.76	Large population, single combined pop., emphasis on ΔF
50-6-15	64	8.5	0.80	Large population, single combined pop., emphasis on ΔF

[1] 24-4-10 represents the ASI breeding program as at 2007

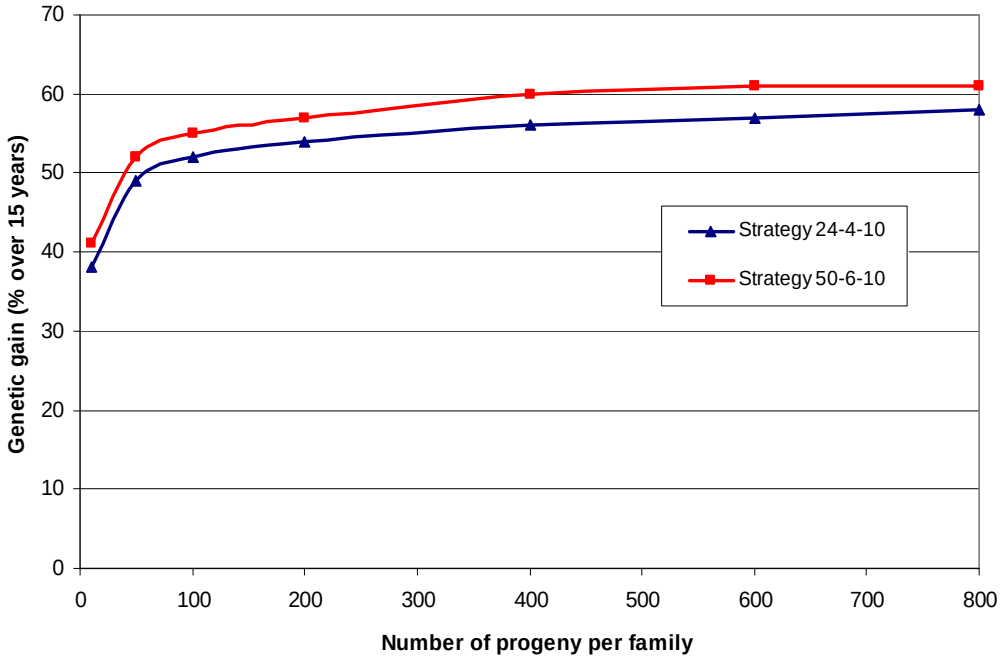


Figure 4.2 Effect of varying numbers of selection candidates per family on the genetic gain (%) over 15 years of selection for breeding strategies 24-4-10 and 50-6-10.

The number of progeny per family available for selection was assumed to be 800 per year. Situations may arise where numbers are reduced, in which case selection intensities would be reduced and the predictions from the simulations overestimated. Therefore, the effect of numbers of progeny per family on gains was investigated. As the numbers per family decreased, genetic gain decreased slowly until family size reaches approximately 50, after which genetic gains dropped rapidly (Figure 4.2). Breeding strategies with different numbers of families or different restrictions on sibling selection showed a very similar response. For all strategies, the threshold for a rapid increase in the loss of genetic gain was approximately 50 progeny per family. Operationally, it is unlikely that the number of progeny available per family will drop below 50 in any year class and, therefore, genetic gain is not likely to be severely affected by low numbers of progeny per family. In a simulated mass selection breeding program, Bentsen and Olesen (2002) found that increasing the number of offspring per family from 5 to 150 approximately doubled the response to selection, which aligns with the findings of this study.

4.3.2 Rate of inbreeding

Different breeding strategies resulted in important differences in the rate of inbreeding (ΔF). As a general rule 1% per generation is the upper threshold of an acceptable ΔF if the aim is to create a long-term sustainable breeding population. ΔF is influenced by the population size and the numbers of related animals that are selected (Table 4.2). It decreased with increasing population size because the scope to select superior and unrelated individuals between families is higher. ΔF increased with increasing numbers of siblings selected and, without genetic links across year classes, ΔF always exceeded acceptable thresholds without strong restrictions on the number of siblings selected per family (that is, allowing no more than four sibling selections per family). This trend is less pronounced with more families in the population due to the increased flexibility to select unrelated animals. This means more siblings can be selected with increasing population size to achieve the same ΔF.

Inbreeding was lowest (ΔF = 0.66%) for the breeding strategy 50-4, which had the largest number of families and least number of siblings selected. Breeding strategy 40-4 is another that kept inbreeding at an acceptable level and would be logistically easier to implement. All other breeding strategies with discrete year classes resulted in ΔF higher than 1%, with one breeding strategy having more than twice the acceptable threshold. In a small population it appears inbreeding cannot be managed safely even with low family selection intensity. In the strategy with 24 families, inbreeding thresholds were exceeded even when only four selections were made from each family. For these population sizes, within family selection is likely to be the only safe option.

Inbreeding rates well below 1% indicate that the breeding strategy is conservative and higher numbers of related animals could be safely selected to increase genetic gains. Therefore 50-6 could be regarded as a better balanced strategy with acceptable inbreeding and slightly higher ΔG than 50-4.

4.3.3 Single population or discrete year classes

Breeding program strategies with discrete year classes were contrasted with strategies where a single population is formed with genetic links. Strategies tested were 24-4 and 50-6, both of which had unacceptable inbreeding when managed as discrete year classes. The creation of genetic links between year classes also improves genetic evaluation, but in this part of the study the focus was on the effect on ΔF.

Merging discrete year classes into a single population appears to be an effective way of managing inbreeding, even when populations are small (Table 4.2). This may seem surprising, but can be explained by the two year generation interval which creates two unrelated populations in the absence of genetic links. The use of siblings of the previous year's broodstock introduces unrelated individuals and, as a consequence, reduces ΔF. With

increasing percentages of related individuals for the genetic links, this effect is less beneficial. The effect on ΔF is initially pronounced, but decreases with time.

An interesting finding is that formation of a single population can reduce ΔF in the medium term to an acceptable level, as is demonstrated in breeding strategy 24-4 compared with 24-4-10. Without genetic links between year classes, the current breeding population (with 24 families) is too small to be sustainable in the medium to long term unless unrelated broodstock are introduced. Similarly, ΔF was unacceptable for strategy 50-8 with discrete year classes, but acceptable when managed as a single population.

4.3.4 Two stage selection

The effects of within family selection that is imperfectly correlated with the breeding objective can cause a significant reduction in potential genetic gains (Table 4.3). For the strategy 50-6-10, this may reduce gains by approximately one-third which would reduce gains per generation from 8.5% to 5.2%. Although the effects of imperfect selection were not simulated for other strategies, the magnitude of the change is expected to be similar. The rate of inbreeding will be unaffected by changes to the individuals selected at the within family selection stage.

The degree to which gains are reduced by imperfect family selection will be influenced by the extent to which non-breeding objective traits are targeted. If there is little selection emphasis on other traits, then the loss of gain will be largely due to selection of animals that do not have the ideal balance of breeding objective traits. In this case, approximately 90% of gains would be expected (scenario 2, Table 4.3). If there is strong selection emphasis on selecting for other traits, then the degree of loss of genetic gains will depend on the correlation between those other traits and the breeding objective. The loss of genetic gains is estimated to range between approximately 60 to 75% (scenarios 3, 4 and 5, Table 4.3). For the ASI breeding program, no information is available on the relationship between secondary traits and the breeding objective traits and, therefore, precise estimates of the effects of this sort of selection are not possible.

Table 4.3 Proportion of genetic gain per year (%G) achieved when within family selection is imperfectly correlated with the breeding objective. Gains were estimated for a single strategy (50-6-10).

Scenario	Correlation of selected individual with ideal (r^2)	%G achieved	Actual gain per generation in 50-6-10 (%)
1. Perfect within family selection	1.0	100	8.5
2. Visual inspection of within family candidates	0.8	90.6	7.7
3. Secondary trait selection with favourable correlation	0.2	76.6	6.5
4. Secondary trait selection with no correlation	0.0	68.8	5.9
5. Secondary trait selection with adverse correlation	-0.2	61.0	5.2

4.4 IMPLICATIONS TO THE ASI BREEDING PROGRAM

The strategy simulations provide some clear guidelines for the ASI breeding program with respect to population size, population structure, and selection strategies. The main implications for the breeding program are described below.

Population size

A small population size (24 families per year), with discrete years classes is unsustainable, even with very limited between family selection. In this study, the minimum level of between family selection was 1:2 and, at that level, it was not possible to safely manage inbreeding. With a population of 24 families per year and discrete year classes, then selection would need to be limited to within family selection only.

If discrete year classes are essential, a low level of between family selection (1:2) can be safely achieved by increasing the population to 40 families per year. Inbreeding is relatively low in such a population and, therefore, this is a sustainable strategy with regard to inbreeding. A further increase to 50 families per year, with the same selection strategy, provides a very low risk strategy without the need to completely limit between family selection.

Expanding the capacity of family production to 50 families offers advantages and is recommended. It offers greater gains. Although the differences in gains between strategies are not large, the combined effect of these over a decade will be significant. An expanded capacity also offers a greater safety margin in the case of failures. It is not uncommon for families to be lost at different stages of the production. With a small population it is likely that loss of families will impact on inbreeding. A larger number of families will also offer the ability to safely use mating designs that involve multiple matings, such as a 2 x 2 design. More matings and the higher selection intensity will offer additional benefits to those shown in these simulations.

Population structure

The simplest and most effective way of reducing the inbreeding risk is to manage the population as a single unit rather than as discrete year classes. In the simulations, this was done by using genetic links for 10% of broodstock. For a population of, say, 40 families with 80 broodstock (a 1 x 1 design) this would mean using 8 parents with full-siblings that were used as broodstock in previous year classes. Successive year classes would therefore have some common grandparents and genetic links would be via cousins (coefficient of relationship of 0.125). This would require the use of two, three and possibly four year old broodstock. In practice, it has been possible to use two, three and four year old broodstock. This would be expected to provide more robust genetic links and there is no reason not to continue this practice.

Between family selection

For a population of 50 families per year which is genetically linked to other year classes, a between family selection intensity of 1:3 is sustainable. In practice, this allows 6 individuals to be selected from each family. If the population size is reduced to 40 families per year, then a between family selection intensity of approximately 1:2 is recommended. This would allow 4 individuals to be selected per family.

Within family selection

Imperfect within family selection has the potential to limit potential gains. Currently, this is done as a visual inspection of breeding candidates on a family-by-family basis. This is unlikely to have severe consequences when selection is focussed on breeding objective traits. Some inaccuracies will occur because a visual inspection cannot assign correct economic weights for multi-trait selection. It is likely that 80 to 90% of potential gains will be achieved.

Imperfect family selection will have more severe consequences if the selection component focuses on non-breeding objective traits. When targeting non-breeding objective traits, it is possible that only 60% of potential gains may be achieved. Therefore, selection of secondary traits should be done only after careful consideration of their value and, ideally, with some knowledge of their genetic relationships with objective traits.

4.5 FUTURE DEVELOPMENT

These simulations assumed a single male by single female mating design (1 x 1) and this was not varied. The high fecundity of both males and female and the ability to strip-spawn Pacific

oysters means there is flexibility in the mating designs that can be used. Therefore the possibility of other mating designs and their effects could be considered in the evaluation of future breeding strategies. There are two aspects to the effects of different mating designs. Firstly, they determine the selection intensity for a particular sex. And secondly, they influence the level of relatedness in the population. If the mating design increases the usage of either sex (e.g. 2 x 1 or 1 x 3) or increases the usage of both sexes (e.g. 2 x 2), then fewer animals are selected, better animals can be selected and the selection intensity increases. This increases the genetic gains but increases inbreeding. Mating designs other than 1 x 1 produce half-sibs within year classes. Currently restrictions are applied on the numbers of full-sibs that can be selected from one family. If mating designs other than 1 x 1 are considered, then restrictions would need to be applied to the selection of half-sibs to manage inbreeding.

These simulations also assumed a single heritability and different assumptions for heritability would influence results. Heritability is one of the main factors influencing the rate of genetic gain. It describes the proportion of phenotypic variance that is due to genetics. The larger this proportion, the greater the genetic gains. Many production traits of economic interest have heritabilities around $h^2 = 0.3$ and, with current estimates, the heritability of the index appears to be very close to this value (see Table 2.4). However, for some traits in the index the genetic parameters are not well estimated (such as survival and uniformity) and therefore it is possible that the heritability of the index may vary. With all other parameters kept constant, a trait with a heritability of $h^2 = 0.15$ would have resulted in only half the genetic gain of what has been demonstrated in this study. Similarly, if the heritability of the trait would be doubled ($h^2 = 0.6$), the genetic gains would have doubled.

4.6 CONCLUSION

Computer simulations have been successfully used to explore future options for the ASI breeding strategy. Stochastic simulations were used, and these had the advantage of being able to simulate breeding options in an exact way, and of using past selection history as a starting point. Therefore, these simulations should be regarded as an accurate representation of future breeding.

A future breeding strategy should be based upon an annual family production of 40 to 50 families, and these families should be genetically linked cross year classes. In each year class, at least 10% of broodstock should have links to a previous year class and, due to the use of strip spawning, these links will be via sibling broodstock. For such a population, a between-family selection intensity of 1:2 to 1:3 will optimise gains whilst safely managing inbreeding. During the within family selection stage, which is the second-stage of the selection process, attention must be given to ensure within family selection is aligned to the breeding objective. This strategy will deliver gains of about 4% per year, or 8% per generation and will maintain inbreeding at what are conservatively considered acceptable levels ($\Delta F < 1\%$ per generation).

APPENDIX 4.1
Stage-one simulation software

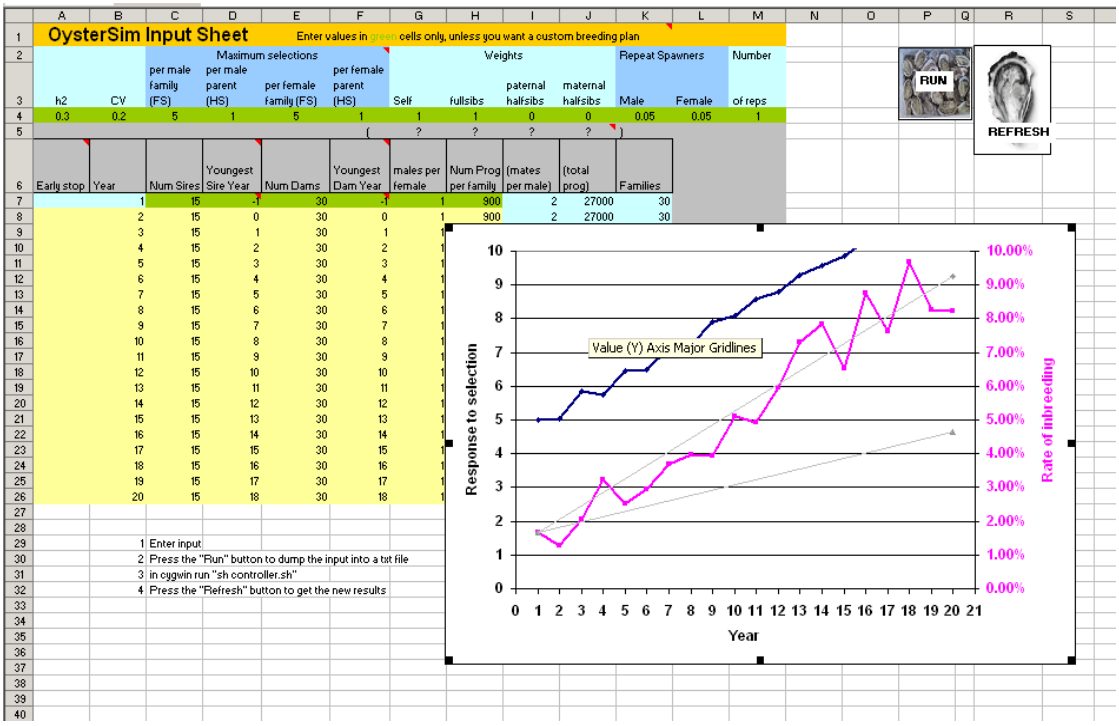


Figure A4.1 Screenshot of the stage-one simulation software, with the graphical interface. This software was used to prepare a shortlist of potential breeding strategies for the detailed analysis in the second stage of the simulations.

Chapter 5

Breeding strategy development

Matthew Cunningham, Peter Kube, Sonja Dominik and Benjamin Finn

5.1 INTRODUCTION

5.1.1 Background

A successful breeding strategy is the amalgamation of many different facets. It must begin with a clearly defined and long term breeding objective. It needs to be built upon knowledge of the genetic inheritance of the traits in the breeding objective. The specific details of activities can only be defined and undertaken with knowledge of the biology and, in particular, the reproductive biology of the animal. An ongoing data gathering, or trait measurement, program is always necessary. And commercial gains are only achieved if the strategy is able to ensure benefits are channelled to commercial producers.

An overarching need is for logistical planning to bring all activities together and ensure the scope of activities fits with available resources. The focus of this chapter is on that logistical planning. It outlines the previous and the new breeding strategies, describes the main elements of each strategy, and summarises the principle differences between the two.

The new breeding strategy was developed over a three year period. Input was received from ASI staff, research partners, industry representatives, and the commercial hatcheries (Cameron of Tasmania and Shellfish Culture). The starting points were the needs to accommodate the newly defined economic breeding objective (Chapter 2) and the findings of the breeding strategy simulations (Chapter 4). It was also recognised that any new strategy must be planned to match the resources available to ASI. The Pacific oyster industry is small in comparison to international oyster industries and other Australian primary industries and, therefore, large increases in resources for breeding are not possible. An additional focus for the strategy deliberations was on the deployment pathway of selectively bred material to commercial growers, both now and in the future.

5.1.2 Need

Operational experience with the existing breeding strategy and the breeding strategy simulations identified shortcomings and opportunities for improvement. Importantly, it was found that the strategy that was being used was unsustainable due to the long term risk of inbreeding. The commercial deployment pathway was also problematic. It was dependent upon the use of four year old broodstock and this caused serious impediments to the supply of genetically improved seed by commercial hatcheries. The breeding strategy proposed has been developed to address these needs and overcome these constraints.

5.1.3 Objectives

The objectives were to develop a logistically feasible breeding strategy which, firstly, maximises genetic gains in commercially important traits whilst keeping inbreeding at acceptable levels, and secondly, provides commercial hatcheries with high quality broodstock which are easy to spawn and in volumes which are suitable for commercial production.

5.2 PREVIOUS STRATEGY

5.2.1 Main features of old strategy

A flow chart of the previous breeding strategy is shown in Figure 5.1. The main principles and underlying rationale of this strategy are described below.

Breeding objective

At the commencement of this project, the primary selection trait was shell shape. This was driven by a need to correct shape after unintended and undesirable changes had occurred when selecting for growth rate. Meat condition and growth rate were secondary traits.

Breeding population

The breeding population consisted of 24 families per year class and the generation interval was two years. In the past, breeding population broodstock were sourced from different year classes which resulted in a single population structure. However, the needs of the commercial deployment pathway (described below) dictated that only two year old broodstock be used for family production which has created discrete and non-overlapping year classes.

Progeny testing and measurement

Families were taken from the nursery site to progeny test sites at approximately 9 months after fertilisation. They were tested on two sites in South Australia and two in Tasmania. On each site, families were grown in three replicate baskets of 100 individuals per basket. Measurements were made at age 20 months on about 50 individuals per family per site.

Selections

Selections were made using a two-stage approach. Firstly, families were selected using average family performance within a year class. There were no strict guidelines for the acceptable level of between family selection, however, it is approximately 1:2. Secondly, individual animals were selected from within the selected families. This was done based on stock inspections without measurements and with reference to breeding objective traits and additional traits (such as other aspects of shell shape).

Commercial deployment

Commercial production occurs via commercial hatcheries and spat originating from the breeding program genetic stock are marketed as ‘Thoroughbred’ spat. ASI receives a $2.00 royalty per thousand spat sold. This strategy was designed to provide progeny tested lines, or proven crosses, for commercial production. This has resulted in a ‘backward’ selection strategy in which selected stock are taken from previous generations rather than new generations.

Commercial lines were chosen at the completion of progeny testing based on family performance data and stock inspection. A selected family was recreated as best is possible using full-siblings of the original parents (these are aunts and uncles of the individuals in the selected family). The commercial lines produced by the hatcheries are therefore double-cousins of the tested family (with a coefficient of relationship is $r = 0.25$). These broodstock were four years old when provided to commercial hatcheries. Only about 150 to 200 of each family were able to be kept due to the logistical requirements of maintaining stock for that length of time. From these, commercial hatcheries typically found 20 to 30 animals suitable for use as broodstock.

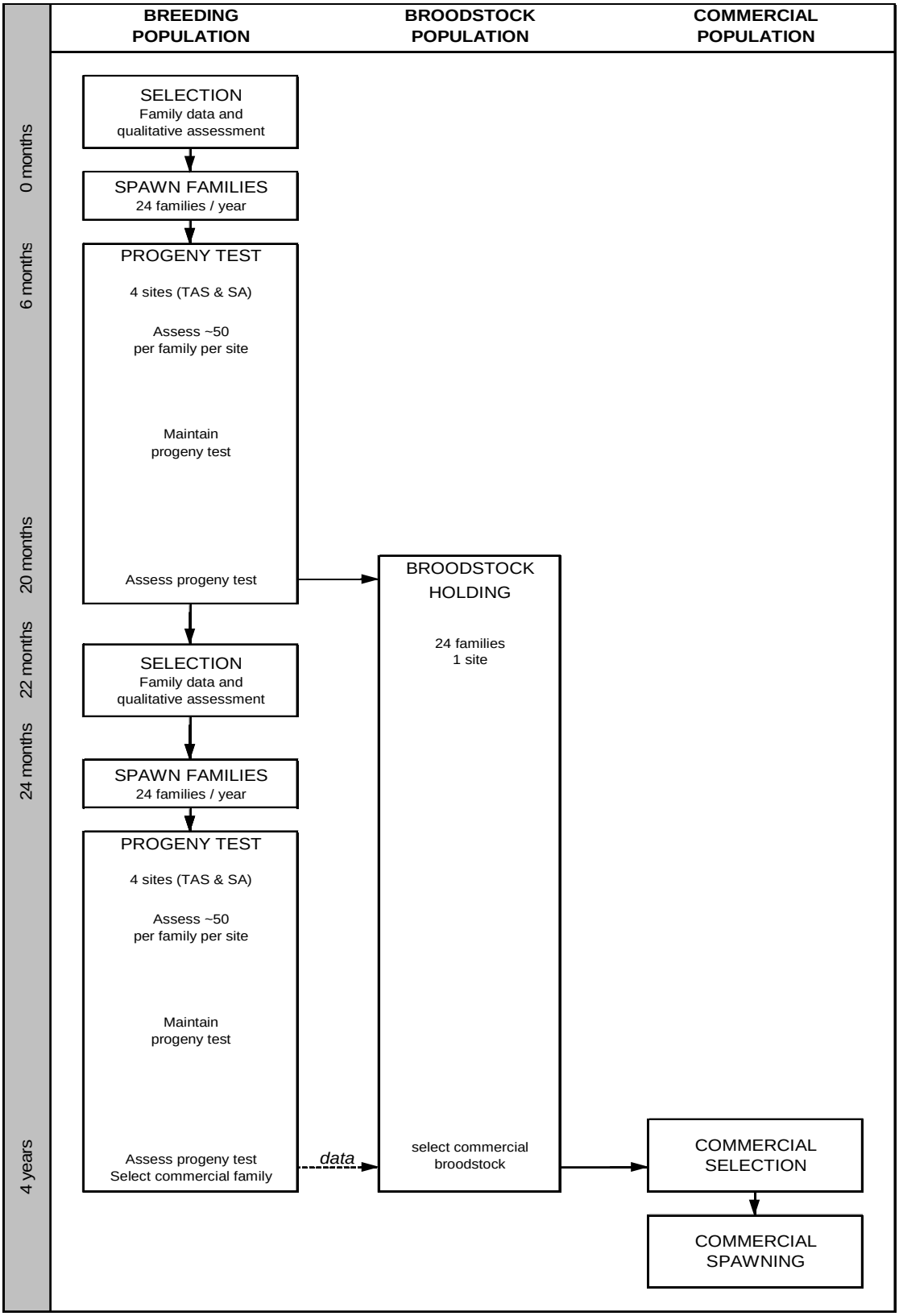


Figure 5.1 Flow chart of the annual activities of the breeding population and commercial deployment activities for the previous ASI breeding strategy. The cycle of activities is shown for a single year class. In practice, two year classes are in production at any point in time resulting in two parallel streams of activity, offset by 12 months.

5.2.2 Constraints of old strategy

Under the previous breeding strategy, genetic progress was constrained by the small population size (24 families per year). This resulted in very little scope for between family selection. The breeding program was seeking to improve multiple traits and there was limited scope to select families that had acceptable qualities for all traits. This problem was particularly critical when selecting for commercial deployment. The computer simulations (Chapter 4) have subsequently shown that there was no level of within family selection that was acceptable without causing long term risks of inbreeding. The only alternative would have been to revert to a strategy based solely on within family selection, or to continually infuse new genetic material into the breeding population. New genetic material would, however, be largely unselected and that would slow genetic progress.

Complexities surrounding commercial deployment resulted in significant constraints to commercial uptake of the breeding program genetic stock. The desire to commercialise only progeny tested lines meant that broodstock were four years old when supplied to the commercial hatcheries. Broodstock at this age are difficult to condition, due to both size and age, which often results in poor sperm and egg quality. This can lead to failures in the production of commercial batches. In addition, opportunities for hatcheries to produce the same commercial batch for more than one year are extremely limited due to the age of broodstock. The limited numbers of broodstock that can be provided to the hatcheries is also a problem. In practice, only 150 to 200 broodstock per family are available due to the difficulties and costs of keeping broodstock for four years. Of these, a commercial hatchery would typically only consider 20 to 30 animals suitable for commercial purposes. The result was that hatcheries only had sufficient numbers of broodstock for one spawning per year and year round supply of spat was not possible.

The time lag between the breeding population and the commercial population was another constraint to genetic progress. Broodstock used for commercial production were two generations older than the current breeding population (Figure 5.1). This was dictated by the requirement for using progeny tested families. Therefore there was a slow transfer of genetic gains from the breeding population to the commercial population.

5.3 NEW BREEDING STRATEGY

5.3.1 Main Features of New Strategy

A flow chart of the new breeding strategy is shown in Figure 5.2. The main principles and underlying rationale of this strategy are described below.

Breeding objective

The breeding objective is defined by the trait economic weights (Table 2.2). Current traits included in the breeding objective are growth time, condition time and shell shape. All are of approximately equal importance. Future traits to be included are survival and uniformity.

Breeding population

The annual breeding population has been expanded to 50 families per year (Chapter 4). Genetic links between year classes create a single breeding population as opposed to discrete year classes. Broodstock for the breeding population can be either 2, 3 or 4 year old stock. At least 10% of broodstock must have siblings that were used as broodstock in a previous year class to form adequate genetic links. Annual populations of less than 50 families are tolerable (in the event of hatchery failures). However, between family selection intensity should be relaxed in such circumstances (see following section, Selections). The current mating plan will be a 1 x 1 design (single male crossed with a single female). A 2 x 2 design (each male and female crossed twice) for the top 25% of broodstock is an option which will

provide better performance information. The CUDL rearing system is now used for nursery production (Chapter 6) which allows the expanded population to be produced with existing resources.

Progeny testing and measurement

Families will be transferred from the nursery site to progeny test sites at about 6 months after fertilisation. They will be tested on a minimum of two grow out sites in South Australia and two in Tasmania. Three replicate baskets of 120 animals per basket will be distributed to each site. Measurements will be taken at age 20 months on approximately 50 individuals per family per site. In addition, counts of live animals and empty shell will be made to assess mortality. Electronic data capture systems will be now used for measurements (Chapter 8) and this will allows measurements to be made on the expanded population without the need for additional resources. Surplus spat from the family production will be kept at a broodstock repository as additional commercial broodstock but these animals will not be measured.

Selections

Selections will be made using a two-stage process. Firstly, Estimated Breeding Values (EBVs) will be used in an index to select families. The index will consist of individual trait EBVs weighted by their economic value to measure the economic worth of all families across all year classes. Secondly, individuals will be chosen within selected families. Independent culling will occur at this stage but the main selection emphasis will be on breeding objective traits. If 50 families have been successfully produced in a year class then up to 6 individuals can be selected from each family, giving a between family selection intensity of 1:3. If fewer families have been produced then this selection intensity will be reduced.

Commercial deployment

Under the new strategy commercial deployment still occurs via commercial hatcheries and spat originating from breeding program genetic stock is still marketed as “Thoroughbred” spat with a $2.00 royalty to ASI per thousand spat sold. However, a significant change has been to move to a ‘forward’ selection strategy where commercial broodstock are selected from the most recent generation, rather than previous generations, and larger numbers of broodstock candidates are kept for commercial production.

Commercial lines are now selected using the *predicted* performance of broodstock candidates at the completion of progeny testing, when animals are about 2 years old. Hatcheries nominate crosses that may be of commercial interest and family EBVs are used to predict the performance of those candidate lines. For each commercial line, this involves nominating two parental lines and estimating the performance of the resulting commercial line as the average EBV of the parental lines. Hatcheries also inspect the stock of the broodstock candidates. A short list of candidate commercial lines is then incorporated into the family production program of the breeding population as a single pair cross. The hatcheries inspect the progeny of this cross (or family) at approximately 6 months age as a final validation of their commercial selections. So far, it has been easy to accommodate the requests of the hatcheries and the needs of the breeding program. Commercial quantities of broodstock animals are then provided to hatcheries as approximately 2.5 year old stock.

Significant broodstock culling occurs at the completion of progeny testing according to the needs of the breeding program and based on a family’s likely commercial importance. This is done in conjunction with commercial hatcheries and allows higher numbers of commercially important families to be retained as potential broodstock. In addition, excess stock from the family production are available at the broodstock repository.

Decisions regarding commercialisation are now made by the Hatchery Reference Group. The group comprises of representatives of ASI, Cameron of Tasmania and Shellfish Culture. The group is open to new members who have a commercial relationship with ASI.

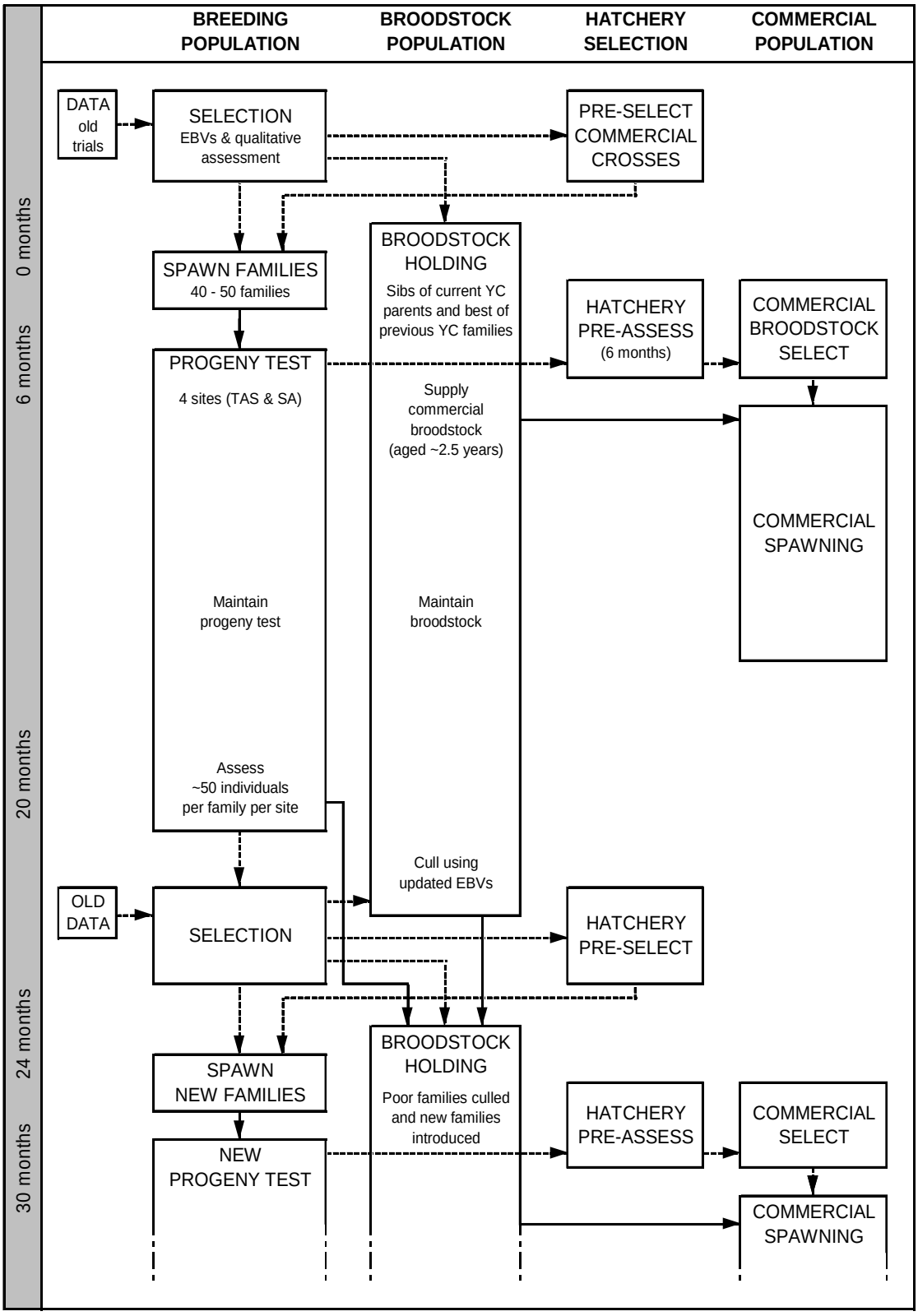


Figure 5.2 Flow chart of the breeding population and commercial deployment activities for the new ASI breeding strategy. Solid lines show the flow of animals and hatched lines the flow of data. The cycle of activities is shown for a single year class (YC). In practice, two year classes are in production at any point in time resulting in two parallel streams of activity, offset by 12 months.

5.3.2 Advantages of the new strategy

Production of 50 families will lead to increased genetic gains in commercially important traits whilst allowing inbreeding to be kept at an acceptable level. Extra gains will be achieved through higher between family selection intensity in the breeding population. Inbreeding will be managed by increasing the numbers of families produced and by moving to a single population structure (as opposed to discrete year classes).

This strategy will also provide greater commercial genetic gains. Previously, the genetic gains in the commercial population lagged the commercial population by two years (or one generation). Gains from the breeding population will now flow more quickly to the commercial population. This will provide an additional one off step-up in the genetic merit of the commercial lines as the new strategy is adopted.

The commercial hatcheries will now have many more options available as commercial lines. Previously, they were forced to choose between 24 families, and generally chose a single commercial line. Now they have potentially over one thousand options, and have the ability to select different commercial lines for different circumstances.

This strategy provides significant advantages with regard to the supply of commercial broodstock. Broodstock are now supplied to the commercial hatcheries as 2.5 year old animals and this overcomes many of the limitations of the previous strategy, which was based on the supply of four year old broodstock. Typically, four year old broodstock were difficult to spawn and allowed for only a single production run at a specific time of the year. The supply of younger broodstock means conditioning and spawning will be much easier and commercial production more successful. Far larger numbers of younger broodstock can be supplied which will allow more production runs and flexibility with scheduling of production runs at different times of the year. Larger numbers of broodstock also provides opportunities to condition extra broodstock to allow for contingencies in the event of a commercial batch failure. The use of younger broodstock increases the length of time those broodstock are available for commercial use which allows the option of repeated supply of the same commercial lines to growers who request a repeated supply of the same stock. Commercial production of the same family will be possible for at least two, and possibly three, breeding seasons.

A trade-off with this strategy is the move away from progeny tested commercial lines. However, the six month pre inspection provides an opportunity for commercial hatcheries to validate their commercial crosses at the stage where the spat would be sold commercially. This gives the hatcheries some confidence that their selected commercial lines will be commercially acceptable.

The ability for commercial hatcheries to have input into the breeding decisions of the program is an integral part of the commercialisation of the program. The formation of the Hatchery Reference Group has provided the hatcheries with direct input into the program. This gives the hatcheries confidence that the breeding program is progressing in a manner that is compatible to their operational requirements and the requirements of their customers, who are the oyster growers.

5.4 FUTURE DEVELOPMENT

It is likely that further development of the breeding strategy will be necessary as the program evolves and commercial requirements change. The Hatchery Reference Group is ideally placed to assist in the future development of a Pacific oyster breeding program whose breeding strategy is compatible to the needs of the Australian oyster industry.

5.5 CONCLUSION

The new breeding strategy has been fully adopted by ASI and the commercial hatcheries. ASI has now increased its targeted production from 24 to 50 families per year. It is anticipated that no extra hatchery and data collection resources will be required to accomplish this. Hatcheries now have access to high numbers of younger and better quality broodstock and are performing forward crosses for their commercial lines using animals from the latest progeny tested year class. In the first year of adoption this has led to a 200% increase in Thoroughbred spat production compared to the previous year. The breeding program is now geared to translate increased customer demand for Thoroughbred spat into increased production and sales. The commercial hatcheries, which remain the only pathway to commercialise the outcomes of the breeding program, now have more input into the breeding program through the formation of the Hatchery Reference Group. This group includes representatives of ASI and hatcheries that have a commercial relationship with ASI. The group makes decisions on breeding and operational decisions in order to assist with commercialisation of the breeding program. This has given the hatcheries confidence that the breeding program is compatible with their commercial requirements now and in the future.

Chapter 6

Hatchery systems for family production

Benjamin Finn and Matthew Cunningham

6.1 INTRODUCTION

6.1.1 Background

ASI has had to change its approach to annual family production over the course of this project. The reliance on access to commercial hatchery facilities for annual family production has presented problems. As hatcheries face increasing production demands from a rapidly growing industry, the capacity for the commercial sector to provide time and space to ASI has diminished. ASI has been forced to look for alternative options. Consequently, the Tasmanian Aquaculture and Fisheries Institute (TAFI) were approached to provide hatchery facilities and the 2009 year class of families were produced at their Taroona facility. However, the need to find more innovative and efficient methods for family production still exists despite the change of hatchery facility.

This chapter describes the equipment and husbandry techniques used to produce pedigreed families for the breeding program. It identifies problems encountered, system constraints and the development of new technologies that are aiding ASI as the breeding program endeavours to reach its target of 50 families per year.

6.1.2 Need

The strategy simulations recommended that the breeding program produce 50 families annually to provide a sustainable breeding program and to deliver increased genetic gains. ASI does not own hatchery facilities and rents hatchery facilities from commercial hatcheries through a tendering process. Under this arrangement, the commercial hatchery supplies high quality water, microalgae and floor space. ASI provides all larval rearing and nursery systems, management of the production run, and staff to complete the work. Previously, static 140 l larval rearing tanks were the production method used. However, it was not possible to double family production using this approach as access to space and time at commercial hatcheries was limited. This meant that simply purchasing more tanks or doing two separate family production runs was not possible. As a result, there was a need to develop a new hatchery system which allowed a doubling of annual family production but fitted within the existing constraints.

6.1.3 Objectives

The original objective of this part of the project was to develop specifications for a hatchery system that was capable of producing 50 families annually within the staff and financial resources available to the ASI breeding program. The implementation of this system exceeded the original goals of this project.

6.2 CUDL REARING SYSTEM

The CUDL (Cawthron Ultra-Density Larval) rearing system, developed by the Cawthron Institute in New Zealand, has been adopted. It has been used to produce the 2008 and 2009 year class families. A schematic of the whole system is shown in Figure 6.1 and a photograph of the system in operation at TAFI is shown in Figure 6.2. It is a flow through system and a key feature is the small size (2.5 l) of the larval rearing vessels (Figure 6.3). It uses less water and algae than the previously used 140 l static larval tanks. It also occupies far less floor space than a static system. The CUDL system developed allows 32 families to be produced simultaneously in a small floor space (4 m x 2.5 m).

Implementation of this system has not been without difficulty. Only partial success was achieved for the 2008 year class families with 12 families produced from a target of 30. The nature of the arrangement with the commercial hatchery meant only limited time, water and microalgae was available for the family production run and, consequently, only limited preliminary trials of the system were possible.

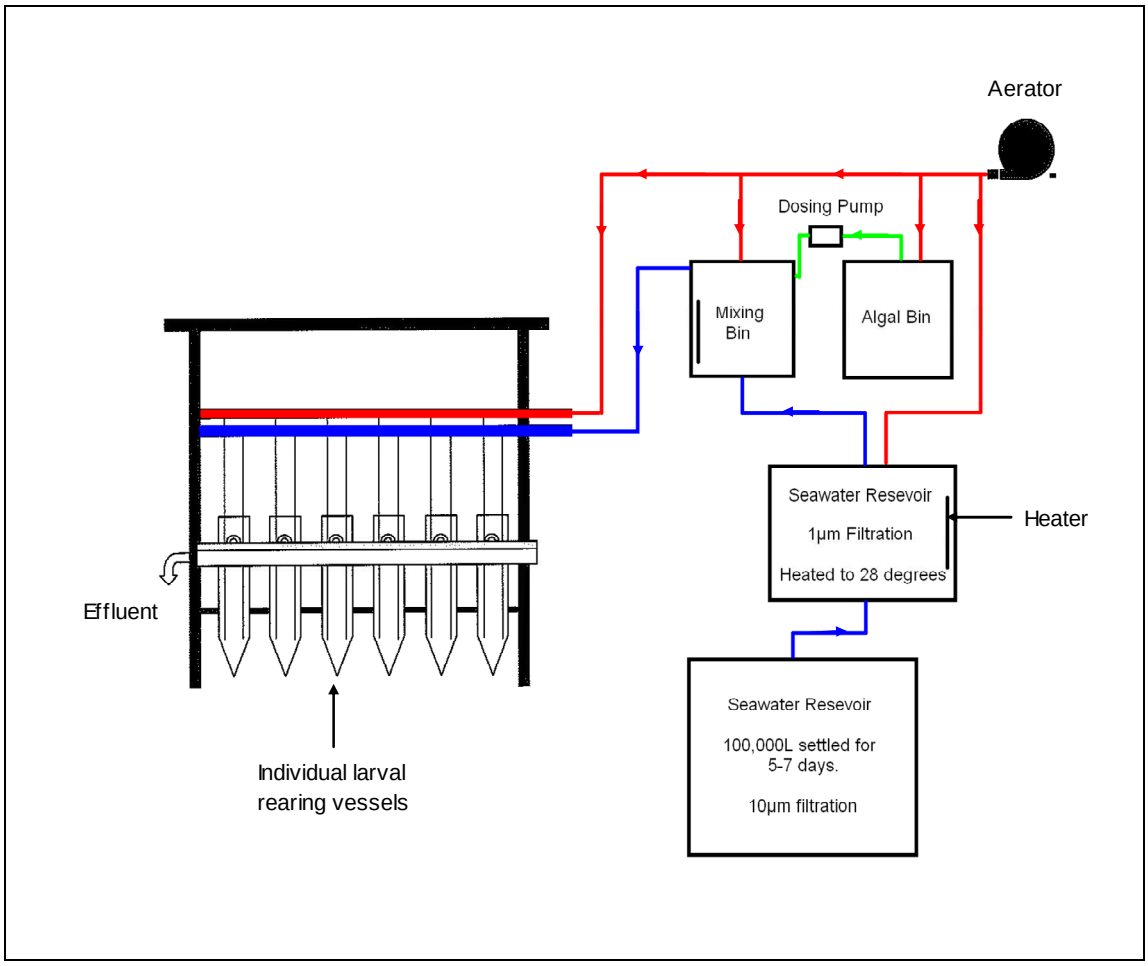


Figure 6.1 A schematic diagram of the CUDL (Cawthron Ultra-Density Larval) rearing system. The seawater line is shown in blue and the air line in red. A total of 32 larval rearing vessels are used with this system, with each vessel containing a single family (there is no replication of families in larval rearing vessels).

Figure 6.2 The CUDL rearing system at the Tasmanian Aquaculture and Fisheries Institute (TAFI) hatchery in Taroona, 2010. Larval vessels are in the blue cradles (foreground, left hand side), algal and mixing bins are on the low stand (foreground, right hand side), and the seawater reservoirs are in the background.

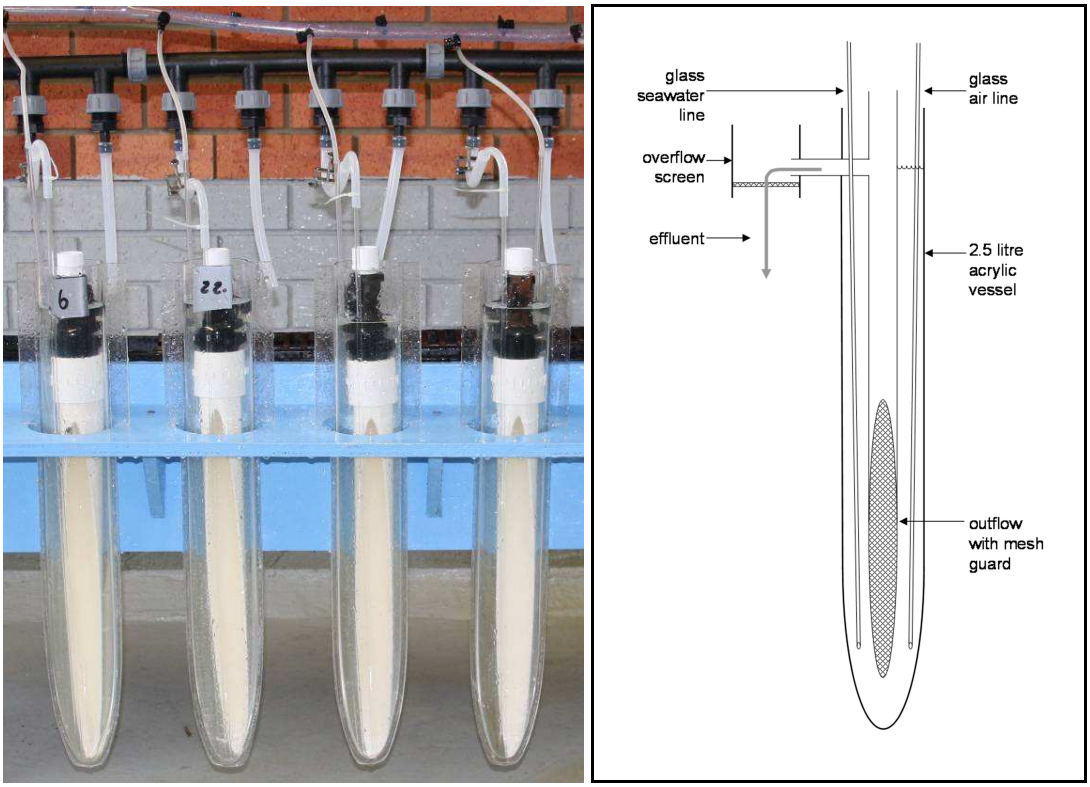


Figure 6.3. Detail of the larval vessels of the CUDL rearing system, and schematic showing the components inside the vessels.

6.3 2008 HATCHERY SEASON

The 2008 hatchery season presented many problems and the following is a description of the problems encountered and the solutions developed.

Problem: Poor fertilization and incubation of oyster larvae in 20 l buckets caused by water quality issues, power failures and poor vessel shape.

Solution: Incubate oyster larvae in 140 l fibreglass tanks for the first 24 hours. These tanks have a larger volume so that water quality issues are reduced and the impact of possible power failures is minimised.

Problem: The larval vessel is made from a two piece mould which is glued together. This left a cavity along the seam of the join which became a trap for oyster larvae. These larvae died and became a source of bacterial proliferation within the culture. The dead larvae were impossible to remove from the cracks and, despite disinfection of the vessel, continued to be a cause of infection.

Solution: Existing moulds were repaired using a Water Clear Ridge Polyurethane resin which was applied to the seam of the moulds. This process eliminated any cracks and left a smooth finish in which larvae were not trapped. Ideally new techniques need to be developed to produce a seamless mould.

Problem: General bacterial loading resulting from running the system for back to back larval runs. Poor results from the first spawning and a time lag to the second attempt meant that the system was running for twice as long as normal. Although the system was cleaned and disinfected regularly, absolute cleaning was not possible. Any organic matter not removed became a site for bacterial contamination.

Solution: Do not run the system for more than two weeks. In addition, duplicate water delivery pipe work so that the system can be dismantled and air dried regularly.

Problem: Screens became blocked by algae. *Isochrysis* sp. can be a problematic strain because it is prone to cell clumping. This can cause blocking of the screen which then results in the vessels overflowing and loss of larvae.

Solution: Do not use *Isochrysis* sp. in the diet. Instead use *P. lutheri* which has similar nutritional value but is not prone to clumping. Add an overflow to the vessel, which needs to have an increased screen size, in case screens become blocked. The vessel will then overflow to the backup screen.

6.4 CUDL SYSTEM PROTOCOLS

A total of 42 families were produced in the 2009/10 hatchery season, which is the most ever produced by ASI. The target of achieving 50 families per year is possible. Knowledge gained from the 2008/09 hatchery season ensured larval rearing techniques had been reviewed prior to spawning and measures were taken to counteract problems (see section 6.3). Whilst not all families produced in 2009/10 were reared exclusively in the CUDL system, families spent the majority of their larval cycle in that system.

The 2009/10 hatchery season highlighted the importance of feed quality during the early larval stages when using the CUDL system. Use of algae prone to 'clumping' when larvae are being retained on the 43 µm spears had deleterious effects on larval health, primarily due to reduced water quality and reduced flow rates (due to blocked screens). The overflowing of culture vessels early in the larval cycle due to screen blockages remained the greatest obstacle. Reducing the daily feed rate failed to fix the problem and it became clear that screen blockages would always occur if algal quality was poor. A potential solution may be to hold larvae in 140 l tanks until they are retained on 75 µm screens and can be placed onto a

CUDL vessel with 63 µm mesh on the spears. Screen blockages dramatically reduced once larvae were retained on 63 µm spears.

6.4.1 Larval rearing

Fertilisation is done in 20 l buckets containing filtered seawater at 24°C (Figure 6.4). Fertilised eggs are transferred to static 140 l cylindro-conical fibreglass tanks for incubation after polar body release. When D-veliger larvae are observed, typically at between 16 to 20 hours, larvae are screened over a 43 µm nylon mesh and retained larvae stocked into the CUDL system culture vessels. These vessels have a 2.5 l volume and receive 1 µm filtered seawater at an initial rate of 60 ml per minute, via a glass straw. The outflow is a PVC pipe cut diagonally, forming a 'spear', and covered with 43 µm nylon mesh to prevent the larvae from escaping. Throughout the initial 48 hours of larvae stocking, it is essential that aeration is blown gently, but directly, over the nylon screen surface of the spear to prevent the screen blocking (mainly due to clumping of algal cells within the vessel). If this is not done, the system will overflow or pressure on the nylon screen will cause the screen to tear.

The initial 48 hours, when larvae are on 43 µm screens, is the most problematic. Good quality algae and seawater are vital and attrition is high with substandard conditions. A stocking density of one million larvae per vessel appears suitable and does not adversely affect water quality. Slightly underfeeding larvae at this time can help to avoid problems such as screen blockages. The system has been fitted with overflow screens in the event of blockages or screen breakages (Figures 6.3 and 6.5). Survival of larvae caught on these screens was variable but, overall, this was not a major cause of family failures.

Chaetoceros calcitrans is the major component of the diet (up to 75%) during the early larval stages due to its small cell size and non-clumping tendencies. The remaining portion of the diet is either *Pavlova lutheri* or Tahitian *Isocrysis*. A diet of 50% diatom and 50% flagellate is used after larvae are retained on a 75µm screen.

Figure 6.4 Fertilisation of families occurs in 20 litre buckets and they are then moved to 140 litre static tanks for incubation.

Once larvae are retained on a 75 µm screen the mesh size on the spear in the culture vessel is increased to 63 µm. Flow rates can be increased to 75 ml per minute but care must be taken to avoid overfeeding. Larvae should be moved to this screen size as soon as possible. Husbandry can become complicated at this stage as some vessels may have spears with the larger screen sizes whilst others have spears with a 43 µm mesh. If necessary, the larval density in vessels with a 63 µm spear mesh should be reduced, and flow rates reduced. Reducing the larval density to approximately 300,000 larvae per vessel helped maintain good water quality and constant growth.

Larvae are moved to a 90 µm spear when they are retained on a 110 µm screen. Flow rates are then increased to 100 ml per minute. It is important not to over feed as settlement approaches as larvae will bind to any chains or clumps of algae as they become pediveligers. Aeration needs to be increased slightly at this stage and the glass straw positioned such that it allows for both water movement over the spear and prevents the larvae from dropping out of the water column and becoming static on the bottom of the culture vessel.

Culture vessels, spears, glass straws and PVC fittings need to be cleaned daily. Hot freshwater is used with a bottlebrush to clean the culture vessels and glass straws, and PVC fittings and spears are hosed with freshwater and cleaned with a scourer. The algal header tank and the dosing pump are also cleaned daily by rinsing with a dilute chlorine solution and freshwater. The main header tank (or mixing bin) is cleaned every second day, also using a dilute chlorine solution and freshwater. All other pipe work is cleaned twice weekly and the seawater reservoir tank is cleaned weekly.

Figure 6.5 Effluent from each larval vessel passes through an overflow screen (in the centre of the photograph) which is placed over the central effluent gutter. These screens trap larvae in the event of a screen blockage or a screen breakage.

6.4.2 Static larval culture

When using static larval culture, larvae are fertilised and incubated in 140 l cylindro-conical fibre glass tanks (Figure 6.6). There are sufficient tanks allow the culture of 20 individual families concurrently. Larvae are cultured as described in Helm (2004). Water exchanges and cleaning of tanks, emersion heaters and airlines is done every second day.

Static larval culture has been a necessary back-up. When problems occurred during the development of the CUDL rearing system larvae were transferred to the 140 l tanks to ensure their survival. In the short term, static culture is expected to continue as a back-up method, but as experience is gained and protocols for the CUDL system are refined it is expected that static culture will no longer be required.

6.4.3 Settlement techniques

Larvae that are ready to metamorphose are screened over a 225 µm nylon mesh before being washed into a downwelling pot with a 180 µm mesh. The pot is labelled with the family code before being placed in an epinephrine solution for approximately one hour. The epinephrine solution consists of 0.03 g of epinephrine bitartrate salt dissolved in one litre of seawater. After exposure to the epinephrine solution, the pot is rinsed gently and thoroughly with seawater before being returned to the downwelling system (see section 6.4.4). Epinephrine treatments are performed daily and every day spat are removed and placed into a separate pot. A 365 µm screen is used to separate spat from larvæ. Epinephrine treatments can continue for up to a week.

Figure 6.6 CUDL rearing system in the foreground and the static 140 litre culture vessels in the background. The static larval culture system has been used as a back-up system in the event of a failure of the CUDL system during the development period.

6.4.4 Nursery rearing

Early nursery rearing is conducted in a downwelling system. Spray bars are used to pass seawater through the downwelling pots. The spray bars also keep the larvae moving within the pot and stop most larvae from settling on the sides of the pots as they metamorphose. Larvae/spat are cultured in this system until the spat are retained on a 500 µm screen. They are then placed into an upwelling system. At this point a highly aerated and vigorous environment is no longer needed as the spat are not metamorphosing and there is no risk of them adhering to a substrate (such as the side of the pot). Therefore, this system does not have spray bars. The seawater flows into the system and up through the mesh on the bottom of the pot before going to effluent. As the spat grow, screen sizes on the upwelling pots are increased to accommodate the increased flow rates required to maintain nutrition. Spat remain in the upwelling system until they are 2240 µm retained and are then put into seed trays and grown at a nursery site.

6.5 FUTURE DEVELOPMENT

Flow through larval rearing systems are higher risk systems than static systems. As a result the CUDL rearing system will require ongoing development before it can be safely used as a stand alone larval rearing system.

The lack of assured and long term access to a suitable hatchery site presents both strategic planning issues and technical difficulties. Protocols for the CUDL rearing system need to be fine-tuned to specific site conditions to be effective and reliable. A long term agreement for hatchery space is critical to build upon the progress that has been made with this system in previous seasons.

6.6 CONCLUSION

The CUDL rearing system has been incorporated into the ASI selective breeding program and the production of 42 families for the 2009/10 hatchery season is a positive step towards implementing changes to the selective breeding program.. The system's major advantages are its small space requirement and need for less water and algae. However, it has been difficult to implement and has been used with mixed success in the first two breeding seasons. A number of problems have been encountered. Many of these problems were resolved resulting in increased success for the 2009 breeding season but more development is still needed. Hatchery systems will continue in a transitional phase over the coming seasons where both CUDL flow-through systems and static systems are in use but ultimately it is expected that the CUDL system can be used as a standalone system.

Chapter 7

Genetic evaluation of the ASI breeding population

Peter Kube

7.1 INTRODUCTION

7.1.1 Background

A genetic evaluation system refers to the methods and procedures used to determine the genetic merit of individuals in a breeding population. Measures of genetic merit are the basis for parental selections for the next generation of breeding and therefore are fundamental to the implementation of all breeding programs. The genetic merit of an individual cannot be seen directly because the appearance of an individual is influenced by both environmental factors and genetic factors. Experiences with selective breeding in other industries have shown that the environmental influences are nearly always greater than the genetic influences. However, genetic merit for most commercial traits can be reliably estimated by measuring the performance of an individual's progeny in a 'progeny test'. There are different methods for processing the data generated by progeny testing, and the genetic evaluation system refers specifically to the methodology used. However, all methods calculate an Estimated Breeding Value (EBV) which is a numerical value that measures the genetic merit for each trait. By definition, an EBV is the predicted performance of the offspring of that individual.

The standard statistical method used for genetic evaluation in modern breeding programs is Best Linear Unbiased Prediction (BLUP). The advantages of BLUP as the genetic evaluation system for selective breeding have been well documented (e.g. Kinghorn *et al.* 2000, White *et al.* 2007) and the adoption of BLUP offers similar advantages to the ASI breeding program. Specifically, the advantages to the ASI program are:

1. Different heritabilities for each trait will be accounted for when making selections. For example, condition has a much lower heritability that other traits and selection on family means would effectively place a lower selection emphasis on this trait.
2. Data across all year classes is used to estimate genetic merit. The ASI breeding program is an advanced generation program with nine generations of performance data and a complex pedigree structure that forms genetic links across all generations. The data from past generations cannot be used when using family means for current selections.
3. Comparisons of genetic merit can be made across year classes. When using family means, good comparisons can be made within year classes but no comparisons are possible across year classes. Comparisons across year classes are particularly important as the breeding strategy moves from a population of discrete year classes to a single population, as recommended in Chapter 4.
4. Estimates of genetic gain for each trait are possible. These estimates can be used to produce a genetic trend across generations.
5. EBVs can be used in conjunction with economic weights, as described in Chapter 2, to enable selection decisions that optimise economic value.

7.1.2 Need

To date, the ASI breeding program has used family means to estimate EBV. Families were ranked on the basis of their mean performance for each trait and then desirable individuals were selected within the top ranked families. Family means can be a simple and effective means of estimating genetic merit, particularly for organisms like oysters which can produce large numbers of progeny per family. However, selective breeding programs in all industries have recognised that improved statistical methods, coupled with the high capacity of modern computers, allow better estimates of genetic merit and therefore better selections. The method of choice for all major breeding organisations today is BLUP. Examples of the application are BREEDPLAN for beef cattle, LAMBPLAN for sheep and TREEPLAN for forest trees (BREEDPLAN, 2009, LAMBPLAN 2004, McRae *et al.* 2004). BLUP provides better estimates of genetic merit by using data on individual performance, performance data of all known relatives across all generations, heritabilities of each trait, and the relationships between different traits.

7.1.3 Objectives

The objectives of this component of the project were to specify the genetic evaluation system that is required for the enhanced ASI breeding strategy. This involved, firstly, developing a data coding system and to recode the ASI data so that it could be used in a BLUP analysis. Secondly, it involved an evaluation of different genetic models and the estimation of genetic parameters that could be routinely used for EBV estimation. And thirdly, it involved developing a standard way of reporting EBVs for ASI to use for both decisions about selections for the breeding population and for commercial deployment decisions.

BLUP analysis was used to estimate the EBVs for broodstock selection in the 2008 and 2009 breeding seasons. The implementation of the BLUP EBV evaluation exceeded the original goals of this project.

7.2 COLLATION OF THE ASI DATA

7.2.1 Objective traits and selection traits

The economic weights study (Chapter 2) identified five traits that were economically important for Pacific oyster production and these combine to form the newly developed profit index for the Australian Pacific oyster industry. These traits are listed and defined in Table 7.1. Breeding programs typically do not directly measure breeding objective traits because they can be difficult or impractical to measure in a progeny test. In stead, other traits are used as selection traits which are simple to measure and well correlated to objective traits. The selection traits and the current status of the operational protocols for each of these are listed in Table 7.1.

Table 7.1 Objective and selection traits for the Australian Pacific oyster selective breeding program.

Objective trait	Definition	Selection trait	Status
Growth time	time required for the shell to reach a marketable shell size	shell length at 22 months	In use, satisfactory
Condition time	time required for the meat to reach a marketable size	wet meat weight / total weight at 22 months	In use, but R&D needed
Survival	percentage of input seed that is saleable	not currently measured	Not used R&D needed
Shell shape	width to length ratio (width index) of the shell at market size	shell width / shell length at 22 months	In use, satisfactory
Uniformity	the proportion of a batch that move to the next unit size at each grading	not currently measured	Not used R&D needed

There are no routine measures in place for survival and uniformity. Some survival data has been collected. However, there is a need for a thorough genetic analysis of existing data, and the collection and analysis of new data before this trait can be routinely used as part of selection decisions. Condition data has been collected and used in selection decisions but current genetic knowledge of this trait is limited and genetic selection is expected to improve with research. For uniformity, there is no data and research is needed to determine ways in which to assess and select for this trait.

7.2.2 Genetic material

As at November 2009, the breeding population consisted of 10 progeny tested cohorts, each with a small number of families. The size and structure of the breeding population is summarised in Table 7.2.

Table 7.2 A summary of the ASI pedigree data as at September 2009 (up to and including the 2007 year class). These data were used for the genetic evaluation for selections for the 2009 year class.

Cohort number [1]	Spawn year [2]	Number families	Number parents	Number progeny tests	Source cohort for parents (f = founder)	Number selections	Number measured progeny
f	-	-	85	-	-	-	
1	1996				f		0
2	1997	37	60	4	f, 1	67	3,353
4	1999	40	64	1	f, 2	64	993
5	2000	19	30	1	2, 4	59	458
7	2001	17	37	1	2, 4, 5	45	460
9	2002	34	66	2	f, 4, 5, 7	12	777
11	2004	20	39	4	f, 2, 4, 5, 7	55	1801
12	2005	10	11	1	f, 4	15	500
13	2005	23	43	4	5, 9, 11	27	1,305
14	2006	24	47	4	f, 4, 7, 9, 10, 11, 12	0	4,320
15	2007	24	32	5	f, 12, 14	0	4,740
TOTAL		248	429	27		344	18,707

[1] Cohorts 3, 6, 8 and 10 are mass selection cohorts with no pedigree data (see Ward *et al.* 2005) and are not included here.

[2] Spawning has occurred from November to January and therefore one season can encompass two calendar years. For consistency, spawning year is defined as the start of summer. For example, a spawning occurring in January 2000 is labelled as the 1999 spawning year.

The breeding population originates from 85 founder broodstock all of which originate from the Tasmanian landrace population (see English *et al.* 2000 for a summary of Pacific oyster introductions to Tasmania). The majority of founders (92%) were animals sourced from commercial Tasmanian hatcheries and therefore had undergone some degree of mass selection prior to their inclusion in the breeding population. A small number of founders (8%) were sourced from wild Tasmanian populations. Most founders were introduced at the outset of the breeding program with the spawning of the 1997 year class. However, small numbers of extra founders have been introduced at most spawnings (see Table 7.2). The genetic analysis assumes all founders come from a single population.

The standard procedure has been to produce a single cohort each year. The only exception has been for 2005, where two cohorts were produced. A total of 429 parents have been used of which 197 were males and 232 were females. The crossing design was a mixture of single pair crosses, crosses where males were mated with multiple females, and crosses where females were mated with multiple males. Actual crossing designs (males by females) used

have been 1 x 1, 2 x 1, 1 x 2, 2 x 2, 1 x 3, 3 x 1, 3 x 2, and 1 x 5.[3] Of the total families produced, 46% were represented by some form of half-sib relationship and 54% were all full-sibs. However, only 13% of parents had been involved in multiple crosses. Families for cohorts 2, 4 and 9 were produced in two separate spawning runs up to four weeks apart (see Ward *et al*. 2005 for specific details). All other cohorts were produced in a single spawning run.

The genetic linkage between progeny test data in different cohorts occurs through full-siblings that are used as broodstock in different spawning years. The common ancestors between cohorts are therefore two shared grandparents which form an uncle/aunt to nephew/niece relationship between cohorts. The coefficient of relationship between the genetic link animals is r = 0.25. There are many of these linkages between cohorts (see Table 7.2 and Figure 4.1) and, consequently, sound genetic links between cohorts. For example, the 2005 spawn year (cohort 13) has 43 parents of which 10 are linked to 2002 spawn year (cohort 9), 34 are linked to 2004 spawn year (cohort 11) and 23 are linked to the 2006 spawn year (cohort 14). A result of these many linkages is the formation of a single breeding population as distinct from a populations of discrete year classes. There are no parent-progeny relationships between cohorts in the progeny test animals because individual identities of broodstock are not retained.

The genetic evaluation uses all breeding population data with known pedigrees collected since the inception of Pacific oyster breeding in 1997. Therefore, the data records used for the genetic analysis expands with every successive year class produced. For the analysis done in September 2009 in preparation for the 2009 spawning season, the data set contained records for 19,115 animals from 10 year classes. (Although a spawning had been done in 2008, the progeny test had not been completed and therefore no data was available for this report.)

7.2.3 Summary of the measurement data

In total, data were available for eight traits, of which five were measured traits and three were derived traits. This data is summarised in Table 7.3. Using this data, genetic analyses were able to be done for three of five selection traits in the profit index (length, condition, and width index). Genetic analyses were also done on two additional traits that are not part of the industry profit function (total weight and depth index). These additional traits are termed secondary traits. Although profit has not been directly linked to these in the current economic model, it was considered important by industry that these be available for consideration at selection decisions.

Table 7.3 A summary of the measurement data as at September 2009 (up to and including the 2007 year class). These data were used for the genetic evaluation for selections for the 2009 year class.

Trait	Description	No. records	Trait category
Length	Length of shell, dorsal to ventral (mm)	18,159	Index trait: EBVs calculated
Width	Width of shell, posterior to anterior (mm)	18,143	No EBVs calculated
Depth	Depth of shell (mm)	18,151	No EBVs calculated
Total weight	Total wet weight (g)	13,359	Secondary trait: EBVs calculated
Meat weight	Wet meat weight (g)	10,163	No EBVs calculated
Width index	Derived: = width / length	18,134	Index trait: EBVs calculated
Depth index	Derived: = depth / length	18,139	Secondary trait: EBVs calculated
Condition	Derived: = meat weight / total weight	10,143	Index trait: EBVs calculated

[3] For the first family spawning (Cohort 2), splitting of sperm was done as part of a trial design to estimate non-additive genetic effects. In other spawnings, splitting of sperm and egg batches was done when skewed sex ratios within selected families caused shortages of males or females.

A total of 27 progeny tests have been conducted on seven different farm sites. The locations of farm sites are shown in Table 7.4. All sites are commercial farm leases where rack space has been made available for progeny testing. Each year class is usually progeny tested on four sites, although for some year classes (2001, 2002 and 2004) only one progeny test site was used, and for the 2005 year class only two sites were used. A full complement of the families for each cohort has been used in all progeny tests.

Families are grown in commercial oyster baskets. The mesh size of the baskets used increases during the grow-out from a 6 mm to a 20 mm mesh size. A basket contains 100 animals, and on each site three replicate baskets are used. The field design is a completely randomised design, with no blocking structure. The grow-out regime used for the families differs to that used for commercial animals in that no size grading or machine rumbling is done. Families from cohort 2 were separated into a small and large size grade before they left the hatchery. The small and large size grades were, respectively, from 20 to 50% of size classes and from 50 to 80% of size classes.

Table 7.4 Commercial farm sites used for progeny testing families.

Site name	Site number	Location	Latitude	Longitude
Pittwater	1	Tasmania	42.82°S	147.48°E
Coles Bay	2	Tasmania	42.09°S	148.23°E
Smithton	3	Tasmania	40.08°S	145.09°E
Coffin Bay	4	South Australia	34.61°S	135.48°E
Smokey Bay	5	South Australia	32.39°S	133.90°E
Cowell	8	South Australia	32.75°S	136.92°E

7.2.4 Data coding system

The data system needed for a breeding program is dependent on the type of genetic evaluation system. Estimation of genetic merit using BLUP requires pedigree records and performance data for individual animal records. To enable a BLUP analysis of the ASI data, the data needed to be recoded to meet the following requirements:

1. All individuals used as broodstock and used in progeny tests needed a unique number.
2. Individual identifier numbers needed to be coded such that older animals (from an earlier year class) had lower numbers.
3. Every individual needed to have a record of its parents.
4. Founder stocks needed to be identified and coded with unknown parents.
5. All families spawned as part of a particular batch needed to be indentified.
6. Progeny test records on each farm needed to be systematically coded to capture field design characteristics.

This system defined a hierarchy of data types (Table 7.5). Data was compiled into two main tables. One was the Pedigree Table, in which the family code was the primary field. The other was the Measurement Table, in which the individual identity was the primary field.[4] Previously, the protocols for the ASI breeding program have been such that no data records were recorded against the actual animal used as broodstock. Consequently, it was not possible to objectively measure how within family selection was applied.

[4] There are additional data needs for the breeding program and these are described in Chapter 9.

Table 7.5 Coding system used for the ASI data to allow BLUP analysis. This system has been used as part of the database development (see Chapter 9).

Category	Field name in database table	Description	Type	Example
Year class	YEAR_CLASS	Group of animals fertilised in same spawning season. Founders are assigned to the 1990 year class.	4 digit number	2008
Spawn run	SPAWN_RUN	Spawning run during which a family was fertilised.	6 digit number	200802
Site	SITE_ID	Farm on which animals are grown	Up to 2 digit number	03
Unit	UNIT_ID	A unit containing individual animals of from a known family	10 digit number (includes YC, site and a 4 digit 'count' within site)	200501001
Family	FAMILY_ID	A group of full-siblings.	7 digit number, 0 for unknown	2008012
Individual	INDIV_ID	Single animal	10 digit number	2008000123

The change in the data coding system represented a significant change in approach to data management. Historically, records have been based on family identities and recoding the data was a painstaking and time consuming task. Most information was available from the published documentation of the breeding program (Ward *et al.* 2005). However, at times it was necessary to go back to original hatchery records to resolve ambiguities. These arose when it was unclear if the same individuals had been used as parents in multiple families through the splitting of egg and sperm batches, or if different individuals from the same family had been used. Recoding also identified errors in some of the measurement data where it was noticed that blocks of data were obviously wrong. These were also resolved by going back to original records or omitted.

7.3 ASSESSMENT OF GENETIC PARAMETERS

7.3.1 Assessment of grading effects

Methods

The nursery grading done for Cohort 2, which was the first major family production, was atypical and not repeated on any other cohorts. A preliminary analysis was done on this cohort to determine if genetic performance was biased by the grading. The aim was to assess genotype x grading effects which, if present, may indicate family rankings are altered by nursery grading.

Traits analysed were length, total weight, width index, depth index, and condition. Analyses were done using the software ASReml (Gilmour *et al.* 2006) to fit univariate individual animal mixed linear models. The model fitted was:

$$Y = \mu + PT + Run + GR + G.GR + Rep + A + D + \varepsilon \qquad (1)$$

Where, Y is the observation on each individual animal, μ is the mean, PT is the fixed effect of the progeny test (4 levels), Run is the fixed effect of spawning date (2 levels), GR is the fixed effect of spat grading (2 levels, small and large), G.GR is the random effect of the genotype by grading interaction estimated by fitting the grading by family interaction, Rep is the random effect of the replicate baskets within family (4 levels), A is the random additive genetic effect for each animal, D is the random non-additive (dominance) genetic effect for each animal estimated by fitting the Sire x Dam effect, and ε is the random residual effect.

Results

The means of the small and large size grades for each trait are shown in Table 7.6. Grading had a statistically significant effect for length and total weight, with the large nursery grade producing larger animals at harvest age. The difference between the small and large grades for length and total weight was, respectively, 7% and 31%. For the width index, depth index and condition, grading effects were small, either statistically insignificant or marginally significant, and of no practical importance.

Table 7.6 Trait means (with standard errors) measured at harvest age for the small and large nursery size grades of Cohort 2 (1997 spawning year).

Source	Shell length (mm)	Total weight (g)	Width index	Depth index	Condition (%)
Small nursery grade [1]	65.6	26.2	56.5	33.0	43.7
Large nursery grade [2]	70.4	34.5	56.1	32.2	42.9
Standard error	1.0	0.9	0.6	0.5	0.3

[1] Small size grades were from 20 to 50% of nursery size classes.

[2] Large size grades were from 50 to 80% of nursery size classes.

Variance components for each trait are shown in Table 7.7. The data of importance from this analysis are the genotype by grading effects. For length, these effects were significantly different from zero, but small and represented only 2% of total variation. For all other traits, genotype x grading effects were statistically insignificant (unlikely to differ from zero). These data indicate that family rankings were not changed by the grading and, consequently, grading effects were ignored in the genetic evaluation. Both low grades and high grades were included and became extra replicates within each progeny test site. The length and weight effects shown in Table 7.6 therefore manifest as replicate effects in all following analyses.

Table 7.7 Variance components (with standard errors) for a combined analysis of the four progeny tests for Cohort 2.

Source	Shell length	Total weight	Width index	Depth index	Condition
Genotype x grading	3.8 (1.7)	0.7 (0.9)	1.2 (0.6)	0.1 (0.2)	0.30 (0.20)
Genotype x environment	18.5 (3.6)	12.9 (2.9)	6.7 (1.4)	2.5 (0.5)	1.74 (0.44)
Replicate	9.7 (2.0)	13.7 (1.9)	2.2 (0.9)	1.0 (0.4)	2.11 (0.30)
Additive genetic	41.1 (28.7)	23.9 (17.0)	15.1 (5.5)	7.6 (8.3)	3.91 (1.48)
Dominance genetic	1.7 (11.8)	1.8 (7.4)	0.0 (0.1)	2.9 (3.7)	0.00 (0.10)
Residual	80.7 (14.7)	58.8 (8.7)	48.2 (3.1)	18.1 (4.2)	8.86 (0.80)

7.3.2 Analyses of individual progeny tests

Methods

Analyses were initially done for each progeny test and each trait individually. Traits analysed were length, total weight, width index, depth index, and condition. This was done as a check on the data for each individual test, and to measure the heterogeneity of variances across progeny tests. ASReml was used to fit univariate individual animal mixed linear models. The model fitted was:

$$Y = \mu + Run + Rep + A + \varepsilon \qquad (2)$$

Where, Y is the observation on each individual animal, μ is the mean for the progeny test, Run is the fixed effect of spawning date within each cohort (2 levels), Rep is the random effect of the replicate baskets within family (usually 3 levels), A is the random additive genetic effect for each animal, and ε is the random residual effect. Additive genetic effects

were estimated using a numerator relationship matrix which was constructed (by ASReml) using the pedigree structure described in the preceding section.

Non-additive genetic effects were ignored in these initial analyses. They could only be estimated in a subset of progeny trials due to the crossing designs used and, where they could be calculated, estimates were mostly imprecise, presumably due to the small data sets. A later analysis combining data across all progeny tests (see section 7.3.3) found very small non-additive effects so it is unlikely the additive effects estimated in these analyses are biased due to non-additive effects.

The models estimated both individual animal breeding values, variance components for all random terms in the model, and standard errors of variance components. It is the variance components and their standard errors that are of particular interest for this part of the analysis. Variance components were also used to calculate heritabilities as:

$$h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_r + \sigma^2_\varepsilon) \qquad (3)$$

Where, h^2 is the heritability, σ^2_a is the additive genetic variance, σ^2_r is the variance due to replicate baskets, and σ^2_ε is the residual variance. Standard errors of heritabilities were calculated using the functions of variance components option in ASReml.

Results

Phenotypic variances, variance components, heritabilities, and standard errors for each trait and for each progeny trial are shown in Tables 7.8 to 7.12. There are large differences in variances components and heritabilities across progeny trials for all traits. For example, heritabilities for shell length vary from 0.21 to 0.81 and there is a 13 fold difference between the lowest and highest estimate of additive genetic variance (Table 7.8). Similarly, heritabilities for width index vary from 0.05 to 0.74 with an 8 fold difference between additive genetic variances (Table 7.10), and heritabilities for total weight vary from 0.07 to 0.87 with a 40 fold difference between additive genetic variances (Table 7.9). Total weight was also analysed after a square root transformation (data not shown). Heritabilities were very similar to those for untransformed data, although the magnitude of additive variance differences was reduced to an 11 fold difference.

The very low heritabilities are most likely due to data measurement errors or data scrambling. Progeny trials that had low and non-significant heritability in one trait always had significant heritabilities in others. For example, Trial 131 had high heritability for shell length and very low heritability for total weight (Tables 7.8 and 7.9). This suggests there is nothing wrong with Trial 131 as a whole, but only with total weight data. The same patterns were seen for other traits and trials with low heritabilities. Therefore a univariate analysis of each progeny trial serves as a useful check on the integrity of the data.

For weight data, there is a clear relationship between the mean of the progeny test and phenotypic, additive and residual variance. Trials with a larger weight have larger variances (Table 7.9). This is not surprising given the large range in mean weights. For shell length, width index and depth index there were no strong relationships between means and variances. Patterns were less clear for condition data. Progeny tests for cohorts 2, 4 and 5 had much higher condition values and this appears to influence variances to some degree. Condition appears to be a variable measure and is probably influenced by husbandry and within site effects. This is indicated by the replicate variance components (Table 7.12), which are measures of the amount of variation between family baskets. These effects were generally high relative to other traits and, for cohorts 13 to 15, were frequently comparable to additive genetic effects.

Table 7.8 Shell length (mm) means, phenotypic variances, variance components, and heritabilities (with standard errors) for each of the 27 Pacific oyster progeny tests. V_p = phenotypic variance, V_{rep} = variance due to replicate baskets, V_a = additive genetic variance, V_e = residual variance, and h^2 = heritability.

Test no.	Cohort	Spawn Year	Site	No fam	Mean	V_p	V_{rep}	(se)	V_a	(se)	V_e	(se)	h^2	(se)
21	2	1997	1	37	61.1	117.0	1.9	(2.3)	53.8	(16.1)	49.7	(9.1)	0.51	(0.12)
22	2	1997	2	37	70.7	254.5	1.7	(5.2)	151.4	(44.9)	105.1	(24.9)	0.59	(0.13)
23	2	1997	3	37	66.2	129.8	0.0	(0.0)	101.8	(25.6)	23.1	(13.1)	0.81	(0.12)
24	2	1997	4	37	73.7	192.9	3.5	(5.8)	70.4	(25.1)	120.5	(16.1)	0.36	(0.11)
41	4	1999	1	40	73.7	145.3	10.8	(4.0)	56.7	(19.4)	79.4	(10.5)	0.39	(0.11)
51	5	2000	1	19	74.1	155.5	6.6	(4.6)	97.0	(42.5)	60.9	(22.6)	0.59	(0.19)
73	7	2001	3	17	82.4	132.8	29.9	(15.7)	80.3	(55.4)	38.4	(28.1)	0.54	(0.30)
93	9	2002	3	34	77.3	118.0	0.0	(0.0)	93.4	(27.0)	26.1	(14.1)	0.78	(0.14)
95	9	2002	5	34	110.9	228.3	18.9	(13.0)	135.3	(56.9)	60.7	(29.6)	0.63	(0.20)
111	11	2004	1	20	96.0	77.0	0.3	(3.1)	45.0	(22.5)	36.4	(12.0)	0.55	(0.20)
113	11	2004	3	20	87.9	63.0	0.2	(2.0)	30.3	(11.5)	35.3	(6.5)	0.46	(0.14)
115	11	2004	5	20	99.9	110.2	1.4	(3.5)	62.9	(24.4)	50.7	(12.8)	0.55	(0.16)
116	11	2004	6	20	99.0	117.6	0.0	(0.0)	109.5	(51.7)	22.7	(26.4)	0.83	(0.23)
125	12	2005	5	10	78.1	128.3	11.9	(7.3)	73.6	(48.1)	55.8	(24.7)	0.52	(0.26)
131	13	2005	1	23	76.6	64.2	5.5	(3.9)	38.1	(18.0)	26.5	(9.6)	0.54	(0.20)
133	13	2005	3	23	89.3	53.3	4.4	(3.4)	11.7	(8.8)	37.9	(5.7)	0.22	(0.15)
135	13	2005	5	23	95.5	134.5	3.9	(5.3)	58.9	(24.4)	70.0	(14.4)	0.44	(0.15)
136 [1]	13	2005	6	23										
141	14	2006	1	24	81.5	118.0	24.0	(5.3)	28.0	(24.4)	68.1	(14.4)	0.23	(0.12)
143	14	2006	3	24	93.0	128.3	5.2	(2.5)	49.8	(17.6)	77.0	(9.9)	0.38	(0.11)
145	14	2006	5	24	106.5	131.8	6.3	(2.8)	67.6	(24.2)	66.5	(12.9)	0.48	(0.13)
146	14	2006	6	24	99.0	105.1	5.5	(2.4)	22.3	(9.8)	79.2	(6.4)	0.21	(0.08)
151	15	2007	1	24	88.2	93.8	9.3	(2.9)	21.2	(10.4)	64.9	(6.1)	0.22	(0.10)
153	15	2007	3	24	74.6	58.3	4.5	(1.7)	13.3	(6.8)	42.3	(4.1)	0.22	(0.10)
155	15	2007	5	24	100.4	120.8	7.8	(3.0)	51.3	(20.8)	64.0	(11.1)	0.42	(0.14)
156	15	2007	6	24	86.6	85.2	5.8	(2.8)	35.2	(17.7)	49.0	(9.5)	0.39	(0.16)
158	15	2007	8	24	92.9	101.0	6.5	(2.4)	59.7	(22.9)	44.8	(11.8)	0.54	(0.15)

[1] No shell length measurements taken for Progeny Test number 136

Table 7.9 Total weight (g) means, phenotypic variances, variance components, and heritabilities (with standard errors) for each of the 27 Pacific oyster progeny tests. V_p = phenotypic variance, V_{rep} = variance due to replicate baskets, V_a = additive genetic variance, V_e = residual variance, and h^2 = heritability.

Test no.	Cohort	Spawn Year	Site	No fam	Mean	V_p	V_{rep}	(se)	V_a	(se)	V_e	(se)	h^2	(se)
21	2	1997	1	37	19.3	55.3	0.5	(1.0)	19.7	(6.0)	25.1	(3.6)	0.44	(0.11)
22	2	1997	2	37	28.6	161.2	10.2	(5.4)	58.4	(22.0)	82.3	(12.8)	0.39	(0.12)
23	2	1997	3	37	31.4	102.0	0.1	(0.9)	58.2	(15.1)	33.3	(7.9)	0.63	(0.11)
24	2	1997	4	37	42.6	282.1	6.2	(7.4)	99.6	(36.0)	95.5	(21.0)	0.49	(0.14)
41	4	1999	1	40	34.4	169.2	19.7	(5.9)	32.7	(17.3)	104.1	(10.1)	0.21	(0.10)
51	5	2000	1	19	36.0	170.0	2.2	(4.3)	71.7	(33.3)	105.2	(19.3)	0.40	(0.15)
73	7	2001	3	17	90.8	534.7	36.0	(41.9)	398.8	(220.3)	160.8	(120.0)	0.67	(0.27)
93 [1]	9	2002	3	34										
95	9	2002	5	34	130.6	1108.1	82.0	(67.8)	548.8	(257.6)	457.1	(140.6)	0.50	(0.19)
111	11	2004	1	20	108.2	363.9	53.1	(38.4)	143.8	(116.9)	205.7	(64.5)	0.36	(0.25)
113	11	2004	3	20	74.8	186.9	1.2	(7.3)	37.7	(21.1)	151.1	(16.5)	0.20	(0.10)
115	11	2004	5	20	95.9	348.1	13.4	(14.7)	105.4	(55.5)	237.4	(32.2)	0.30	(0.14)
116	11	2004	6	20	108.7	389.5	0.0	(0.0)	288.8	(148.1)	139.1	(79.1)	0.67	(0.23)
125 [1]	12	2005	5	10										
131 [2]	13	2005	1	23	51.9	92.6	0.0	(0.0)	6.2	(6.2)	86.8	(8.3)	0.07	(0.07)
133	13	2005	3	23	63.0	108.2	7.3	(6.1)	33.1	(18.8)	69.2	(11.8)	0.30	(0.15)
135	13	2005	5	23	110.4	579.5	0.0	(0.0)	250.2	(98.9)	337.7	(62.5)	0.43	(0.14)
136	13	2005	6	23	61.6	158.5	4.5	(7.8)	169.6	(62.1)	20.3	(32.8)	0.87	(0.20)
141 [2]	14	2006	1	24	51.4	241.4	98.8	(22.4)	18.8	(30.9)	116.6	(16.5)	0.08	(0.13)
143	14	2006	3	24	65.9	246.7	6.6	(4.4)	29.4	(13.7)	208.0	(12.0)	0.12	(0.05)
145	14	2006	5	24	144.7	863.7	38.1	(17.9)	457.0	(162.1)	418.9	(86.4)	0.50	(0.14)
146	14	2006	6	24	81.0	271.7	16.1	(6.6)	44.8	(21.3)	212.9	(15.1)	0.16	(0.07)
151	15	2007	1	24	65.0	202.4	0.0	(0.0)	75.2	(31.8)	128.0	(20.8)	0.37	(0.13)
153	15	2007	3	24	44.0	71.3	8.4	(4.2)	13.6	(9.5)	50.3	(6.8)	0.19	(0.12)
155	15	2007	5	24	110.2	485.3	55.6	(26.5)	225.6	(106.9)	211.9	(60.0)	0.46	(0.17)
156	15	2007	6	24	61.3	141.1	9.7	(8.5)	44.0	(26.7)	89.1	(17.7)	0.31	(0.16)
158	15	2007	8	24	84.0	357.2	12.3	(14.5)	120.2	(57.5)	215.7	(36.6)	0.35	(0.14)

[1] No total weight measurements taken for Progeny Test Numbers 93 and 125

[2] Very low genetic variation for Progeny Test Numbers 131 and 141; data assumed to be incorrect.

Table 7.10 Width index (shell width / shell length x 100) means, phenotypic variances, variance components, and heritabilities (with standard errors) for each of the 27 Pacific oyster progeny tests. V_p = phenotypic variance, V_{rep} = variance due to replicate baskets, V_a = additive genetic variance, V_e = residual variance, and h^2 = heritability.

Test no.	Cohort	Spawn Year	Site	No fam.	Mean	V_p	V_{rep}	(se)	V_a	(se)	V_e	(se)	h^2	(se)
21	2	1997	1	37	0.57	62.5	0.1	(1.1)	28.1	(8.4)	33.3	(5.0)	0.46	(0.11)
22	2	1997	2	37	0.56	105.5	1.4	(2.7)	43.5	(14.8)	65.5	(9.0)	0.39	(0.11)
23	2	1997	3	37	0.57	61.8	0.0	(0.0)	36.2	(9.3)	25.7	(5.0)	0.58	(0.11)
24	2	1997	4	37	0.56	81.4	0.5	(2.6)	12.5	(6.8)	70.0	(6.0)	0.15	(0.08)
41	4	1999	1	40	0.50	51.2	2.2	(1.0)	34.2	(9.7)	18.2	(4.9)	0.63	(0.12)
51	5	2000	1	19	0.52	55.8	6.2	(2.4)	44.8	(20.3)	10.6	(10.5)	0.73	(0.22)
73	7	2001	3	17	0.59	74.2	6.0	(4.5)	52.4	(26.6)	23.0	(13.7)	0.64	(0.24)
93	9	2002	3	34	0.54	60.7	1.0	(1.8)	49.8	(14.9)	16.6	(7.7)	0.74	(0.14)
95	9	2002	5	34	0.52	41.4	1.6	(2.3)	22.5	(9.9)	19.6	(5.6)	0.52	(0.18)
111	11	2004	1	20	0.59	39.3	0.0	(0.0)	25.4	(11.8)	15.0	(6.2)	0.63	(0.20)
113	11	2004	3	20	0.58	37.7	0.9	(1.2)	28.1	(10.5)	10.8	(5.3)	0.71	(0.17)
115	11	2004	5	20	0.58	51.8	0.0	(0.0)	39.2	(13.4)	13.8	(6.9)	0.74	(0.16)
116	11	2004	6	20	0.60	58.8	0.0	(0.0)	35.0	(16.9)	27.2	(9.1)	0.56	(0.20)
125	12	2005	5	10	0.61	62.5	6.5	(3.9)	18.1	(15.5)	41.1	(8.3)	0.28	(0.21)
131	13	2005	1	23	0.62	55.3	8.0	(4.2)	26.0	(14.5)	23.8	(7.8)	0.45	(0.21)
133	13	2005	3	23	0.66	41.4	4.9	(3.2)	10.2	(8.3)	27.6	(5.0)	0.24	(0.18)
135	13	2005	5	23	0.63	49.2	4.1	(2.8)	10.1	(7.1)	35.6	(4.8)	0.20	(0.13)
136 [1]	13	2005	6	23										
141	14	2006	1	24	0.68	69.5	7.1	(2.3)	23.0	(9.6)	39.9	(5.4)	0.33	(0.12)
143	14	2006	3	24	0.57	67.7	0.9	(1.0)	15.7	(5.8)	51.5	(3.9)	0.23	(0.08)
145	14	2006	5	24	0.60	51.4	2.6	(1.1)	20.4	(7.6)	29.7	(4.2)	0.39	(0.12)
146	14	2006	6	24	0.59	56.9	1.3	(1.0)	9.9	(4.1)	46.2	(3.1)	0.17	(0.07)
151	15	2007	1	24	0.66	70.8	2.2	(1.3)	29.1	(10.8)	43.8	(5.9)	0.39	(0.12)
153 [2]	15	2007	3	24	0.69	121.3	12.2	(4.1)	6.3	(7.4)	103.7	(6.2)	0.05	(0.06)
155	15	2007	5	24	0.57	54.1	0.6	(0.8)	20.5	(7.7)	35.7	(4.4)	0.36	(0.11)
156 [3]	15	2007	6	24	0.65	61.3	7.4	(2.4)	0.0	(0.0)	54.0	(3.1)	0.00	(0.00)
158	15	2007	8	24	0.60	46.5	3.0	(1.2)	9.7	(4.9)	35.1	(3.0)	0.20	(0.09)

[1] No shell length measurements taken for Progeny Test number 136 and therefore no width index data

[2] Very low genetic variation for Progeny Test Number 153; data assumed to be incorrect.

[3] No genetic variation for Progeny Test Number 156; shell width data appears to be wrong.

Table 7.11 Depth index (shell depth / shell length x 100) means, phenotypic variances, variance components, and heritabilities (with standard errors) for each of the 27 Pacific oyster progeny tests. V_p = phenotypic variance, V_{rep} = variance due to replicate baskets, V_a = additive genetic variance, V_e = residual variance, and h^2 = heritability.

Test no.	Cohort	Spawn Year	Site	No fam.	Mean	V_p	V_{rep}	(se)	V_a	(se)	V_e	(se)	h^2	(se)
21	2	1997	1	37	0.30	26.6	0.0	(0.0)	20.7	(5.7)	8.2	(3.1)	0.72	(0.13)
22	2	1997	2	37	0.32	39.8	0.0	(0.0)	22.2	(6.6)	19.6	(3.8)	0.53	(0.12)
23	2	1997	3	37	0.33	30.3	0.1	(0.3)	26.7	(6.7)	5.4	(3.4)	0.83	(0.12)
24	2	1997	4	37	0.34	38.2	0.0	(0.0)	14.1	(4.6)	20.0	(2.9)	0.41	(0.11)
41	4	1999	1	40	0.27	17.6	1.6	(0.5)	10.9	(3.4)	7.0	(1.7)	0.56	(0.13)
51	5	2000	1	19	0.29	18.3	0.8	(0.5)	12.2	(5.3)	6.5	(2.8)	0.63	(0.19)
73	7	2001	3	17	0.34	29.0	5.3	(2.9)	13.7	(10.1)	12.1	(5.2)	0.44	(0.27)
93	9	2002	3	34	0.31	27.7	0.6	(0.8)	26.0	(7.6)	3.7	(3.9)	0.86	(0.15)
95	9	2002	5	34	0.34	22.7	0.2	(0.8)	17.3	(6.1)	4.7	(3.2)	0.78	(0.17)
111	11	2004	1	20	0.35	16.1	0.0	(0.0)	8.4	(4.2)	8.7	(2.3)	0.49	(0.19)
113	11	2004	3	20	0.33	12.0	0.0	(0.0)	6.3	(2.4)	6.3	(1.3)	0.50	(0.14)
115	11	2004	5	20	0.34	13.4	0.0	(0.0)	6.2	(2.3)	7.7	(1.3)	0.44	(0.13)
116	11	2004	6	20	0.34	21.3	0.0	(0.0)	9.5	(4.9)	12.9	(2.8)	0.42	(0.17)
125	12	2005	5	10	0.37	36.2	0.5	(0.8)	33.0	(18.0)	5.5	(9.2)	0.85	(0.27)
131	13	2005	1	23	0.35	21.6	0.9	(0.9)	20.9	(7.9)	3.3	(4.1)	0.83	(0.20)
133	13	2005	3	23	0.31	10.9	0.0	(0.0)	3.1	(1.4)	7.9	(1.1)	0.28	(0.12)
135	13	2005	5	23	0.35	22.4	1.4	(1.1)	9.5	(4.3)	12.2	(2.5)	0.41	(0.16)
136 [1]	13	2005	6	23										
141 [2]	14	2006	1	24	0.43	47.4	13.36	(2.76)	0.0	(0.0)	34.21	(1.60)	0.00	
143	14	2006	3	24	0.32	28.1	0.5	(0.4)	12.4	(4.2)	16.1	(2.3)	0.43	(0.11)
145	14	2006	5	24	0.36	21.8	1.1	(0.5)	6.5	(2.6)	14.7	(1.5)	0.29	(0.10)
146	14	2006	6	24	0.31	19.2	0.6	(0.4)	3.9	(1.6)	14.8	(1.1)	0.20	(0.08)
151	15	2007	1	24	0.31	21.0	1.5	(0.5)	10.5	(4.0)	10.1	(2.1)	0.48	(0.14)
153	15	2007	3	24	0.34	45.4	1.6	(1.0)	5.5	(3.3)	39.1	(2.5)	0.12	(0.07)
155	15	2007	5	24	0.33	29.5	0.5	(0.5)	12.9	(4.8)	18.0	(2.6)	0.41	(0.12)
156	15	2007	6	24	0.30	19.9	1.5	(0.7)	8.3	(4.6)	11.9	(2.4)	0.38	(0.17)
158	15	2007	8	24	0.33	30.9	0.0	(0.0)	22.2	(7.4)	14.5	(3.8)	0.61	(0.14)

[1] No shell length measurements taken for Progeny Test number 136 and therefore no depth index data

[2] No genetic variation for Progeny test number 141; shell depth data appears to be wrong.

Table 7.12 Condition (wet meat weight / total weight x 100) means, phenotypic variances, variance components, and heritabilities (with standard errors) for each of the 27 Pacific oyster progeny tests. V_p = phenotypic variance, V_{rep} = variance due to replicate baskets, V_a = additive genetic variance, V_e = residual variance, and h^2 = heritability.

Test no.	Cohort	Spawn Year	Site	No fam.	Mean	V_p	V_{rep}	(se)	V_a	(se)	V_e	(se)	h^2	(se)
21	2	1997	1	37	43.9	11.96	0.06	(0.24)	8.01	(2.31)	4.52	(1.25)	0.64	(0.13)
22	2	1997	2	37	47.0	23.56	1.59	(0.82)	10.25	(3.69)	11.60	(2.09)	0.44	(0.13)
23	2	1997	3	37	40.2	11.84	0.09	(0.13)	7.51	(1.96)	4.74	(1.03)	0.61	(0.11)
24	2	1997	4	37	42.1	41.65	1.14	(2.00)	8.62	(5.71)	27.03	(4.20)	0.23	(0.14)
41	4	1999	1	40	40.4	67.19	1.37	(0.51)	6.15	(2.22)	7.92	(1.19)	0.40	(0.12)
51	5	2000	1	19	37.6	11.20	1.64	(0.66)	1.34	(1.46)	8.40	(0.97)	0.12	(0.12)
73	7	2001	3	17	16.8	8.28	0.06	(0.52)	5.47	(2.94)	3.51	(1.68)	0.60	(0.24)
93 [1]	9	2002	3	34										
95	9	2002	5	34	18.5	5.38	0.25	(0.29)	3.73	(1.50)	1.97	(0.81)	0.63	(0.18)
111	11	2004	1	20	16.0	4.72	0.00	(0.00)	2.39	(1.27)	2.63	(0.74)	0.48	(0.20)
113	11	2004	3	20	14.7	5.13	0.00	(0.00)	2.17	(0.91)	3.09	(0.54)	0.41	(0.14)
115	11	2004	5	20	18.3	8.67	0.49	(0.42)	3.93	(1.83)	4.89	(1.00)	0.42	(0.16)
116	11	2004	6	20	19.7	8.72	0.47	(0.59)	4.07	(2.66)	4.54	(1.48)	0.45	(0.24)
125 [1]	12	2005	5	10										
131	13	2005	1	23	17.6	7.15	1.25	(0.61)	1.65	(1.38)	4.37	(0.80)	0.23	(0.18)
133 [1]	13	2005	3	23										
135	13	2005	5	23	21.3	7.19	0.00	(0.00)	3.94	(1.45)	3.40	(0.84)	0.54	(0.15)
136	13	2005	6	23	19.8	10.61	0.00	(0.00)	3.19	(1.23)	2.79	(0.73)	0.53	(0.16)
141	14	2006	1	24	14.1	7.23	0.92	(0.47)	0.97	(0.87)	5.42	(0.68)	0.13	(0.12)
143	14	2006	3	24	17.4	6.55	0.60	(0.35)	1.27	(0.73)	4.69	(0.57)	0.19	(0.10)
145	14	2006	5	24	18.0	7.98	2.44	(0.70)	2.20	(1.42)	3.36	(0.80)	0.27	(0.16)
146	14	2006	6	24	20.5	7.78	1.26	(0.48)	2.46	(1.26)	4.06	(0.77)	0.32	(0.14)
151	15	2007	1	24	18.0	5.44	1.11	(0.39)	0.74	(0.76)	3.69	(0.50)	0.13	(0.13)
153	15	2007	3	24	19.9	6.83	0.52	(0.35)	2.33	(1.22)	4.15	(0.76)	0.33	(0.15)
155	15	2007	5	24	19.2	8.65	1.53	(0.59)	3.01	(1.75)	4.38	(1.01)	0.34	(0.17)
156	15	2007	6	24	17.4	7.80	1.08	(0.62)	1.89	(1.58)	5.04	(1.01)	0.24	(0.18)
158	15	2007	8	24	18.4	10.67	2.97	(0.87)	3.04	(2.11)	4.97	(1.18)	0.28	(0.17)

[1] No total weight or wet meat weight measurements taken for Progeny Test numbers 93, 125 and 133

Genetic evaluation requires homogeneity of variances across different progeny tests. Ignoring heterogeneous variances is known to influence genetic parameter estimates, change selection decisions, and alter estimates of response to selection (e.g. Visscher *et al.* 1999, White *et al.* 2007). Therefore strategies are needed to stabilise variances prior to doing a multisite analysis. One option is to use the phenotypic variance for each progeny test. This is done by dividing all records by the individual trial standard deviation and is widely used (e.g. Visscher *et al*. 1999, White *et al.* 2007). This is a simple adjustment and uses an easily calculated statistic, but it assumes a constant heritability across all progeny tests. A second option is to adjust by the residual variance. Johnston *et al.* (1999) describes a system where this is done after each round of calculations in an iterative EBV analysis. This assumes a constant heritability across all progeny tests and allows the residual variance to float. It is a better scaling factor than phenotypic variance, especially when the model contains fixed effects. A third option is to adjust each progeny test by the additive genetic variance for that test by dividing by the square root of additive variance (e.g. McRae *et al.* 2004). This causes the additive variance for each progeny test to equal one and allows the residual variance to float. It results in every progeny test using a unique heritability rather than assuming a constant heritability across all tests.

For Pacific oysters, heritabilities and genetic variances appear to vary across progeny tests and there would be advantages in scaling variances to a standard additive genetic variance. However, obtaining reliable estimates of individual trial additive variances is problematic. All trials are based on small numbers of families resulting in imprecise estimates of additive variance. This is illustrated by the high standard errors in Tables 7.8 to 7.12. Therefore adjusting each progeny test by the additive genetic variance for that progeny test was not considered a reliable method for this data and was not used.

The use of residual variance to adjust for heterogeneity is appealing, but is limited by the need to make adjustments after each iteration of EBV calculations. Presumably, the system described by Johnston *et al.* (1999) uses purpose built BLUP software and this cannot be easily done in the software routinely used for the ASI EBV estimations (ASReml). Therefore this method was not used, but it remains an option worthy of evaluation and further exploration.

The scaling factor used to adjust for variance heterogeneity was phenotypic variances. This was considered the safest and simplest method. To account for some of the variability in estimates of additive variance, progeny tests with very low heritability estimates were excluded from the genetic evaluation. These are flagged in Tables 7.8 to 7.12.

7.3.3 Analysis of the combined data

Methods

To estimate genetic parameters, a multivariate analysis was done combining data for all traits and using data from all progeny tests in a single analysis. Traits analysed were length, total weight, width index, depth index, and condition. Prior to analysis, variances were homogenised by dividing by the phenotypic standard deviation for each progeny trial (as described in section 7.3.2 Results). Some traits from some trials were excluded from this analysis (see footnotes in Tables 7.9 to 7.12) because the univariate analyses indicated the data were probably wrong. In addition, data points that were flagged by ASReml as having very high residuals were excluded. The threshold used for exclusion was residuals exceeding ± 4 standard deviations.

Analyses were done using ASReml to fit an individual animal mixed linear model. The model fitted was:

$$Y = \mu + PT + Run + Rep + A + D + GE + \varepsilon \qquad (4)$$

Where, Y is the vector of observations for each individual animal and for each trait, μ is the general mean, PT is the fixed effect of the progeny test, Run is the fixed effect of spawning date within each cohort (2 levels), Rep is the random effect of the replicate baskets within a family (usually 3 levels), A is the random additive genetic effect for each animal, D is the random non-additive (dominance) genetic effect for each animal estimated by fitting the Family effect, GE is the random genotype by environment interaction estimated by fitting Family x Site (6 levels of Site), and ε is the random residual effect. Full variance and covariance matrices were fitted for additive genetic effects and residuals. For replicate, non-additive, and genotype by environment effects, variances only were fitted (using the DIAG option in ASReml). Additive genetic effects were estimated using a numerator relationship matrix which was constructed (by ASReml) using the pedigree structure.

Variance components were used to calculate heritabilities as:

$$h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_r + \sigma^2_\varepsilon) \quad (5)$$

Where, h^2 is the heritability, σ^2_a is the additive genetic variance, σ^2_r is the variance due to replicate baskets, and σ^2_ε is the residual variance. Standard errors of heritabilities were calculated using the functions of variance components option in ASReml.

Results

Genetic parameters are shown in Table 7.13. An analysis such as this estimates the genetic parameters of the founder population and, therefore, the data shown represents genetic parameters of the Tasmanian Pacific oyster land race.

Additive genetic variance (V_a) was highly significant for all traits and constituted the major portion of the explained variation. Consequently, heritabilities were moderate to high in comparison to traits in other animal breeding programs. The genetic coefficient of variation (genetic standard deviation / mean – a useful credibility check of data) ranged from 5% to 12% which is well within the expected range. Non-additive genetic variance (V_d) was either zero, or not significantly different from zero for all traits. Although the production of half-sib families was somewhat *ad hoc*, nearly half of all progeny had half-sib relationships. Therefore this is likely to be a sound estimate of non-additive variance in this population and, in EBV estimation, there appears no reason to fit this effect. Genotype by environment effects (V_{gxe}) were significant for all traits, but always relatively small. The magnitude of these effects ranged from 4% to 8% of total variation. Although small, genotype by environment effects should be fitted when calculating EBVs and failure to do so will inflate additive variance estimates. Replicate, or basket, effects (V_{rep}) were also relatively small but significant for all traits. The magnitude of these effects ranged from 2% to 12% of total variation. Replicate effects were small for shape traits, but much larger for growth rate and condition. These effects should also be fitted when calculating EBVs, and failure to do so will also lead to inflated additive variances.

Genetic correlations were all statistically significant, except for that between weight and condition. Correlations were frequently strong, meaning they can have profound implications for genetic selection. Importantly, correlations between shell shape and growth rate were strongly adverse. The correlation between total weight and condition was, surprisingly, zero indicating these are two distinct traits.

Parameter estimates were made as part of the EBV estimates for both the 2008 and 2009 spawning years. The estimates made for the 2008 selections used all data up to and including the 2006 year class, and the 2009 estimates included the 2007 year class data. Parameters did not change with the inclusion of the 2008 year class data. Therefore, these genetic parameters appear to be sound estimates that can be considered standard parameters for the ASI population (or indeed any other populations arising from the Tasmanian landrace). This means that for future EBV calculation it is not essential to re-estimate the genetic parameters.

Table 7.13 Genetic parameters (with standard errors) for selection traits calculated in a multivariate analysis combining all progeny trials across all year classes. For additive genetic and residual components, variances (in normal type) are along diagonals of matrices, and genetic correlations r_g and phenotypic correlations r_p (in italics) are on off-diagonals. Data for all traits was standardised by dividing by phenotypic variance.

Component		Shell length	Weight	Width index	Depth index	Condition
Additive genetic	Shell length	0.48 (0.07)				
V_a (diagonal)	Weight	*0.91 (0.04)*	0.23 (0.06)			
r_g (*off-diagonal*)	Width index	*-0.77 (0.05)*	*-0.38 (0.11)*	0.46 (0.06)		
	Depth index	*-0.87 (0.04)*	*-0.34 (0.11)*	*0.70 (0.06)*	0.50 (0.08)	
	Condition	*0.34 (0.12)*	*-0.05 (0.14)*	*-0.32 (0.12)*	*-0.39 (0.12)*	0.19 (0.06)
Residual	Shell length	0.50 (0.04)				
V_e (diagonal)	Weight	*0.71 (0.02)*	0.63 (0.03)			
r_p (*off-diagonal*)	Width index	*-0.45 (0.03)*	*-0.15 (0.03)*	0.55 (0.03)		
	Depth index	*-0.31 (0.04)*	*-0.02 (0.04)*	*0.37 (0.04)*	0.50 (0.04)	
	Condition	*-0.03 (0.04)*	*-0.01 (0.03)*	*0.03 (0.04)*	*0.03 (0.04)*	0.56 (0.03)
Replicate (V_{rep})		0.06 (0.01)	0.10 (0.01)	0.02 (0)	0.02 (0)	0.11 (0.01)
Genotype x environment (V_{gxe})		0.04 (0.01)	0.04 (0.01)	0.03 (0.01)	0.04 (0.01)	0.08 (0.01)
Non-additive genetic (V_d)		0.00 (0)	0.01 (0)	0.00 (0)	0.02 (0.01)	0.01 (0.02)
Heritability (h^2)		0.44 (0.05)	0.23 (0.05)	0.41 (0.04)	0.40 (0.06)	0.22 (0.06)
Mean (of standardised data)		8.10	4.04	7.70	6.62	8.30

The significance of fixed effects were evaluated using Wald F statistics, which were routinely calculated by ASReml (results not shown). In the EBV calculation, these fixed effects are of no direct use and their inclusion in the model is to remove their influences from the genetic effects. Progeny test had a large and strongly significant effect for all traits, as would be expected, and should always be included. Spawning run had a relatively small effect, and is marginally significant for shell length and weight but not significant for other traits. Failure to include Spawning Run causes a slight increase in additive variance. For example, V_a for shell length increases by 10%, and heritability increases from 0.44 to 0.47.

7.4 ESTIMATED BREEDING VALUES

7.4.1 Methods

Breeding values are presented as family EBVs. They are calculated for profit index traits, for which data is available for three of the five traits. They are also calculated for two secondary traits (see Table 7.3). For each family and each trait, four EBVs are calculated reflecting different intensities of within family selection. These are the best 10% of individuals per family, the best 25%, the best 50%, and no selection (these values are the truncation points). EBVs are expressed as percentage gains over unselected stock.

There are, essentially, three steps in preparing the final EBVs. These are, firstly, to calculate the EBVs for the selection traits and secondary traits. Secondly, to calculate breeding values reflecting different levels of within family selection. And thirdly, to calculate the EBVs for the objective traits and the profit index values.

Selection trait EBVs

Family EBVs were derived from individual animal EBVs. Individual animal EBVs were calculated by fitting the same multivariate model used for genetic parameter estimation (equation 4). This analysis was done with ASReml, using the genetic parameters in Table 7.13 and with maximum iterations set to one. The batch file used is shown in Appendix 7.1. This produces EBVs for each trait, for all measured animals, and for parents. EBVs were expressed in units of genetic standard deviation (by dividing by the additive

genetic standard deviation – see Table 7.13). Family EBVs were calculated as the mean of the Sire and Dam EBVs.

Within family selection EBVs

EBVs reflecting different intensities of within family selection were estimated using the within family standard deviation of the breeding values and the within family selection intensity (*i*). The within family standard deviation of the breeding values was calculated directly from the individual animal EBVs, and distinct values were used for each family. The selection intensity *i* is taken from the tabulated values of the truncated normal distribution for a large sample (for example, Falconer and Mackay 1996 – Appendix Tables). Alternately, *i* can be calculated directly using the following formula in Excel:

$$i = \text{NORMDIST}((-\text{NORMSINV}(p)),0,1,\text{FALSE}) / p \qquad (6)$$

Where: *i* is the selection intensity and p is the proportion of the population with values exceeding the truncation point (either 0.1, 0.25 0.5 or 0 in this case).

Generally, the calculation of family breeding values for each trait and each within family selection intensity can be expressed as:

$$EBVf_{ij} = (\text{Sire-EBV}_i + \text{Dam-EBV}_i) / 2 + \sigma_i \; . \; i_j \qquad (7)$$

Where $EBVf_{ij}$ is the estimated breeding value of the i^{th} family at the j^{th} within family selection intensity, Sire-EBV_i and Dam-EBV_i are the breeding values of the sire and dam of the i^{th} family, σ_i is the within family standard deviation of the breeding values for the i^{th} family, and i_j is the selection intensity for the j^{th} within family selection intensity.

Objective trait EBVs

The EBV calculation shown in equation 7 expresses values in units of genetic standard deviations for selection traits. These values were transformed to a percentage gain in the objective trait using:

$$\begin{aligned} EBV\%_{ij} &= EBVf_{ij} \; . \; GCV \; . \; r_G \\ &= EBVf_{ij} \; . \; CV \; . \; h \; . \; r_G \end{aligned} \qquad (8)$$

Where: $EBV\%_{ij}$ is the estimated breeding value of the i^{th} family at the j^{th} within family selection intensity expressed as percentage gain, $EBVf_{ij}$ is as previously defined (equation 6) and GCV is the coefficient of genetic variation, CV is the phenotypic coefficient of variation, h is the square root of heritability, and r_G is the genetic correlation between the selection trait and the objective trait. Values used are shown in Table 7.14 and these values are intended to represent parameters of a typical Pacific oyster harvest batch. The CVs for growth time, condition time and width index have been estimated from the modelling done as part of the economic weights study (Chapter 2). The value of h is from Table 7.13. Genetic correlations between objective traits and selection traits are assumed values. The genetic correlation for width index has been assumed to be one because it is, in effect, a direct measure of the objective trait.

The Profit Index was then calculated as:

$$PI = W_{gr}.EBV_{gr} + W_{wi}.EBV_{wi} + W_{co}.EBV_{co} \qquad (9)$$

Where: PI is the profit index, W is the economic weight for each objective trait, and EBV is the estimated breeding value for each objective trait. Economic weights are expressed as the change in the cost of production (cents per dozen oysters) per a one percent change in the objective trait and are listed in Table 7.14. Therefore the profit index is also in units of change in cost of production.

Table 7.14 Parameters and economic weights for objective traits in the ASI breeding program.

Trait	Units	Mean	Coefficient of variation	Standard deviation	Heritability h^2	Coefficient of genetic variation	r_G sel-obj traits	Economic weight [1]
Growth time	days	600	15%	90	0.44	6.6%	-0.9	-0.9
Width index	ratio	0.6	15%	0.09	0.41	6.2%	1.0	1.1
Condition time	days	150	15%	22.5	0.22	3.3%	-0.9	-1.3
Weight	g	80	25%	20	0.23	5.8%	NA	0
Depth index	ratio	0.33	15%	0.0495	0.40	6.0%	NA	0

[1] Economic weight is the change in the cost of production (cents per dozen) for each percentage increase.

7.4.2 Results

The EBVs calculated for selections for the 2009 breeding season included the following:

- Data for 247 families, from the 1997 to 2007 spawning years
- Family EBVs for 5 traits (see Table 7.14) and the Profit Index
- Three EBVs for each family and each trait, reflecting different levels of within family selection (no selection, the average of the top 50%, and the average of the top 25%)

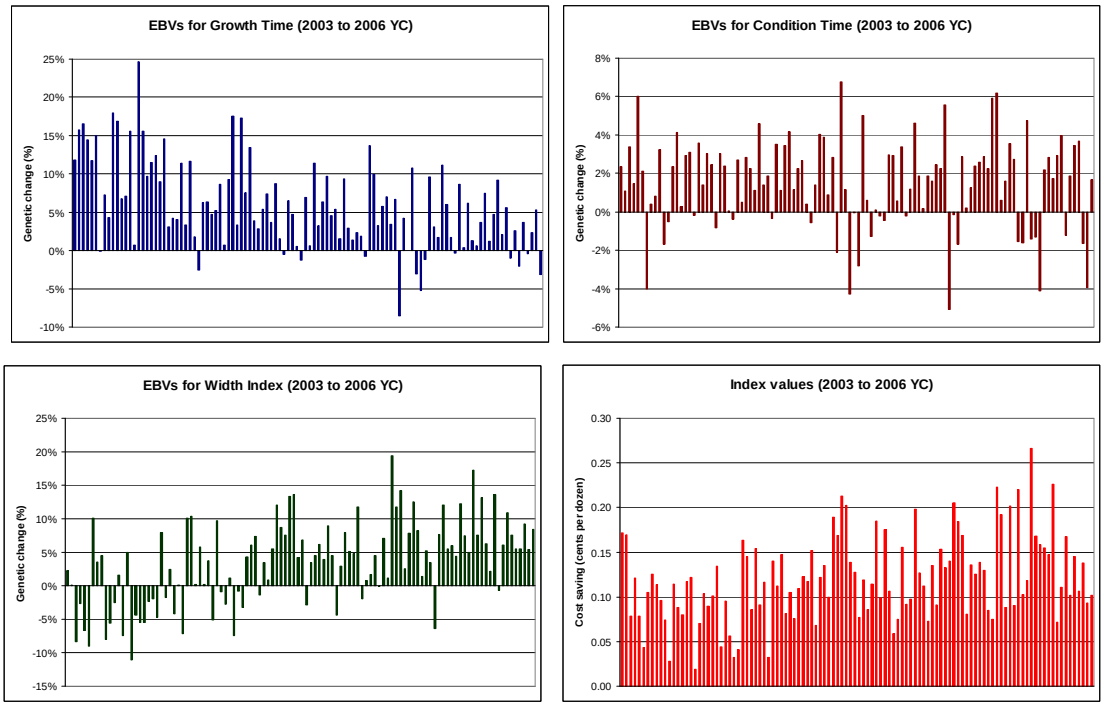


Figure 7.1 EBVs for growth time, condition time, width index and Profit Index. Bars on the charts represent the average of the top 25% of each family. Families are sorted in chronological order with the 2003 year class on the left hand side and the 2006 year class on the right hand side.

A diagrammatic representation of a subset of the EBVs is shown in Figure 7.1. These are the families that were available for selection for the 2008 spawning season. These data also show the genetic trend from 2003 to 2006. The majority of the selection effort was on width index, and an upward trend can be seen for this trait. Selections were made for slower growth due to concerns about poor shape and the belief that fast growth accentuated shape problems, and this trend is also evident. Condition was not considered and no change is evident. There were introductions of new founders at each year class, and these are the families showing the strongly negative EBVs. Index values show a slight upward trend which comes via the change in width index.

7.5 FUTURE DEVELOPMENT

The breeding program tracks records of family selection, but does not record individual records for within family selection. This results in an absence of data on broodstock which limits the quality of the information produced from the genetic evaluation system. It potentially contributes to imprecise or poorly targeted selections. It definitely leads to a loss of information about the genetic merit of the individuals used as broodstock which affects the ability to accurately track the genetic trend across year classes. In oysters, family sizes are large and there is a high potential for genetic change due to within family selection. The need, and challenge, is to develop a system that enables this to happen in a simple, robust and cost effective way.

A breeding program is built upon knowledge of the genetic inheritance of the traits. This knowledge is then translated into a practical work plan that enables data to be collected on these traits and selections made. There is a need to increase the understanding of the genetic control of conditioning. Data is being routinely collected, but there is evidence that this data may be affected by temporal variation and within-site variation. In addition, there is a need to ensure that current measurements do accurately represent the breeding objective desired by industry.

There is also a need to develop an understanding of the genetic control of survival and uniformity. Both are fundamentally important to the profitability of the industry and both are not currently included in the routine assessments. Including uniformity is likely to present a challenge. It is not a conventional trait and case studies where it has been used elsewhere appear lacking.

Consideration of the best way to manage the heterogeneous variances between progeny test sites is warranted. Breeding programs for different species have different approaches and these are determined by the biological, genetic and practical considerations. The need is to identify what is most appropriate for Pacific oysters and implement that in a practical way.

Genotype by environment (gxe) interactions appear statistically significant for all traits. Although they do not appear to be of sufficient magnitude to necessitate regionalised breeding programs, they may offer the opportunity for regionalised commercial deployment programs which could optimise commercial returns for growers. Therefore, there is a need to undertake a detailed gxe assessment to assess the size, repeatability and potential commercial benefits of gxe in the breeding population.

The continued development and maintenance of a database is critical to the EBV system. An EBV system cannot function efficiently without a sound data management system. In particular, there is a need to design and extend the system so that it can effectively manage the within family selection components. There is also a need to consider how EBVs can best be routinely calculated in the medium to long term. ASReml can adequately do this at present, however, most major breeding programs reach a point where they need a more robust and ‘industrial strength’ genetic evaluation system.

7.6 CONCLUSION

A system for a BLUP genetic evaluation has been specified and implemented. This involved recoding all data, estimating genetic parameters, and determining a suitable statistical model. The system developed now calculates EBVs routinely and on an annual basis and has been used for the 2008 and 2009 breeding seasons. This can be done within short time spans due to the data coding systems that have been implemented and due to the sound knowledge of the genetic parameters of the breeding population. The ability to complete this task within a short time span is important because there is limited time between the completion of field assessments and selection of broodstock for the next spawning. The implementation of the BLUP system exceeds the original objectives of this project.

This system will provide significant benefits. The evaluation of genetic merit will be done in a more accurate and robust way. There is now a means to track a genetic trend across year classes and which will provide an accurate and objective assessment of the performance of the breeding program. This system provides a way of integrating the economic breeding objective, as defined by the economic weights, with the selection strategy. A significant change in the breeding strategy has been to manage the breeding population as a single combined population, rather than discrete year classes. This system provides a way of making selections from that combined population. It also provides a way of using all data in selection decisions.

The system of EBVs has been accepted by the hatcheries, whom are the main customers of the ASI breeding program. EBVs have been used to make selections for commercial deployment and, under the current deployment plan forward of projected crosses, they are critical for the decision making process.

Continued development is needed to ensure the needs of the breeding program are met and to ensure the program delivers maximum economic value to industry. Priorities are to develop an understanding of the genetic inheritance of additional traits (condition, survival and uniformity), to incorporate these additional traits into the genetic evaluation system, and to develop a system to record individual records for within family selection.

APPENDIX 7.1
ASReml batch file used for EBV estimation

```
!WORKSPACE S6

ASI Oyster data EBV estimates (Sep 2009 data set)

 Animal 19115 !p
 Sire  191 !a
 Dam  225 !a
 FamID  243 !a
 SpawnRun 2 !a
 PTrial 27 !a
 Cohort 10 !a
 Farm 7 !a
 Unit 1887 !a
 Grade 2 !a
 Len
 Width
 Depth
 Wt_meat
 W_index !*100
 D_index !*100
 Cond
 Len_adj
 Wt_adj
 WI_adj
 DI_adj
 Cond_adj

ASI_Oyster_2009.ped !skip 1 !alpha !make !diag
ASI_Oyster_2009.csv !skip 1 !maxit 1 !nodisplay

Wt_adj Len_adj WI_adj DI_adj Cond_adj ~ Trait Trait.PTrial,
Tr.SpawnRun.Cohort, !r Tr.Unit Tr.Farm.FamID Tr.Sire.Dam Tr.Animal

1 2 4
0

Tr 0 US !+15          !GF
 0.5039
 0.4108       0.6295
-0.2385      -0.0886       0.5463
-0.1547      -0.0109       0.1917       0.5006
-0.0160      -0.0083       0.0133       0.0139       0.5591

Tr.Unit 2
Tr 0 DIAG  0.0647  0.1017  0.0225  0.0249  0.1106 !GF
Unit

Tr.Farm.FamID 2
Tr 0 DIAG  0.0421  0.0415  0.0333  0.0367  0.0752 !GF
Farm.FamID

Tr.Sire.Dam 2
Tr 0 DIAG  0.0018  0.0083  0.0001  0.0182  0.0071 !GP
Sire.Dam

Tr.Animal 2
Tr 0 CORR !+15          !GF
 0.4753
 0.9100       0.2347
-0.7671      -0.3783       0.4634
-0.8697      -0.3383       0.7043       0.5034
 0.3363      -0.0505      -0.3170      -0.3928      0.1902
Animal 0 AINV
```

Chapter 8

Measuring systems

Benjamin Finn and Matt Cunningham

8.1 INTRODUCTION

Data collection is a fundamental component of a selective breeding program. The data is used for the performance evaluation of families (Chapter 7) which, in turn, is used to make selections. Breeding programs require large quantities of data. In the existing ASI breeding program, at least five different measurements are made on approximately 5,000 individuals every year. In the revised breeding program (Chapter 5) this number will double. Breeding programs also require accurate data. The performance evaluations, and therefore the selections, will only be as good as the data on which they are based. When collecting large quantities of data it is essential that systems be developed that ensure data accuracy. The consequence of data errors can either be lost time when data files need manual correction, or inaccurate selections when data errors are undetected.

8.1.2 Need

Current data protocols require large amounts of manual data entry and manual data manipulation. This is inefficient and ASI staff currently spend approximately 20 days per year manually entering data. There is an identified need to expand the family production (Chapters 4 and 5) and more efficient data collection and data loading is needed. In addition, data errors were detected when developing the genetic evaluation system (section 7.2.4) and a significant amount of time was spent correcting these errors.

8.1.3 Objective

The objective of this part of the project was to develop an automated data capture system for the collection and processing of field performance data. Two approaches were evaluated. The first was the use of photographs and image analysis programs for the capture of shape data. The second was the use of electronic measuring equipment capable of directly logging weights and shell length, width and depth data directly to a computer.

8.2 IMAGE ANALYSIS PROGRAMS

8.2.1 Image J

The automated image analysis program ‘Image J’ was evaluated. The aim was to directly obtain shell length, width and depth measurements from photographs. The irregular shape of an oyster has made this difficult.

Image J is a public domain Java image processing program. It can display, edit, analyse and process images. It is able to read different image formats including TIFF, GIF, JPEG, BMP, DICOM, FITS and ‘raw’. It can calculate area and pixel value statistics using user-defined selections and it can measure distances and angles. It supports standard image processing

functions such as contrast manipulation, sharpening, smoothing, edge detection and median filtering.

The ability of Image J to measure images in real units, such as millimetres, was of most interest. Density, or gray scale, calibration is also available for Image J. Here contrasts in colour are used to target objects (in this case oysters) within the image and create a montage (Figure 8.1) from which spatial data can be derived. Custom analysis and processing can be developed using Image J's inbuilt script editor to target particular facets of the imagery analysis (such as length, width and depth).

The main problems that limited the application of Image J were:

1. Physical characteristics of an oyster: Oysters are irregular and jagged by nature and determining a precise, accurate montage is difficult. Photographing oysters on a true vertical plane for depth measures without impacting on the imagery is also difficult. Image J is extremely sensitive to colour changes when analysing the photographs to produce a montage. These problems are fundamentally caused by the morphology and variation in morphology between oysters. This technology is suited for objects that are largely homogenous in colour and shape. Oysters do not fit this description and, consequently, image analysis is unlikely to have application for this purpose.

2. Shadowing: Shadowing and shading occur due to the irregular shape. It was possible to reduce this shadowing using the software features but it was not possible to remove it. A clean, white background, free of shadows, will produce the most accurate results and a quicker processing time. Therefore the camera flash must be used at all times. Photographs taken from directly above minimise shadowing. Image J attempts to separate individual oysters when forming a montage, however, any significant noise (e.g. shadows and marks) can lead to the merging of two (or more) individuals.

3. Light intensity: Image J is highly sensitive to light intensity when analysing batches of photographs taken in the field. Variations in light intensity naturally occur throughout the day due to changes in weather conditions and the positioning/intensity of the sun. These changes require the scripting within the Image J program to be re-written each time a change is detected. Re-writing the script is not difficult, but is time consuming.

Resolving these problems is only likely to provide marginal improvements. Time will still need to be spent formatting and copying measurements from an Image J text file to data files. Data capture systems that can log data directly to a data file are preferred. Therefore the implementation of Image J will not be pursued.

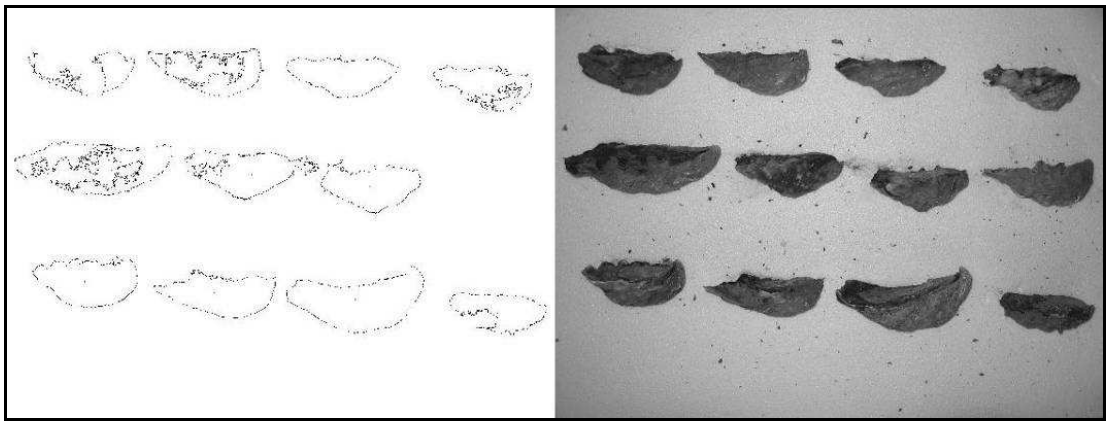


Figure 8.1 Image J montage derived from photograph of oysters.

8.2.2 NiVision

An alternate computer imaging program called NiVision was also trialled. This software also failed to provide reliable data. It was limited by the same problems as were encountered with Image J, which were the irregular shape of an oyster and shadowing. NiVision has been successfully used by the Tasmanian Selected Abalone (TSA) breeding program where length measurements for over five hundred abalone were taken from photographic images. However, abalone have a regular shell shape with a smooth edge. Also no depth measurements were required for the abalone breeding program.

8.2.3 Grab It

If measurement data are required from photographs then the software Grab It is an option. It is accurate, uninfluenced by shadowing and compatible with Microsoft Excel for easy data management. However, it is labour intensive and requires an object with a known size to be in the field of view to obtain a scale. It is also unlikely to be efficient for processing large numbers of photographs.

Grab It is useful for measuring multiple objects within a photograph. Point-to-point measuring is used to produce a length measurement (after setting the scale). Grab it is the only imagery software trialled where depth measurements were possible. This was because props used to hold the oysters vertically did not impact on the accuracy of the depth measurement. The major advantage of this system is its simplicity and that multiple measurements can be taken from the one image. Grab It is uncomplicated to navigate and relatively easy to check for human error.

8.3 ELECTRONIC DATA COLLECTION SYSTEM

An electronic data capture system has been developed and successfully implemented. This system uses an electronic balance to measure weights and electronic callipers to measure shell dimensions. Both log directly to a laptop computer. The system hardware is illustrated in Figure 8.2. Data is logged into an Excel file, and the standard file template used is illustrated in Figure 8.3.

This system was used for the progeny trial measurements in 2009 and has demonstrated both increased efficiency and increased accuracy. Previously upon returning from the field, manual data entry has taken at least two days per site to complete. With this system data processing can be completed in less than one hour for each progeny test site. This system has been designed to be applicable to all facets of ASI's field work and is easily re-formatted to accommodate future year classes.

8.3.1 Electronic weight capture

Weight data is collected at the start, middle, and end of the family performance trials. In the past a basic set of bench scales has been used and results scribed onto data sheets. The 2007 AusIndustry grant allowed the purchase of new equipment for more efficient and accurate data collection. This included the purchase of a NUWEIGH JAC 828 balance which has a data output cable for transferring data directly to a computer.

The advantages of the new system are:

- Increased reliability of data (no errors from scribing)
- Increased efficiency
- 'One-touch' data capture
- Data logged directly into Microsoft Excel format.

A computer software program 'Winwedge' has allowed easy transfer of data from the balance directly to Microsoft Excel. Without this software, data is logged as a text file and must be manually transferred into Excel. The ability to write directly to Excel reduces the time spent formatting data and reduces the capacity for errors when manually transferring data.

8.3.2 Electronic callipers

The collection of shape data is a routine part of the measurement program and there is an ongoing need to collect data on shell length, width and depth. Electronic callipers provide a way to collect this data accurately and quickly. Previously, measurements had been made with manual Vernier callipers. The electronic callipers provide a means of logging data at the push of a button. This eliminates errors involved with manually reading and transcribing data. It is also far quicker. It was hoped that this system could be operated by a single person. However, a second person is required to ensure calliper measurements are accurate and are logged correctly.

Mititoyo callipers are being used. A variety of products were trialled. Most would only run via custom made company software packages which made it difficult to directly log data into a Microsoft Excel. The Mititoyo callipers log data directly into Excel eliminating the need for transferring text from one format to another. Directly logging of the data reduces data entry time. A disadvantage with the Mititoyo callipers is their incompatibility with the software Winwedge. This means that the operator needs to manually move to a new row after completing measurements on an individual animal. The electronic callipers are waterproof, which is essential and given the work environment. However, regular lubrication, maintenance and cleaning is essential.

Figure 8.2 ASI's electronic data capture system

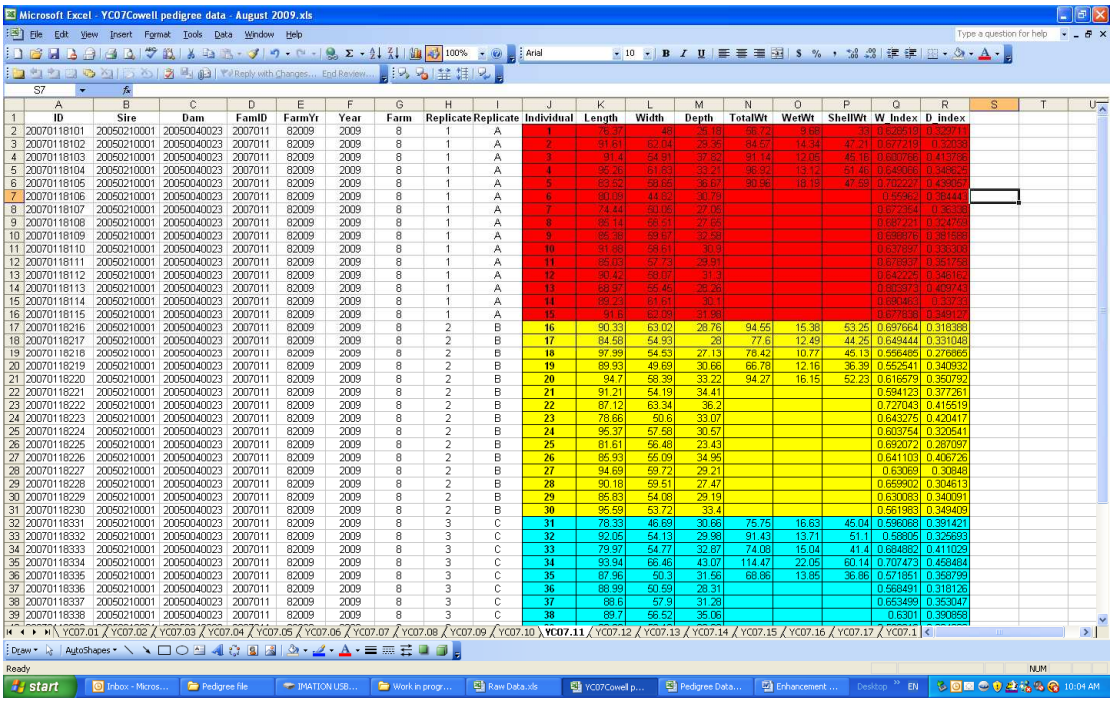


Figure 8.3 Screen-shot of the Microsoft Excel data collection template.

8.3.3 Data processing

The database (Chapter 9) has been designed to be compatible with the field data collection system. Field data will be converted to a standard file format and loaded directly into the database. All data will be loaded as a file to ensure complete traceability of data. No keyboard entries into the database are permitted. The standard file will be a .csv file (and easy and standard conversion from an Excel format) and will have the following fields that ensure all data is unambiguously identified:

- Unit, or basket, number (a prior database load will have placed a record of family identity against each unit number)
- Progeny test site
- Individual number (a sequential count of each measured individual in each unit)
- Trait code (such as WT for weight and LEN for length)
- Date (the date on which field measurements were done)

On loading, there will be a series of data checks to ensure data is 100% accurate. If errors occur the file load will be stopped to allow errors to be corrected.

8.3.4 Photographic archive

A photographic archive of all families is being developed. The aim is to photograph each family four times (spat, 6 months, 12 months, and 18 months) at each progeny test site. The reasons for this are to:

- Provide commercial hatcheries with a visual record of the stock across different growing sites throughout time. This will be used to support EBV data and give hatcheries greater confidence when selecting families for commercial deployment.
- Allow ASI to retrospectively identify any important traits or characteristics that are not recorded through data measurements.

- Provide a means of checking for the presence of visual characteristics that may be undesirable. Although EBVs are used for selection decisions, there will be traits that are not measured and these traits will not have EBVs.

The photographic archive is stored on an external hard drive with a backup that is kept off-site. It is easily transportable and accessible when in the field. The catalogue of images proves useful when visually gauging growth since the last stock handling and when promoting the breeding program to growers.

8.4 FUTURE DEVELOPMENT

As more traits and different measurement methodologies are developed the measuring systems will need to be updated. It is expected that these will be able to be included as part of the current system and should not require a complete redesign of the system.

8.5 CONCLUSION

The data capture system developed has resulted in increased efficiency and accuracy of data collected for the selective breeding program. Image analysis methods for the collection of shape data were evaluated but these proved unsatisfactory. The system adopted is one using electronic callipers and balance to log directly to a laptop computer with data templates. A photographic record of families is also kept. The data system has substantially reduced the time required to collect and process data and will enable the collection of data on 50 families without sacrificing data accuracy or increasing the resources required for this task.

Chapter 9

Specification of a database for the ASI breeding program

Peter Kube and Matthew Hamilton

9.1 INTRODUCTION

Data is integral to a selective breeding program. Selective breeding programs generate large quantities of data on an ongoing basis. This is predominantly records of pedigrees and records of performance. Together with the breeding animals, data forms the core intellectual property of a selective breeding program. The loss of either will result in a failed program. For the data, 'loss' may include the inability to access the data in time to meet biological deadlines, and failure to trust the accuracy of archived data. Therefore it is essential that a system be developed to ensure the data is secure, data is accurate, and data can be accessed in a timely and easy manner.

ASI does not have a data management system. Data has been collected over 10 years, and there are now large quantities of data representing a large investment and a valuable resource. This data has not been systematically stored and is held in different formats. Data collected in the early years of the breeding program is in danger of being lost as personnel change. There is, therefore, an urgent need to develop a data management system. This need is heightened by the approach now being taken for the genetic analysis (see Chapter 7) where there is a reliance on data records from all year classes.

9.1.1 Objectives

The objective of this part of the project was to develop the first stage of a database. Specifically, the aims were to:

- Develop and specify a database design suited to the specific needs of the revised ASI breeding program.
- Implement that design to the point where the majority of historical data could be loaded and stored in a secure way and where data could be output to meet the routine needs for genetic analysis.

It is accepted that the database will need ongoing development. This will include the ongoing checking and fixing of flaws in the initial design, inclusion of additional load features, and the design of more streamlined data outputs.

9.3 DATABASE DESIGN

The approach taken has been to develop a purpose built database to suit the workflow and design of the ASI Pacific oyster breeding program. The two main principles have been to:

- Provide software to enhance the decision making process, not to make decisions
- Design software that is adapted to the needs and activities of the user, not software that dictates changes in work activities

9.3.1 Intended users

The main users of the database will be ASI, who are the breeding program staff. They are responsible for the selective breeding activities and, therefore, are responsible for the data collection and data management. These users will need access to the database on an ongoing and regular basis. They will be responsible for uploading of the data and will also have the capacity to run customised reports associated with regular events.

The provider of genetic evaluation services (i.e. the person calculating estimated breeding values) will also be a regular user. Typically, this will require an annual download of all measurement and pedigree data, and an upload of estimated breeding values.

Another group of possible users are those involved with managing research projects associated with selective breeding. Both researchers and ASI would benefit from systematic and safe data storage.

9.3.2 Software and hardware

The software used for the database is Oracle and the database will be programmed using PL/SQL. The database is housed on a CSIRO server (in Hobart) and is accessible to breeding program staff and any other remote users via an internet browser and high speed internet connection. The web interface uses Oracle Application Express, which requires no software to be loaded by the user.

The database needs to be managed and maintained by a database administrator, who is a trained database specialist. The database administrator will be responsible for providing user assistance via phone or email. Documentation has been prepared that gives detailed user instructions, fully describes the database design, the lists the specific data checks done at loading (not shown here).

9.3.3 Database design principles

The key principles that influence the database design are as follows:

- Database inputs are ‘EVENT driven’. Data is generated when something is done to the breeding population (such as a fertilisation, measurement or animal movement) and this is described as an ‘EVENT’.
- These events determine the type of data captured and the way it is loaded into the database. Each EVENT generates a unique set of data, and the data generated by that EVENT has a standard format.
- In practice, events follow a logical sequence (e.g. families must be fertilised before individual family members can be measured) and data loads must occur in that same sequence.
- Individual animal records are the basis of the data. However, the breeding strategy does not involve individual animal tagging and it is not possible to follow repeated records of the same individuals. The oyster growing baskets, termed ‘units’ in the database, are the lowest order repeated measure. Every unit has a unique number.
- All data is loaded as a file, and the file load associated with every data record is maintained by the database. No keyboard entries into database tables are permitted. If errors are detected, then the file is rolled-back, amended, and reloaded.

9.3.4 Categories of records

The main data categories in the database are as follows:

1. **Spawn Run:** A spawning event that occurs over a short period of time (e.g. one or two days). All families must be assigned to a spawn run.
2. **Year class:** A group of animals all fertilised in the same spawning season. A year class will be created annually and every family must be assigned to a year class. A year class is defined by the beginning of the summer (e.g. a spawning in January 2009 is defined as the 2008 year class).
3. **Family:** A full-sib family (i.e. both parents are known).
4. **Individual:** A single animal from a known unit. Individual animals are not usually tagged but an operational identity can be entered for an animal if required.
5. **Site:** A site where animals are spawned, progeny tests are conducted and/or broodstock are held.
6. **Unit:** A vessel containing animals from a single family. Units may be nursery tanks, progeny test units, broodstock holding tanks, conditioning tanks etc.

9.3.5 Hierarchy of inputs

Events have a hierarchy and must be entered in a particular order. Events lower in the hierarchy cannot be entered until those above have been entered. For example, before measurement data can be loaded, it is necessary to enter details of the unit the animals reside in through the EVENT 'Define Unit'. Figure 9.1 shows the hierarchy of events and the standard database inputs are as follows:

1. EVENT 'Input Founder'
2. EVENT 'Define Fertilisations'
3. EVENT 'Define Site'
4. EVENT 'Define Unit'
5. EVENT 'Input Trait Descriptor'
6. EVENT 'Input Unit Measurement'
7. EVENT 'Input Individual Measurement'
8. EVENT 'End Unit'
9. EVENT 'Input Selection Measurements'
10. EVENT 'Input EBVs'
11. EVENT 'Input Activity Details'

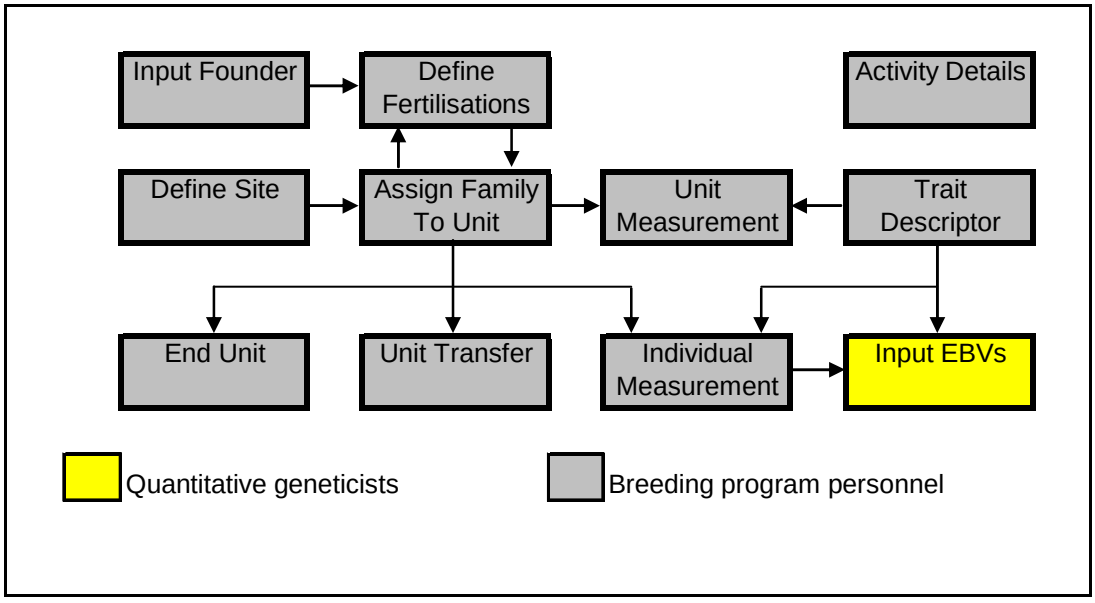


Figure 9.1 Flow chart showing the order of data generating events of the selective breeding program. In practice, these events occur in a specific order and the data must be loaded into the database in that order.

Table 9.1 Summary of database tables

Table Name	Data Stored	EVENT loading data
LOADED_FILES	Details of the files uploaded to the database	All events - details are automatically recorded whenever data are uploaded
FAMILY	Family Dam and Sire	Define Fertilisations
SITE	Site ID and description	Define Site
UNIT	Unit ID, Family ID and description	Define Unit OR Selected Animal Transfer OR End Unit
INDIVIDUAL	Individual animal data	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurements
FOUNDER	Species, source and comment on founder	Input Founder
TRAIT_DESCRIPTOR	A description of each selection trait (i.e. measured traits) and objective trait (i.e. traits for which EBVs are calculated)	Input Trait Descriptor
MEASUREMENT_UNIT	Measurement data for units by trait and date	Input Unit Measurement OR Selected Animal Transfer
MEASUREMENT_INDIV	Measurement data for individual animals by trait and date	Input Individual Measurement OR Selection Measurement
ACTIVITY	Diary of all activities done in association with the breeding program	Input Activity Details
EBV	EBV data for individuals	Input EBVs

9.3.6 Database tables

Input data are stored in 11 database tables, which are briefly describe in Table 9.1. All data are entered into these tables by loading files and no data is ever loaded via keyboard entries. As data are loaded, the following actions occur:

- data checks are made (described in the database manual)
- the details of the load file are recorded, including the user, date, time and file name
- a reference to that file is held against every data record to enable checks of the source individual data records and roll-backs of data records if errors of found (database procedures have been written to automatically perform file roll-backs)

Data are loaded into the database as comma separate values (CSV) files. Such files are most easily created in a spreadsheet application such as Microsoft Excel but, once created, they can be viewed in a standard text editor, such as Microsoft Notepad, for error checking purposes.

A conceptual schema of the database, which defines the relationships between tables and their fields, is shown in Appendix 9.1.

9.3.7 Data formats

Categories of records are encoded in a specific way (Table 9.2). This ensures there are no ambiguities between records. For example, a family record can never be confused with an individual record, which can never be confused with a unit record. Some categories of records are assigned by the user and others by the database. Those which are assigned by the user are checked by the database to ensure they are valid (suitable format and not already used).

Table 9.2 Data formats for important data categories

Category	Field name in table	Description	Type	Format	Example	Assigned by
Year class	YEAR_ CLASS	Fertilisations in same spawning season. Founders assigned to 1990YC	4 digit number	| YC | |_ _ _ _|	2008	User
Spawn run	SPAWN_ RUN	Hatchery run when family fertilised.	6 digit number	| YC | count | |_ _ _ _|_ _ |	200802	User
Site	SITE_ID	Site/farm on which animals are held	Up to 2 digit number	| count | |_ _ |	03	User
Unit	UNIT_ID	Typically a basket containing a family	10 digit number (count unique within site & YC)	| YC | SITE | count | |_ _ _ _| _ _ |_ _ _ _ |	200501001	User
Family	FAMILY_ ID	A group of full-siblings.	7 digit number, 0 for unknown	| YC | count | |_ _ _ _ |_ _ _ |	20080012	User
Individual	INDIV_ID	Single animal	10 digit number	| YC | count | |_ _ _ _|_ _ _ _ _ _ |	2008000123	Database

9.4 FUTURE DEVELOPMENT

The work completed represents the first stage of the database development. The future developments that are necessary are to:

- Design and implement a system that allows recording of within family selection of broodstock. Currently, the breeding program tracks records of family selection, but does not record individual records for within family selection.
- Design and implement data output features that streamline the genetic evaluation process.

- Identify and design data output features that assist with the day-to-day management of the breeding program.
- Identify and source all historical data from the breeding program and implement a process of getting this data systematically loaded into the database.
- Implement a feature that allows ASI to obtain a complete backup of all data tables, on demand, that can be stored independently of the CSIRO system.

9.5 CONCLUSION

A data management system that is tailored to the ASI breeding program has been designed and implemented. This will ensure all future pedigree and performance data is recorded in a systematic, accurate, and secure way. It will make the data management aspects of the breeding program more efficient, thereby saving time for those involved with data management aspects of the breeding program. And it is an important component in facilitating the move to the BLUP based genetic evaluation process.

There are still developments needed to complete and streamline the system. The most important of these are the recording of within family selection and the data reporting.

APPENDIX 9.1
Conceptual schema of the database

LOADED_FILES			
FK	**FILE_ID**	Integer	All events
	FILENAME	Text	All events
	USER_NAME	Text	All events
	OPERATION	Text	All events
	DOCUMENT	Text	All events
	DTTM	dd/mm/yyyy	All events

FAMILY			
FK	**FAMILY_ID**	Integer	Define Fertilisations
	SIRE_INDIV_ID	Integer	Define Fertilisations
	DAM_INDIV_ID	Integer	Define Fertilisations
	YEAR_CLASS	Integer	Define Fertilisations
	COHORT	Integer	Define Fertilisations
	SPAWN_RUN	Integer	Define Fertilisations
	FERT_DATE	dd/mm/yyyy	Define Fertilisations
	FAM_COMMENT	Text	Define Fertilisations
FK	**FILE_ID**	Integer	Define Fertilisations

SITE			
FK	**SITE_ID**	Integer	Define Site
	SITE_NAME	Text	Define Site
	LOCATION	Text	Define Site
	COMMENT	Text	Define Site
	OWNER_DETAILS	Text	Define Site
	OWNER	Text	Define Site
FK	**FILE_ID**	Text	Define Site

UNIT			
FK	**UNIT_ID**	Integer	Define Unit
FK	**FAMILY_ID**	Integer	Define Unit
FK	**SITE_ID**	Integer	Define Unit
	UNIT_REP	Integer	Define Unit
	UNIT_TYPE	Text	Define Unit
	UNIT_COMMENT	Text	Define Unit
	START_DATE	dd/mm/yyyy	Define Unit
	END_DATE	dd/mm/yyyy	End Unit
	END_NOTICE	Text	End Unit
FK	**FILE_ID_NEW**	Integer	Define Unit
FK	FILE_ID_END	Integer	End Unit

INDIVIDUAL			
FK	**INDIV_ID**	Integer	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement
	OPERATIONAL_ID	Text	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement
FK	**UNIT_ID**	Integer	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement
	DATE	dd/mm/yyyy	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement
	SEX	Text	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement
	COMMENT	Text	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement
FK	**FILE_ID_NEW**	Integer	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement
FK	FILE_ID_SEX	Integer	Define Fertilisations OR Input Founder OR Individual Measurement OR Selection Measurement

FOUNDER			
FK	**INDIV_ID**	Integer	Input Founder
	SPECIES	Text	Input Founder
	LOCATION	Text	Input Founder
	DETAILS	Text	Input Founder
FK	**FILE_ID**	Integer	Input Founder

TRAIT_DESCRIPTOR			
FK	**TRAIT_CODE**	Text	Input Trait Descriptor
	TRAIT_DESC	Text	Input Trait Descriptor
	UNITS	Text	Input Trait Descriptor
	METHOD	Text	Input Trait Descriptor
	MIN_VALUE	Number	Input Trait Descriptor
	MAX_VALUE	Number	Input Trait Descriptor
	VAR_TEST	Y/N	Input Trait Descriptor
FK	**FILE_ID**	Integer	Input Trait Descriptor

MEASUREMENT_UNIT			
FK	**UNIT_ID**	Integer	Input Unit Measurement
FK	**TRAIT_CODE**	Text	Input Unit Measurement
	MEASURE_DATE	dd/mm/yyyy	Input Unit Measurement
	RESULT	Number	Input Unit Measurement
	COMMENT	Text	Input Unit Measurement
FK	SELECT_DATE	Integer	Selected Animal Transfer
FK	**FILE_ID**	Integer	Input Unit Measurement

MEASUREMENT_INDIV			
FK	**INDIV_ID**	Integer	Input Individual Measurement OR Selection Individual Measurement
FK	**TRAIT_CODE**	Text	Input Individual Measurement OR Selection Individual Measurement
	MEASURE_DATE	dd/mm/yyyy	Input Individual Measurement OR Selection Individual Measurement
	RESULT	Number	Input Individual Measurement OR Selection Individual Measurement
	COMMENT	Text	Input Individual Measurement OR Selection Individual Measurement
FK	SELECT_DATE	Integer	Selection Individual Measurement
	SELECTED	Y/N	Selection Individual Measurement
FK	**FILE_ID**	Integer	Input Individual Measurement OR Selection Individual Measurement

ACTIVITY			
	YEAR_CLASS	Integer	Input Activity Details
	ACTIVITY	Text	Input Activity Details
	START_DATE	dd/mm/yyyy	Input Activity Details
	END_DATE	dd/mm/yyyy	Input Activity Details
	STAFF	Text	Input Activity Details
	DETAILS	Text	Input Activity Details
FK	**FILE_ID**	Integer	Input Activity Details

EBV			
FK	**FAMILY_ID**	Integer	Input EBVs
FK	**TRAIT_CODE**	Text	Input EBVs
	PERCENTILE	Integer	Input EBVs
	EBV_DATE	dd/mm/yyyy	Input EBVs
	RESULT	Number	Input EBVs
FK	**FILE_ID**	Integer	Input EBVs

The primary key is the unique identifier in each table. It may be a single data field or a combination of data fields. In the schema shown here, the primary key is defined by the data fields in the top portion of the box (down to the line dividing the box).

FK = foreign key. A foreign key is a data field in one table that matches and can be linked to a data field in another table.

Chapter 10

Benefits and adoption

This project will benefit the Australian Pacific oyster industry by providing a selective breeding program that reduces the cost of oyster production. All project outputs have been adopted and included in the Australian Seafood Industries (ASI) selective breeding program. Therefore the flow of benefits to industry is assured.

Five genetic traits that influence the cost of production have been identified. With current knowledge, the breeding strategy can select for three of these traits. This selection strategy is expected to reduce the cost of production by 2% every year. This represents a cost saving of $0.07 per dozen per year. At current production levels and industry uptake of ASI material, this will provide the industry with an annual and ongoing benefit that will accumulate at the rate of $200,000 per year.[5] This project has identified two additional traits that need to be included into the breeding objective. When selecting on these additional traits, the breeding strategy is expected to reduce the cost of production by 4% every year, or by $0.16 per dozen per year.

This project also guarantees the sustainability of the selective breeding program. A breeding strategy has been chosen that can safely manage the conflicting needs of selecting to make rapid genetic gains against maintaining diversity to avoid inbreeding and provide the opportunity for gains well into the future. In adopting this approach, the ASI breeding program is contributing to the long term sustainability of the Australian Pacific oyster industry.

The hatchery and measurement systems developed as part of this project have also been adopted by the breeding program. They are integral to providing a practical way of implementing the revised breeding program with the resources available.

Adoption of a new breeding strategy which directly caters for the requirements of commercial hatcheries has been a major catalyst for increasing the flow of benefit to industry. The adoption of this strategy by the commercial hatcheries has resulted in successful production of ASI commercial lines in the first season. As a result, commercial sales of Thoroughbred oyster seed have doubled over the last 12 months (from 2008/09 to 2009/10). ASI is now poised to be able to take advantage of the rapidly increasing grower demand for this product. The formation of the Hatchery Reference Group has strengthened ASI's commercial relationship with Australia's two largest bivalve hatcheries, Shellfish Culture and Cameron of Tasmania. The commercial hatcheries have been satisfied that Thoroughbred spat offers no significant commercial risk to their businesses. This has been a large step forward for the breeding program and the industry.

These advances, coupled with increasing grower demand for Thoroughbred families, should see increased industry benefit from this project.

[5] Industry benefit calculation assumes total output is 14.3 million dozen per year (ABARE 2008) and industry uptake of ASI Thoroughbred stock is 20%.

Chapter 11

Conclusion

The overall goal of this project was to revise, or to enhance, the ASI breeding program to ensure that it delivers economic value to the Australian Pacific oyster industry. This goal has been achieved. Substantial revisions have been made to the breeding strategy and these have been adopted and implemented in the tactical plans of the breeding strategy. The objective of the breeding program is now firmly focused on decreasing the cost of production of oysters. Economic benefits will be, increasingly, realised by the industry as selectively bred oysters (marketed as Thoroughbred oysters) are produced by growers.

Prior to this project, there had been difficulties in defining a clear breeding goal. This occurred because the Pacific oyster production system is relatively complex and intuitive decisions about the relative trait weightings did not necessarily give good economic outcomes. The problem was successfully addressed using an economic approach to objectively identify the important biological traits and calculate their economic value. There are still knowledge gaps in understanding the way in which biological traits influence profit, however, processes have been developed to address these gaps and systems implemented to allow easy integration of new information to fine-tune the breeding objective. The breeding objective is defined in terms of cost of production for an oyster grower and, therefore, does not consider consumer preferences. Given that oysters are essentially a luxury item, this may be a limitation and is an area requiring research.

The breeding strategy used by ASI had been small and simple. It appropriately represented the resources available to that program up to that point. However, there was a desire to accelerate gains and concerns had been expressed about the sustainability of the breeding strategy. In addition, the work done on economic breeding objectives and difficulties with commercial deployment highlighted the need for a revised strategy. Stochastic computer simulations were used to explore breeding options. This process simulated what had been done and what could be done in an exact way. Through this process a suitable strategy was identified and adopted. The simulations allowed the future population size, structure and selection strategy to be defined in a precise way. The breeding program is able to proceed with the knowledge of what genetic gains are likely and with the knowledge that genetic diversity will be sufficient to allow ongoing gains without the risk of inbreeding.

A direct flow on from the revised breeding strategy has been the need for new systems to support the breeding program. There were four main components to this, all of which have been successfully implemented. The first is a new nursery system capable of producing an expanded population (of 50 families annually). The system adopted is an ultra high density larval rearing system (the New Zealand Cawthron system). The second is an updated genetic evaluation system that provides more accurate selections, allows a move to a different population structure (a single population rather than discrete year classes), and allows selections for the new commercial deployment system (based on prediction of forward selections). The system adopted is one that calculates estimated breeding values using BLUP methodology. The third system is electronic data collection for field measurements. Data is now directly logged to computers allowing the field measurement program, which is now doubled in size, to be achievable with no extra resources. The fourth system is a new database. This has been specifically designed to meet the needs of the new breeding strategy.

It is also sufficiently flexible to meet any changing future circumstances. The system work is ongoing. There will be additional development work on the database, and a mate allocation system needs to be developed.

Significant changes have been made to the commercial deployment strategy. These have been possible due to the revised breeding strategy. The previous commercial deployment system was based on the use of four year old broodstock. This caused difficulties with conditioning and spawning in commercial hatcheries and locked-in a breeding strategy that was sub-optimal. The new commercial strategy uses forward selections (selections from the most recent progeny trial). This allows commercial hatcheries to use younger broodstock (two year old), allows much larger numbers of broodstock to be provided to hatcheries, and provides a vastly greater number of commercial selection options through the use of estimated breeding values to 'design' commercial lines.

This project has clearly identified the future research needs for the selective breeding program. Firstly, there is a need to expand knowledge of the genetic control of conditioning (which is the marketability of the meat). Secondly, there is a need to fully understand the genetic control of survival and determine how this can be included into the breeding strategy. And thirdly, there is a need to develop and understanding of uniformity in growth rate, determine if there is a genetic basis to this, and identify other options for managing this trait.

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Appendix 1 Intellectual property

The prior intellectual property that project partners brought to this project is:

1. The breeding population animals, the pedigree records and the performance data relating to those animals; owned by Australian Seafood Industries P/L (ASI).
2. Computer code for strategy simulations; owned by CSIRO
3. Underlying computer code for the database; owned by CSIRO.

The intellectual property arising from this project is:

1. Economic weights for the Pacific oyster breeding program
2. Breeding strategy for Pacific oysters
3. Database schema design for the ASI breeding program

The intellectual property arising from this project that is not jointly owned by all project partners is:

1. The breeding population animals, the pedigree records and the performance data relating to those animals generated during the life of this project; owned by ASI
2. Economic weights spreadsheet calculator; owned by CSIRO and ASI
3. Business Plan for ASI; owned by ASI

Appendix 2 Project staff

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