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**Genetic Improvement in a Texel
Breeding Operation: A case study
&
Maximising Pedigree Accuracy for
Genetic Gain: A comparison of DNA-
assigned parentage and lambing book
assigned parentage**



A report prepared on behalf of

Landcorp Farming Limited

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Genetic Improvement in a Texel Breeding Operation: A case study
&
Maximising Pedigree Accuracy for Genetic Gain: A comparison of
DNA-assigned parentage and lambing-book assigned parentage

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Abstract

There were two main aims to this research. The first was to carry out an investigation of the genetic gain of Landcorp Farming Limited's Waikite Texel breeding operation. This was in order to identify factors that may have been limiting ΔG and the financial return of the system and make recommendations for improvement.

It was found that the achieved mean ΔG of 33¢/ewe/year was less ($P < 0.05$) than that predicted for the Innervalue Fat Index at 97¢/ewe/year. Financially the system was found to have made a net return over the course of the studied period; however, this was less than what was predicted as possible. The main cause of this shortfall was the majority of genetic selection being imposed on live-weight BVs rather than Index values. This investigation also found that there was little room for improvement in the ewe and ram generation intervals with hogget mating and maintenance of current levels being recommended for L. While the ram selection intensity had little room for improvement, the ewe selection intensity did and this is achievable by imposing less selection pressure on structural traits and more on genetic merit.

The second aim of this research was to compare lambing-book dam records and DNA-assigned dam records in order to identify management practices that would target the minimisation of pedigree identification error. Triplets and lambs born to older dams were found to be the groups most at risk of having incorrect lambing-book data, while singles had a lower mean probability that the DNA identified dam was correct.

Although DNA parentage testing was not found to financially benefit a system, it did offer the opportunity to reduce pedigree error through the use of a variety of practices. These practices include: single sire mating of ewes, lambing ewes in mobs of equal or near equal proportions from each sire group, lambing in mobs based on scanning rank, carrying out two or more checks per day on ewes during lambing, and increase the number of markers used in the DNA parentage assignments of groups most at risk from incorrect parentage assignment if financially feasible.

Preface

The figures presented in this research are estimates only and intended to give a guide to improving system management rather than being exact performance figures. They should therefore be used accordingly.

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Chapter 1 Introduction

New Zealand has long been recognised as a world leader in pastoral agriculture (Morris, 2008) and in 2009 agriculture was reported to contribute 12% to New Zealand's annual GDP (Ministry of Agriculture and Forestry, 2010b). An important part of New Zealand agriculture is the sheep production sector which, in 2009, produced lamb exports to the value of NZ\$2.57 billion (Ministry of Agriculture and Forestry, 2010b). A key feature of the sheep industry over the last 20 to 30 years has been the increase in production per head.

Between 1984 and 2010 there was a 53% decrease in breeding ewe numbers (from 70 million down to 32.6 million) (Statistics New Zealand, 2010). Despite this, lamb production decreased by just 14% (from 375,000 tonnes in 1984 down to 323,000 tonnes in 2010) (Statistics New Zealand, 2010). This was a result of an increase in production per head with Davison (2000) reporting that, in 1986/87, the average carcass weight of lambs was 13.2kg and the national average lambing percentage was 98% and by 1990 these values had increased to 16.5kg and 114% respectively (Davison, 2000). Morris (2008) reported that as of 2008, these averages increased further still to 17.5kg and 121% respectively. Such gains have been the result of improvements in both genetics and management practices (Davison, 2000; Morris, 2008). Nevertheless, Morris (2008) reported that the productivity and efficiency of New Zealand agriculture needs to continue to improve in order for New Zealand to remain competitive on the world market. Genetic improvement is a tool that has been, and can continue to be, utilised to achieve this. High levels of efficiency and accuracy are important in achieving such gains but, in order for this efficiency and accuracy to be achieved, it is important that those making on-farm management decisions are aware of levels of performance and how specific management practices can be utilised to optimise rates of gain.

Chapter 2 Literature Review

Harris & Newman (1994) listed four main components needed by an industry in order to carry out effective genetic improvement programs. These were: a structure that allows dispersal of genes from the nucleus to the commercial sector; a computer database and the capacity to carry out complex statistical procedures; economic breeding objectives that target improved returns of a nucleus system and its commercial farming clients; and a testing and selection scheme for traits of economic importance targeting optimum genetic gain. The first two requirements are initialised and run by the industry whereas the later two take place on an individual farm level.

2.1 Sheep Industry and Genetic Improvement

2.1.1 Industry Structure

Livestock breeding industries commonly consist of a nucleus breeding sector and commercial production sector, sometimes with a multiplier tier in between the two (Blair & Garrick, 2007). The New Zealand sheep industry commercial sector was reported by Garrick et al. (2000) to hold around 98 – 99% of the total sheep numbers with the remaining 1 - 2% present in nucleus or multiplier flocks. The nucleus sector carries out genetic improvement while the commercial farmers enable the industry effect of this genetic gain to be realised financially (Blair & Garrick, 2007). This is achieved with the purchase and utilisation of high genetic merit breeding stock in commercial systems to produce improved offspring on a commercial scale (Blair & Garrick, 2007). In the sheep industry, this genetic improvement is generally passed along to the commercial sheep farming sector in the form of ram sales (Garrick et al., 2000; Amer et al., 2007). The benefits of this improvement to commercial farmers will therefore be related to the rates of gain being achieved by nucleus breeders.

Rams are typically sold at the age of two or three years old if they are not selected to be used for breeding in the stud flock. Rams of the highest genetic merit are commonly selected and used as nucleus sires before being sold as mixed age rams. Because of this there is a lag between the realisation of genetic improvement in the nucleus flock and this

improvement being passed onto the commercial flock which is commonly twice the generation interval (Blair & Garrick, 2007).

Sometimes there is a shortage of high genetic merit rams and demand from the commercial sector cannot be met, or these rams are simply too expensive for many commercial farmers to purchase (Blair & Garrick, 2007). In such cases, multiplier flocks act between the nucleus and the commercial sectors by purchasing high genetic merit stock and multiplying numbers through breeding (Blair & Garrick, 2007). This practice does however, increase the genetic lag which can extend to as much as four times the generation interval (Blair & Garrick, 2007).

Benefits of genetic gain in the nucleus are only available to the industry as a whole with this diffusion of improved genetics from the nucleus through to the commercial sector (Harris & Newman, 1994). Rather than all the nucleus flocks carrying out genetic improvement programs however, Garrick et al. (2000) estimated that only 10% of nucleus flocks contribute to the genetic improvement achieved by the industry. For genetic improvement to be realised in an industry it is essential that animals in the nucleus flock are genetically superior to those of the commercial and multipliers flocks (Rae, 1964) and that genetically superior sires are purchased by commercial farmers (Amer et al., 2007).

2.1.2 Sheep Improvement Limited

Genetic gain in the New Zealand sheep industry is largely facilitated by Sheep Improvement Limited (SIL) which provides a national database for sheep genetic improvement (Geenty, 2000). SIL is a farmer owned system that stores genetic and phenotypic data which enables the calculation of BLUP breeding values and genetic trends (Newman et al., 2000). Geenty reported in 2000 that there were 300 flocks in the SIL database. In 2009 this had risen to over 1000 (Young & Wakelin, 2009). Of these, 740 were carrying out performance recording while a little over 300 flocks only recorded flock pedigrees (Young & Wakelin, 2009).

In New Zealand, investment into genetic improvement in the sheep industry nucleus was reported by Amer (2009) to be substantial "...by a wide range of public and private entities...". The performance of flocks part of genetic improvement programs varies widely with Amer (2009) reporting that, of the flocks within the SIL system from the 2007 Advanced

Central Evaluation (SIL - ACE), a small proportion of high genetic merit flocks were achieving high levels of index gain (150¢ or more per year) and continuing to make improvement in SILs terminal and dual purpose indices. These were considered leading flocks and were trailed by the majority of the flocks achieving at average, or just below average, genetic gains (around 50¢ per year) (Amer, 2009). This author does however, state that these results do not completely represent the ram breeding industry and that selection based upon physical characteristics remains a prominent factor in achieving less than optimal gain in genetic improvement systems.

2.2 On Farm Genetic Improvement

In the past, it has been common for commercial farmers to use subjective measurements when purchasing breeding rams (Simm, 2000; Amer et al., 2007). Nonetheless, the physical appearance of an animal is the result of both its genotype and the environment it is produced, and lives, in (Lynch & Walsh, 1998; Simm, 2000). Thus, under this type of selection, animals reared in favourable environments are selected over those from less than optimum environments, potentially overlooking animals that are genetically superior for targeted production traits (Hazel, 1943). Continuous phenotypic selection will result in a degree of genetic improvement due to the additive genetic contribution to the trait, known as the heritability, which is inherited from the parents (Hazel, 1943) however; this form of selection is not the most efficient means of livestock improvement. Improvement of performance by genetic selection will give cumulative benefits (Davison, 2000) that have the ability to be expressed in different production systems every year given sufficient environmental resources (Wright, 1939; Beilharz, 1998).

Carrying out genetic improvement of a system involves the selection of genetically superior animals to pass on genes to the next generation (Morris, 1980). Genetic gain in a system will act to improve system efficiency and productivity even though achieving high rates can be expensive (Blair & Garrick, 2007). The incentive to breeders to carry out this genetic improvement is mainly in the form of financial return from additional production and the sale of high genetic merit rams to the commercial sector (Harris & Newman, 1994). Despite this, Garrick et al. (2000) reported that, in the New Zealand sheep industry, there is a gap

between the genetic merit of rams being sold and the price that is received for them. Return on investment from genetic improvement is an important factor determining industry use and development of genetic gain technologies. On an industry scale, Amer (2009) reported that the costs incurred when achieving genetic improvement will generally be outweighed by industry benefits. Nevertheless, the costs and benefits realised on an individual farm scale will be an important factor determining the investment into, and utilisation of, new and existing technologies and improved selection programs, and thus the level of genetic gain achievable.

Breeding scheme design is limited by the mating ratios and reproductive rates of livestock as well as the specific traits in which improvement is desired (Harris & Newman, 1994). These factors contribute to the need for many genetic improvement programs to balance the components of genetic gain in order to optimise, rather than maximise, rates being achieved (Garrick et al., 2000). This optimal genetic gain will be unique to each system depending on what is considered acceptable management practice and financial performance.

2.2.1 Breeding Objectives

The breeding objective or breeding goal of a genetic improvement system is a list of traits in which improvement is desired although; some traits of preference of the individual farmer may also be included (Simm, 1994; Blair & Garrick, 2007). Traits selected are commonly those which will directly affect the income and expenses of commercial clients farm systems (Harris & Newman, 1994; Blair & Garrick, 2007). A broad selection of traits will enable breeders to target a broad customer base, or more specific traits can be utilised in order to target a smaller, more specialised, proportion of the commercial clientele (Harris & Newman, 1994). The sheep industry consists of many separate breeds (Garrick et al., 2000). Each of these breeds has a specific breeding objective and, furthermore, each individual ram breeder has a breeding objective unique to each system (Garrick et al., 2000). In livestock production, terminal breeds understandably focus the majority of selection on lamb production, mature live-weight and the efficiency of growth (Rae, 1982; Harris & Newman, 1994).

The breeding objective is commonly written in the form of a linear equation that includes the estimated additive genetic merit, or estimated breeding value (EBV), of the traits weighted by a monetary value, called the relative economic value (REV), which represents the relative financial importance of each trait to the breeding system (Conington et al., 2004). It is not always possible to measure traits in the breeding objective on a live animal therefore traits which are genetically correlated can be used. Traits on which selection is performed, and sources of information (individual and/ or relatives) are known as the selection criteria (Dickerson & Hazel, 1944; Christensen, 1994).

In order for genetic improvement to occur there must first be variation in the genetic values of the selection criteria in a population so animals of superior genetic merit can be selected for breeding (Weller, 1994; Blair & Garrick, 2007). There must also be a measure of genetic merit of individuals available to allow this selection to take place (Hazel, 1943). The calculation, and ranking, of the additive genetic merit of individual animals for production traits will allow for the continued improvement of production levels (Simm, 2000).

2.2.2 Genetic Variation and Prediction of Genetic Merit

The phenotypes of most livestock production traits are quantitative and generally have a normal distribution in a population. This means there will be measurable properties of variation between individuals and the population mean (Lynch & Walsh, 1998). The variance (σ^2), and hence the standard deviation (σ), is a measure of how much difference there is in a population for a trait undergoing selection (Blair & Garrick, 2007). Genetic variation of a population is essential for genetic improvement to take place and the greater the variation of a trait, the greater the potential for rapid rates of genetic gain to be achieved (Lynch & Walsh, 1998).

The phenotype (P) of an animal is the sum of genetic (G) and environmental (E) effects. As a result the phenotypic variance in a population will result from genetic and environmental variance (Hazel, 1943). This shows how individuals with superior performance potential due to their genetics may be passed over for an individual given an advantageous environment under phenotypic selection (Hazel, 1943). The prediction of genetic merit, and therefore

genetic improvement, requires the separation of the genetic and environmental components (Hazel, 1943).

The environmental component can consist of three different types of effects. These are:

- Group effects – pertaining to particular contemporary groups made unique by factors such as age, rearing and production environments and differences in management
- Permanent effects – affecting individual animals for the duration of their lifetime
- Temporary effects – affecting individuals for a short period of time

The genetic component of a phenotype consists of additive and non-additive gene actions and it is the additive component that is measured as the genetic merit of an animal. This is referred to as the breeding value (BV). Variation in the genetic merit of individuals in a population will be caused by differences in gene frequencies and gene expression.

In order to determine the degree of expression resulting from additive genetic variance the variance and covariance components of traits in the population must first be calculated from phenotypic information (Harris & Newman, 1994). This involves investigation of the regressions and correlations between both, information on relatives, and information on different traits (Garrick, 1991).

Breeding Values

Livestock production traits are affected by quantitative trait loci (QTL) on the chromosomes which contain numerous alleles (Mayo & Franklin, 1998). The actual effects of specific alleles at these sites are generally not known but QTLs have observable effects on an individual's performance (Mayo & Franklin, 1998). Because the exact effects of the alleles, or how they interact with each other and the environment, are not known the true breeding value (TBV) of an individual cannot be measured (Mayo & Franklin, 1998). Instead the genetic merit of an animal must be predicted to give an estimated breeding value (EBV) (Hazel, 1943).

The first step in making this estimation is to determine the variance and covariance components of traits in the population using phenotypic information (Harris & Newman, 1994). This involves investigation of the regressions and correlations between both, information on relatives, and information on different traits (Garrick, 1991). Next, statistical methods are used to separate the genetic and environmental effects. In the evaluation of genetic merit it is desirable to give an estimate which is based upon the observations on a trait/s that gives the most accurate prediction of true breeding value (Henderson, 1949; Garrick, 1991). That is, a method that minimises the prediction error variance (PEV). PEV is the variation of an individual's actual performance around the mean. The combination of available phenotypic information to predict breeding values, and the further combination of EBVs and REVs to give a value for overall genetic merit, involves the use of selection index theory and best linear unbiased predictor or BLUP.

Selection Index

Selection indices use principles of best linear predictor (BLP) to give individuals an overall value of genetic merit based upon their performance, as calculated from a number of different sources or on a number of different selection traits (Rae & Andreson, 1982). There are two types of indices commonly used in genetic improvement programs, a family selection index and an economic index. A family selection index allows for the combination of all available information on an individual and it's relatives to give an EBV for each trait selected upon (Hazel, 1943). An economic index uses EBVs in conjunction with relative economic values in order to predict the genetic merit of individual animals for these traits.

These indices are presented in the form of a linear equation:

$$I = b_1P_1 + b_2P_2 + \dots + b_nP_n$$

Where I = Index merit

b = regression co-efficients

P = phenotypic measurement adjusted for environmental effects

The regression coefficients are values derived to give the weighting of the phenotypic records which will result in the greatest prediction accuracy, and thus the best correlation between the EBV and the TBV, from the available information (Hazel, 1943). For a family index, these values will depend upon the heritability of the trait/s, the source of the information and the number of records available. Thus, an important aspect of the use of multiple records on relatives is that the amount of information utilised in family indices will vary depending on the age of the individual and the source/s of the information used. This means that older animals with more records available will tend to have higher accuracies of prediction than younger animals with fewer records. In an economic selection index, traits are weighted with an economic value (Simm, 2000). This value can be derived to target maximum profitability or efficiency of an operation and, as with family index regression coefficients, are calculated as those which will optimise the genetic gain achieved by an operation (Simm, 2000).

Selection indices are beneficial from the view that selection of replacements based upon index values will result in genetic improvement in all targeted traits included in the index, compared to just one trait at a time (as with tandem selection) (Hazel, 1943). They also have the advantage in allowing for the selection of traits that can only be expressed in one of the sexes (i.e. number of lambs born), or by rendering the individual incapable of passing on its genes (i.e. carcass traits), through the use of records on related individuals (Hazel, 1943).

The shortcomings of BLP practices include the adjustment of phenotypic records for known environmental effects. The size of this adjustment is assumed and therefore, has the potential to over, or underestimate the size of the actual effect. As a result, this can incorrectly predict the additive genetic component of a trait being selected for. This method of combining information also means that differences in management between individuals are not accounted for and values cannot be compared between age groups. In addition, BLP methods require that different weighting factors be used for each class and for different numbers of records which results in a large number of calculations required for each individual. Because of these faults, a method that can account for these is more commonly used. This method is best linear unbiased predictor (BLUP).

Best Linear Unbiased Prediction

Because BLP and BLUP are “best” they both target the minimum prediction error variance to give the greatest EBV accuracy. BLUP involves statistical procedures using linear models similar to those of selection indices to combine all or some of the available phenotypic information on an individual and its relatives to calculate EBVs (Henderson, 1949; Garrick, 1991). It differs from BLP analysis in that it allows for the adjustment for permanent environmental effects, such as age and environment, by treating them as fixed effects (Henderson, 1949; Rae & Anderson, 1982). Random effects are the animals themselves (Garrick, 1991). When fixed effects between relatives are not known, use of BLUP allows for the inclusion of information on relatives and removes any bias resulting from adjustment for contemporary group effects (Garrick, 1991). It also allows for the comparison of EBVs across years and contemporary groups given that there are genetic relationships between them (Rae & Anderson, 1982; Garrick, 1991). As with economic BLP indices, BLUP analysis of multiple traits can be combined in a mixed model equation to give an overall selection index value.

Selection on BLUP BVs is well known to be a more efficient form of selection than phenotypic selection, even in small, closed populations (Kuhlers & Kennedy, 1992). When selection is based on BLUP derived EBVs younger animals in the population will be of higher genetic merit than older animals although the accuracy of breeding values in these individuals will be lower due to fewer records available on the individual (Bijma & Wooliams, 1999; Simm, 2000).

2.2.3 Components of Genetic Gain

There are several factors that affect the rate of genetic gain achieved by a system and these are used in the following equation to predict the genetic gain of a system:

$$\Delta G = \frac{\bar{i} \times r_{TI} \times \sigma_T}{L}$$

Where ΔG = genetic gain per year

\bar{i} = selection intensity

r_{Ti} = accuracy of selection

σ_T = variance in the objective (genetic variance)

The individual components of this equation are discussed in detail below but it is first important to note that these factors are interdependent and changing one will have an effect on at least one of the other factors (Blair & Garrick, 2007). The particular management practices of a system will determine the population generation interval and selection intensity while practices involved in genetic prediction, including performance measurement and recording, will determine the accuracy of selection (Harris & Newman, 1994; Blair & Garrick, 2007). The genetic variance of a population is controlled by the flow of genes within, to and from the system (Harris & Newman, 1994; Blair & Garrick, 2007). System production levels, especially the number of offspring produced per year, will therefore affect both the financial performance of an operation and determine an upper limit of genetic gain achievable (Rae, 1982). The effects of genetic selection will also depend largely on the efficiency of technologies utilised (Everett, 1984) and genetic improvement will only occur if performance recording and selection on traits that are economically important take place (Garrick et al., 2000).

Blair & Garrick (2007) stated that the theoretical maximum genetic gain achievable in sheep populations is 3.4 genetic standard deviations although, such rates are expensive and involve a large labour input. In New Zealand sheep production systems, the level of gain that will be most cost effective is like to be around 0.3 genetic standard deviations (Blair & Garrick, 2007).

Generation Interval

The generation interval (L) is a measure of the rate at which breeding parents in a population are being replaced by younger, higher genetic merit stock (Rendel & Robertson, 1950; Lynch & Walsh, 1998). As a result, a short L is preferable when high rates of genetic gain are targeted (Lynch & Walsh, 1998; Simm, 2000; Blair & Garrick, 2007). It is calculated

as the average contribution of each age group to the next generation (Bijma & Wooliams, 1999; Blair & Garrick, 2007).

In the sheep industry the overall L is commonly around three to four years despite the minimum achievable being two years when first mating ewes and rams at six months of age (Blair & Garrick, 2007). Although it is possible to improve upon the current industry average, it is impractical to decrease this too far because the reproductive rate of sheep, especially ewes of a younger age, would result in insufficient offspring being produced to maintain flock size while improving the intensity of selection (Blair & Garrick, 2007). To maintain flock size ewes must be retained in flocks for at least 2.5 – 3 years (Blair & Garrick, 2007). Another limitation that may restrict the significant reduction of L is the fact that the EBVs of younger animals are predicted with less accuracy than those of older animals with more information available (Blair & Garrick, 2007). These features of L show that, although high rates of genetic gain are desirable, they are not always practical within the current system and/ or industry environment (Blair & Garrick, 2007).

Other than actively culling older animals to reduce L, selection based largely upon BLUP EBVs containing parental information, or on a selected trait of high heritability, in a system carrying out genetic improvement will favour individuals born to younger parents, thus decreasing the L (Bijma & Wooliams, 1999). Christensen (1994) reported that this practice is likely to optimise L. If such selection occurs then the calculation of L as the contribution of each parental age group to the next generation may overestimate the genetic gain (Bichard et al., 1973). As a result the L calculated based upon the average parental age of replacement parents is likely to be a more accurate method of calculation (Bichard et al., 1973).

The nature of the L will depend on the structure of the breeding population (Villanueva et al., 2000). When each age group is a separate unit and there is no breeding between them the generations are discrete but when there is breeding between animals of different ages the generations overlap (Hill, 1974; Villanueva et al., 2000). When a population has overlapping generations the selection process, and thus the intensity of selection, will be affected (Hill, 1974).

Selection Intensity

The selection intensity (\bar{i}) is a measure of the genetic superiority of the animals chosen as replacements in a population undergoing selection (Hazel, 1943; Lynch & Walsh, 1998). This superiority is measured in standard deviation units of the chosen replacements over the mean of the population from which they were selected (Blair & Garrick, 2007). If a smaller proportion is selected, the average genetic merit of the selected animals can be greater than if a larger proportion is selected, therefore allowing a greater genetic gain (Simm, 2000; Blair & Garrick, 2007). Increasing \bar{i} by increasing the percentage of animals selected based upon BLUP calculated genetic merit will also result a decreased L due to animals from younger parents having a higher genetic merit (Bijma & Wooliams, 1999).

As with L, \bar{i} is limited by the number of replacements which can be produced by the breeding population each year, and how many of these are required to replace animals culled for age and lost through deaths (Hazel, 1943). This reflects the need to balance \bar{i} and L. Although the maximum \bar{i} value is 3.4 if 0.1% of candidates are chosen, Blair and Garrick (2007) report that values of between 1.3 and 1.7 are common averages over rams and ewes in the New Zealand sheep industry. Due to the fact that the ewe to ram ratio can be as high as one ram to 500 ewes, selection upon the male population is often more intense than the female population (Blair & Garrick, 2007). Selection of the top 1% of ram lambs and the top 46% of ewe lambs as replacements, if 130% of lambs (lambs available at selection over ewes mated) are available for selection, would result in \bar{i} of 1.8 (Blair & Garrick, 2007). Increasing the number of lambs available at selection to two per ewe mated will increase this further still to 1.9 (Blair & Garrick, 2007).

There are several different types of selection that can be utilised in animal breeding systems and each of them has different effects on the intensity of selection. Mass selection is carried out based the level of performance of individuals from records of phenotype performance on the individual (Rendel & Robertson, 1950). This method does not allow for the selection of animals on sex limited or difficult to measure traits so does not optimise rates of genetic gain (Rendel & Robertson, 1950). Independent culling levels involve culling a number of the bottom performing animals for each trait sequentially during each selection event. This however, is only effective when the traits measured are those in the objective.

In systems with overlapping generations the usual, and most beneficial form of selection is that of truncation selection when a threshold breeding or index value is chosen, above which are the individuals selected as replacements (Villanueva et al., 2000). Because animals from a variety of parental age groups, or individual age groups, are selected each group will have a different distribution of breeding values (Villanueva et al., 2000). This selection can be performed on either the offspring produced each year or across the entire breeding population (Villanueva et al., 2000). If truncation selection on the offspring is utilised in a system, genetic gain will be increased due to the increase in average genetic merit of those selected (Bichard et al., 1973). This practice will also decrease the average parental age of a system (Bichard et al., 1973). It should be noted that, as animals born to younger parents will be favoured by this practice, it is likely to increase the inbreeding in a population (Bijma & Wooliams, 1999; Villanueva et al., 2000).

Accuracy of Selection

The accuracy of selection (r_{TI}) is a measure of how much the EBV of an animal, as calculated from available phenotypic data, reflects the TBV of an animal (Lynch & Walsh, 1998). This accuracy is generally presented for individual traits or index values for each individual in a population (Macbeth, 1994) and is the correlation between the predicted genetic merit and the true genetic merit, thus having values of between 0 and 1.0 (Blair & Garrick, 2007). Highly accurate selection will have values close to 1.0 but commonly in the sheep industry values are between 0.2 and 0.4 unless extensive progeny testing is carried out in a system (Weller, 1994; Blair & Garrick, 2007).

As previously mentioned, accuracy will largely depend upon the source of information with which genetic merit is calculated, the amount of information available and what degree of trait expression is controlled by additive genetic variance (the heritability) (Harris & Newman, 1994; Lynch & Walsh, 1998). The heritability of traits cannot be controlled and as it increases, the additional value of information on relatives, and more records on the individual, decreases (Garrick et al., 2000). In contrast, the source of information and the amount of this available will depend on farm management practices. This means that these

can be manipulated to optimise accuracies within the confines of the production environment.

Given that \bar{i} is somewhat restricted by the replacement rate of a population, and that the genetic variance is a result of the gene frequency of the population and the rate of inbreeding, significant opportunity for control exists in the accuracy of prediction (Hazel, 1943). Accuracy can be increased by utilising more performance information on an individual and/ or its relatives, especially those closely related to the individual. Nevertheless, this also means that the selection accuracy will be greater in older stock due to the availability of more information on the individual and any siblings and/ or offspring (Villanueva et al., 2000). The collection of additional records on an individual, and/ or its siblings or progeny, will also often increase L and the costs involved in measurement and analysis of phenotypic information (Christensen, 1994; Simm, 2000).

Nevertheless, during selection, the accuracy will be decreased from that predicted by giving some animals preference to selection not based upon genetic merit or based on traits not included in the objective (Everett, 1984). Such preference may result from the culling of individuals based on undesirable physical traits and/ or health defects or the preference of older, higher producing stock over younger animals with lower levels of production (Everett, 1984). These points highlight the need to balance the components of genetic gain to achieve optimum, rather than maximum levels.

Variation in the Objective

As with the genetic variance mentioned previously, variance in the objective is a measure of how much difference there is in the additive genetic merit of a population for a given trait or index (Lynch & Walsh, 1998; Blair & Garrick, 2007). It will depend of gene frequencies and gene expression and is largely uncontrollable using farm management practices but introducing individuals from outside populations will increase genetic variation, as will increasing the number of replacements selected (Blair & Garrick, 2007). An important point to note is that, as genetic improvement takes place, the variation in population decreases, as it does if the number of individuals selected as replacements decreases (Blair & Garrick, 2007).

2.2.4 Other Considerations

Assumptions in Calculating Genetic Gain

BLP, or selection index, practices are based on several assumptions (Rae & Andreson, 1982). These assumptions are that mating is random, no genetic trend is occurring in the population and records are adjusted for environmental effects (Rae & Andreson, 1982). BLUP practices remove the need to assume there is no genetic trend and adjust for environmental effects. However, an important assumption in both BLP and BLUP is that there is no genotype by environment interaction. That is individuals within the contemporary groups have not been given any preferential treatment with regards to their genotype.

Lambing Hoggets

The mating of hoggets has numerous advantages to a genetic improvement system, mainly through the potential to decrease L and increase \bar{i} , subsequently increasing genetic gain (Bijma & Wooliams, 1999). The mating of ewe hoggets can also result in more lambs present at weaning, and subsequently more lambs available for selection, potentially increasing the \bar{i} as well as increase revenue from lamb sales (Simm, 2000; Kenyon et al., 2006)). Nevertheless, the extent of these effects will depend on the existing age structure of the breeding flock and the number of hoggets producing replacements (Bijma & Wooliams, 1999; Simm, 2000) which is often not the case if subjective selection of replacements takes place as hogget lambs are smaller at weaning (Kenyon et al., 2006).

The mating of hoggets, especially ewe hoggets, is likely to increase the health and feed costs involved in the production of additional lambs (Ratray et al., 2007). Extra feed must be dedicated to hogget live-weight gain in order for puberty to be attained and pregnancy achieved (Ratray et al., 2007). High feeding levels must continue throughout pregnancy and after parturition in order to allow for the continued growth and development of the hogget as well as that of the lamb (Ratray et al., 2007). The additional health cost associated with breeding a ewe hogget is around \$9.10/head (vaccine, drenching and scanning) but it should

be noted that this does not include the cost of additional labour or time required to carry out these additional tasks.

Inbreeding and Genetic Variation

The rate of inbreeding occurring in a flock will depend on its size (Rae, 1964) and will occur over time as a result of genetic selection unless outside animals are introduced (Christensen, 1994). There is a possibility that inbreeding can have negative effects on the number of offspring born and survival rates, therefore reductions in \bar{i} and L of a population (Kuhlers & Kennedy, 1992). Variation of traits within a population is lost by inbreeding but will also occur as a result of selection (Kuhlers & Kennedy, 1992; Blair & Garrick, 2007).

Rate of inbreeding per generation (as in Everett, 1984) is estimated as:

$$Inbreeding = \frac{1}{8m} + \frac{1}{8f}$$

Where: ΔF = rate of inbreeding per generation

m = the number of breeding males

f = the number of breeding females

Parentage Identification and Genetic Gain

When estimating genetic merit prior to the availability of DNA parentage testing, it was assumed that offspring were accurately assigned to correct parents (Banos et al., 2001). Nevertheless, any errors in the assignment of parents to a generation of offspring will have an adverse affect on the genetic gain achieved, mainly through a decrease in the accuracy of selection (Long et al., 1990; Crawford, et al., 1993). The percentage of pedigree errors present will depend on several factors including the method used to determine parentage and how this procedure was carried out.

Effect of Pedigree Errors on Genetic Gain

The extent to which genetic gain is affected by pedigree errors will depend upon the extent to which pedigree is utilised in the estimation of breeding values (Long et al., 1990; Crawford, et al., 1993). In systems which utilise BLUP estimation of genetic merit, such is the case for many New Zealand breeding systems carrying out genetic improvement programs including Landcorp Farming Limited, pedigree errors can have a significant effect on the accuracy of genetic gain due to the heavy reliance of this method on pedigree data (Long et al., 1990; Banos et al., 2001; Cardoso & Tempelman, 2003). The effect of such errors also increases if both parents of an individual are wrongly identified rather than just one (Long et al., 1990). Pedigree errors will also have a significant effect in systems that utilise progeny testing to assess the genetic merit of sires (Banos et al., 2001; Visscher et al., 2002).

Pedigree errors can adversely affect heritability estimations and correlation co-efficients as paternal half-sib analysis of variance relies upon performance information on the sire (Van Vleck, 1970; Long et al., 1990; Banos et al., 2001; Visscher et al., 2002). As heritability increases, there is a decreased importance of information from relatives (Sise et al., 2001; Dodds et al., 2005), although pedigree error will still have a negative effect on heritability and correlation co-efficients. Visscher et al. (2002) reported an estimated effect on heritabilities of any trait to be:

$$1 - p^2$$

Thus:

$$h_{PE}^2 = h^2 \times (1 - p^2)$$

where p = the rate of errors in the pedigree

h_{PE}^2 = heritability with errors in the pedigree

The decrease in the accuracy of EBV calculation can also have an adverse effect on the selection intensity (Banos et al., 2001; Cardoso & Tempelman, 2003) as errors give rise to the potential that replacements of a lower than optimal EBVs will be selected if they have incorrectly been recorded as the relative of a high genetic merit individual or family (Banos et al., 2001; Cardoso & Tempelman, 2003).

Banos et al. (2001) found that, on a population scale US Holstein dairy herd, the mean losses in false identification due to offspring of lower merit being assigned to a high genetic merit bull were balanced by the gains resulting from the incorrect assignment of high genetic merit offspring to low genetic merit sires. Despite this the losses and gains for individual sires did not generally balance and effects on individual sire EBV was greatest for those of high and low values (Banos et al., 2001). This is because of the strong possibility that any incorrectly assigned offspring will be of a lower or higher genetic merit in comparison to a sire's true offspring (Banos et al., 2001). Such errors were largely the result of human error in recording and identification of bulls and semen straws (Banos et al., 2001; Visscher et al., 2002). Furthermore, Banos et al. (2001) reported that various reports have found up to 25% of parents in dairy populations worldwide have been incorrectly assigned due to errors in recording and/ or identification.

The effect of pedigree errors on genetic gain was found by Crawford et al. (1993) to be, in comparison to a pedigree assignment that is 100% correct, about 6% if 100 progeny are tested at an error rate of 80%. If the percentage of correct pedigrees increases to 90% this error decreases to about 2% (Crawford, et al., 1993). Similarly, Long et al. (1990) found that a 20% error rate in parentage identification resulted in a 9.3% reduction of genetic gain in a pig population.

The effect of error rates on genetic gain will vary between sires and dams if only one parent is incorrectly matched. Dodds et al. (2005) reported a 1% decrease in the genetic gain if 10% of of the dams and progeny in the system were not genotyped compared to a situation where 5% were not genotyped. In comparison a decrease of 1% of genetic gain was achieved when just one of 10 sires was not genotyped.

Parentage Identification Recorded at Lambing

Common practice in sheep breeding systems is to identify and record offspring at birth through the monitoring of lambing ewes which is carried out at regular intervals over the lambing period. Inspection is made of lambing paddocks and newborn lambs are tagged and record is made of the presumed dam (Dodds et al., 2005). Nevertheless, in large scale breeding systems such a practice is often time consuming and expensive to carry out as it requires the input of skilled labour (Dodds et al., 2005; Crawford et al., 2007). Single sire mating and records of ewes in each ram group are commonly used for the purpose of parentage identification in these systems in order to reduce the number of possible parentage combinations for individual lambs (Sise et al., 2001). This practice also imposes restrictions on the management options of a system and can have the additional effect of reducing pregnancy rates if there is a fault with the performance of a sire (Dodds et al., 2005).

In an effort to minimize the cost, many systems will carry out a check of ewes lambing just once or twice a day, assuming that any new lambs belong to the dam they are observed to be suckling from and following. This can create inaccuracies in the assignment of parentage. Ewes approaching parturition commonly display maternal behaviour to lambs born to other ewes and such behaviour can lead to the "stealing" of lambs (Alexander et al., 1983). These stolen lambs often bond to, and suckle from, these ewes making observations of parentage based upon suckling activity somewhat inaccurate (Alexander et al., 1983).

Alexander et al. (1983) reported that Romney ewes and lambs under good pasture conditions have a rate of lamb separation from the correct dam of around 8%. Blair & Garrick (2007) reported that rates of lambs being stolen from their dam of between 6 and 18% had been recorded in various studies. These rates will increase with increased stocking rates, increases in the number of ewes lambing in a given time period in a paddock, ewe disturbance near lambing, an increase in the number of multiple births and lack of mothering experience among ewes (i.e. younger ewes) (Alexander et al., 1983; Crawford, et al., 1993). Alexander et al. (1983) concluded that the identification and parentage recording of lambs at birth is more accurate than the assignment of parentage based on suckling observations in a ewe flock and, in conjunction with the mis-mothering rates reported by

Blair & Garrick (2007) this suggests that frequent checks on lambing ewes is required to minimise pedigree errors in cases of manually recorded pedigrees. The findings of Crawford et al. (1993) and Dodds et al. (2005), which revealed that the level of management dedicated to the recording of parentage data is reflected in the percentage of pedigree errors in pedigree records, support this. New Zealand flocks kept in large paddocks with a high ratio of ewes to shepherds can show error rates as high as 15% (Crawford, et al., 1993). In contrast, more intensively managed flocks can achieve error rates of less than 1% (Crawford, et al., 1993). Sise et al. (2001) reported error rates of around 10% for singles, and higher for multiple births, have been recorded in the past.

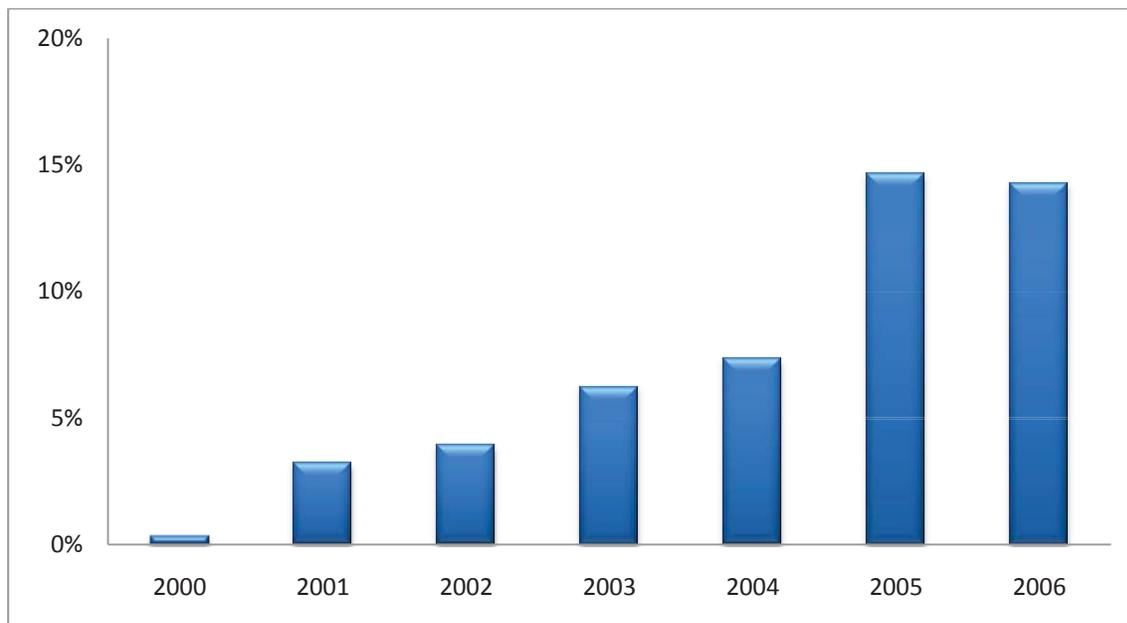
DNA Parentage Identification

Technology developments present an alternative method to assess the parentage of offspring in a breeding system. DNA parentage uses a DNA sample from the offspring (in sheep this is commonly in the form of a blood or tissue sample taken at docking) and DNA markers to either assess manually recorded parentage to confirm or refute recorded parents, or to assign parents from a group of potential sires and dams (Dodds et al., 2005). Any mismatch between two or more markers excludes an animal as a potential parent of an individual (Bolormaa et al., 2008).

Use of DNA Parentage in New Zealand Agriculture

DNA parentage identification has the potential to increase the genetic gain of a system where pedigree error is present and increase the economic return as a result (Banos et al., 2001). This method first became available to commercial sheep breeders in 2000 and since has been adopted by many large scale breeding systems (Crawford et al., 2007) and McEwan (2009) reports that, in the deer industry, 30% of the nucleus breeders carrying out parentage recording are utilising DNA parentage.

Figure 2.1 Adapted from data from Garrick et al. (2000) and Crawford et al. (2007) this graph shows the estimated percentage of the New Zealand nucleus flock animals that are DNA parentage tested by *Genomnz™*, one of the major companies providing such services in New Zealand.



If the average trend from Figure 2.1 of a 2.3% increase in the number of individual animals in the sheep industry DNA parentage tested each year continued through to 2011, and all DNA parentage tests carried out used a number of informative markers, then an estimated 26% of animals born in the nucleus would have a 10% chance (Blair & Garrick, 2007; Bolormaa et al., 2008) of being assigned the correct parentage. This leaves 74% with the potential of having pedigree error rates of up to 15% (Crawford, et al., 1993; Sise et al., 2001).

Using DNA Parentage - Some Costs and Benefits

Initially, DNA samples from sires can be taken prior to mating and those from the ewes taken at scanning (Pfizer Animal Genetics, 2011). These records, and those from subsequent offspring, can be used to develop a data base of potential parents (McEwan, 2009) that would only require the addition of samples from any purchased breeding animals.

The use of highly accurate DNA parentage can provide several benefits to a breeding system. There is the potential for less labour to be involved in tagging and recording lambs at birth

which also means fewer disturbances to ewes during lambing (Dodds et al., 2005; Crawford et al., 2007). The reduced need for labour intensive lambing also means that lambing, if desired, can be carried out in larger paddocks with rougher terrain and more natural shelter such as scrub and bush. Nevertheless, this is only possible if no record of birth weight or litter size at birth is required (Dodds et al., 2005). Litter size estimations made by DNA parentage from samples collected at docking cannot be considered accurate (Dodds et al., 2005) as they do not include any lambs that have died prior to docking. The elimination of the need for single sire mating would also mean that less grazing space is occupied by small mobs, reducing the labour required in managing several small flocks (Dodds et al., 2005; Crawford et al., 2007). Taking samples for the purpose of DNA parentage identification also allows for the identification of individuals with both desirable and undesirable genes and the resulting information can be incorporated into selection criteria (Pfizer Animal Genetics, 2011). However, the majority of these benefits do depend on the DNA being highly accurate and the cost of such analysis will also be an important factor which must be considered.

DNA parentage assessment can be expensive (Sise et al., 2001; Dodds et al., 2005) and requires accurate recording of lamb identification during the sampling period which is often a busy and potentially stressful time for farmers. The accuracy of parentage records from DNA parentage assignment depends largely upon the number of DNA markers used and the heritability of the trait/s in question (Dodds et al., 2005; Blair & Garrick, 2007). Dodds et al. (2005) reported DNA parentage in situations where there are few potential parents to be "typically very reliable". When more potential parents (26) are involved Sherman et al. (2004) reported a unmistakable sire assignment of 86% using 11 microsatellite markers. Using more markers increases the likelihood that matched parents are correct but as the number of markers used increases, so will the cost of analysis (Sise et al., 2001; Dodds et al., 2005; Blair & Garrick, 2007). Both Blair & Garrick (2007) and Bolormaa et al. (2008) reported that, when many informative markers were used, the accuracy approached 100%. The amount of information that must be derived by the process of DNA parentage, and therefore the cost of processing, can be reduced by continuing to record the rams, ewes in each mating group and the ewes and lambs in each lambing group (Dodds et al., 2005). Because of this, the use of DNA parentage as the only method of parentage identification in

a farming operation is not the most cost effective practice and it should be combined with other practices (Sise et al., 2001)

Sise et al. (2001) investigated three breeding scenarios in order to investigate options that would allow for DNA parentage to be carried out while keeping costs involved at a minimum. Two of these scenarios investigated single sire mating, one involved maintaining ewes mated to individual sires in separate mobs until lambs were tagged and the other involved running all ewes as a single flock until lambing and then split into mobs containing equal proportions of each sire group. The third scenario involved a single mating group for all ewes and rams. The second scenario gave the largest percentage (56%) of lambs assigned a single parent combination and 21% had two parent combinations. This percentage increases with the number of sire groups per paddock as it reduces the number of potential dams per paddock. Single sire mating and lambing in sire group mobs resulted in 31% of lambs with unique parentage assignment (1 pair) and 19% with two possible parent combinations.

Additional factors to consider when using DNA parentage include the possibility of unmatched, or incorrectly matched, offspring due to the occurrence of spontaneous mutations in the DNA although the rates of such mutations tend to be low (Bolormaa et al., 2008). Assigning DNA parentage also becomes more difficult when individuals within the parent population are more related and therefore have more genes in common (Dodds et al., 2005).

The assumption of correct pedigree made when analysing genetic gain (Banos et al., 2001) can lead to error in systems where lambing beats are the only source of pedigree information. The margin for error using this practice, especially in large systems, is considerable and errors can have adverse effects on the genetic gain and therefore the financial performance of a system. As a result, it is of interest to all ram breeders, whether carrying out DNA parentage or not, to be aware of the advantages and disadvantages involved in the use of this technology and to be able to implement practices that minimise pedigree error while maintaining financial efficiency.

2.3 Financial Implications of Genetic Gain

Morris (2008) reported that low cost production systems in New Zealand are essential to allow competition on a world market scale. It is still important however, to continue to improve the productivity and efficiency of agricultural production (Morris et al. 2008). Amer et al (2007) found that genetic gain in the United Kingdom sheep and beef industries contributed financial benefits to the industry that were greater than the costs imposed in achieving them. Factors that influence the degree of this benefit included the extent to which rams from performance recorded population are used in the nucleus, the extent to which rams from genetically improved flocks are utilised in the industry and the level of genetic improvement being achieved in the nucleus population (Amer et al., 2007).

An important point to note when considering these systems is that high rates of genetic gain can be expensive and the costs associated with these returns are incurred directly by the nucleus farmer (Amer et al., 2007). As a result, the genetic and financial performance of these operations, and the implications of any changes to management practices, should be considered when making decisions and/ or considering changes to the systems.

2.3.1 Economic Values

Economic values are defined by Hazel (1943) as "...the amount by which profit may be expected to increase for each unit of improvement in that trait." In the calculation of these values Harris & Newman (1994) reported three main categories of economic importance in a breeding system that should be accounted for. These were:

- The income from the product/s produced which itself is dependent on the number of progeny produced.
- The product produced per progeny and the quality of the product
- The expenses of breeding and maintaining the female parent, including feed costs; and the progeny growth expenses.

The increase in environmental resources required by improved animals should be also be factored into the relative economic values for each trait (Hazel, 1943).

Because genetic merit is realised sometime after selection takes place, economic values must be predictions of future benefits of genetic improvement (Conington et al., 2004) which means they must be discounted (Weller, 1994). Nonetheless, these predictions can not be for an extended time period due to the volatility of markets and consumer preferences (Weller, 1994). Weller (1994) states that increasing the number or size of animals in an operation will not necessarily increase the profit achieved, or the economic efficiency, due to a subsequent increase in inputs required to maintain production levels. Thus, economic values will need regular reassessment as the number of offspring and/ or the production per head increases.

The practice of economic discounting is used to measure the future costs and returns associated with economic investment. Its use predicts the value of money invested at time t will be worth at a future date (t_n) (Weller, 1994). This change is the result of interest rates and inflation (Weller, 1994). The rate of this discount is commonly between 5 and 10% in breeding programmes and this includes the effect of inflation, which in turn depends on interest rates, risk and taxes. Traits are also not necessarily expressed at the same stage in an animal's life therefore discounting must be used at different rates for different traits (Harris & Newman, 1994).

The inclusion of discounting in the calculation of profit means that there will be a point beyond which current investment in genetic gain will be equal to zero at some point in the future (Weller, 1994). This point is termed the profit horizon and is commonly set at 10 or 20 years in breeding programs (Weller, 1994).

2.3.2 Financial Considerations in Animal Breeding - Now and in the Future

There are two aspects to consider when analysing the economic aspects of any system. These are the returns received from products produced and the cost required to achieve these returns. The unique nature (operational and management environments) of each production system means that the economics of each system will be specific to each genetic improvement program (Hill, 1971; Conington et al., 2004). Practices targeting improvement in the genetic gain being made will incur additional expenses over and above those incurred

when achieving lower rates of gain and these costs have the potential to outweigh the benefits (Harris & Newman, 1994; Blair & Garrick, 2007). As a result, when considering working farm operations and/ or potential developments in a farming system, a compromise must generally be reached between many factors including labour input and output costs and production response (Everett, 1984; Morris 2008). The current physical and financial environments in which the system operates and the limits of operation must also be considered (Everett, 1984). Because of these considerations, when investigating the genetic performance of current systems and/or potential changes to a current system, a financial analysis of annual and long term costs and returns should be included for consideration (Everett, 1975).

The physical production returns, and thus the financial returns, from genetic improvement are cumulative and permanent (Morris, 1980). Nevertheless, in the calculation of the profit achieved by a livestock breeding scheme, it must be understood that there is a delay between the incurrence of costs in performance recording, selection and breeding and the realisation of the physical and financial benefits which occur months or even years later (Morris, 1980; Weller, 1994). Because of this, the costs incurred by a breeding scheme can be considered as investments and any returns on investment must consider addition to returns due to interest rates and reduction of the value of the investment due to inflation (Morris, 1980; Weller, 1994). As a result of these factors, the accumulation of financial returns is not linear and increases by less each time the gain is expressed (Hill, 1971; Morris, 1980). The time taken to establish selected genetics in a population will also contribute to the non-linear accumulation of profit and how long this establishment takes will depend upon selection and other farm management practices pertaining to genetic improvement (Hill, 1971; Davison, 2000).

A selection event will result in half the genes from the selected animals being passed onto their offspring which means that the improvements made are expressed at different times by different numbers of animals (Conington et al., 2004). This means that the flow of genes through a population must be taken into account both when deriving economic values and calculating the long term financial benefits of a selection program (Banks, 1994; Conington et al., 2004).

Thus, the calculation of revenue and/or profit in an animal breeding program using a multi-trait selection index must account for:

- The flow of selected genes through a population over time
- The extent and frequency of genetic change expression in selected individuals and their descendants
- Differences in the number and timing of the expression of selected traits
- The discounted value of financial investment in the breeding program

Morris (1980) stated that the “biological changes” in a trait multiplied by the associated economic value gives the net dollar returns that can be expected as a result of a single round of selection. The net returns from several traits after one round of selection were calculated by Morris (1980) using index values.

Thus (in a selection index): $\text{Revenue} = \Delta G$

However, this method does not account for the timing differences of incurred costs and realised returns of each trait (Morris, 1980). In the calculation of the discounted returns Morris, 1980 utilised a discount rate on the net return of one round of selection of 1 in the first year and $1/(1 + d')$ in each subsequent year with d' being the annual return on investment percent or the discount rate. The costs of production involved with genetic improvement are already accounted for in the economic values of the selection index. However, to find the profit from a round of selection, the cost of recording trait performance, associated labour, and computing genetic gain per animal must be accounted for (Morris, 1980). Morris (1980) stated expected values of \$1 - \$2 per breeding female for these costs which includes the cost of recording and processing her progeny.

This inclusion reportedly gives the accumulative financial benefits of one round of selection resulting from the produced progeny (Morris 1980). In order to find the accumulative financial benefits of one round of selection upon all progeny produced Morris (1980) computed the sum of the geometric progression:

$$A/(1 - d^x)$$

Where A is the total profit from one round of selection and x is the L.

Not included in the calculations of Morris (1980) is consideration that returns from one round of selection will not be realised in the progeny until the trait/s under selection are expressed in full. Also not considered is a selected profit horizon. Weller (1994) presented an alternative method of cumulative discounted profit calculation from a genetic selection program that includes consideration of the profit horizon, discount rate and the flow of genes through a population.

In the calculation and analysis of return on investment the following formula were presented by Weller (1994):

To calculate cumulative profit up to a proposed profit horizon:

$$P = V \left[\frac{r^t - r^{T+1}}{(1-r)^2} - \frac{(T-t+1)r^{T+1}}{1-r} \right] - \frac{C_c r(1-r^T)}{1-r}$$

Where

P = Profit

V = Genetic gain

$r = 1/(1 + d_i)$

where d_i = rate of inflation

T = Profit horizon (stated by Weller (1994) to be 10 or 20 years in livestock breeding systems)

t = number of years until first return is realised

C_c = annual cost of breeding program

This holds true for one round of selection on the progeny resulting from that selection. However the genes selected for in any one selection event will contribute to the performance of future generations beyond the first (Weller 1994). In this case it is desirable to know the proportions of genes in the population derived from selected animals and the genetic improvement each year resulting from selection for a given time period. The response of one cycle of selection at time t (v_t) is calculated by Weller (1994) as follows:

$$v_t = (\mathbf{Z}^t - \mathbf{Q}^t) \times (y_{m0}G_m + y_{f0}G_f)$$

Where \mathbf{Z} = a matrix describing passage of genes across the male and female age groups of the system

\mathbf{Q} = a matrix describing population structure changes due to ageing

y_{m0} and y_{f0} = vector describing the original genetic makeup of the male and female populations respectively

G_m and G_f = scalars showing the genetic superiority of males and females selected as parents for the next generation

However, given that selection is a process that occurs regularly in any breeding program the total response in any one year will be the result of several past selection events (Weller, 1994). Because genetic improvement depends on additive genetic merit the cumulative genetic merit (V) of any sex-age class at time t can be found from the beginning of the selection period as:

$$V_{(t)} = r_{(t)} + r_{(t-1)} + \dots r_{(1)}$$

2.3.3 Application to Farming Systems

Because farming systems operates in unique physical and financial environments, case studies that track farm specific performance are important tools when increasing, or maintaining, levels of performance (Kuhlers & Kennedy, 1992). In the analysis of genetic improvement systems, case studies allow for the investigation of how system specific management decisions have influenced genetic gain and what adjustments can be made to these to optimise gain. Such studies also allow for the analysis of alternative management practices and investigations of their effects on the current levels of performance. This was observed in a case study of the American dairy industry carried out by Everett (1984). This study found that the difference between the theoretical limit of progress being made and the actual progress was due to decreases in the selection intensities and accuracies of

selection. The main reasons for this were: the selection of replacements based on non-production traits; low selection intensity on Index values; incorrect genetic evaluation due to preferential treatment of individuals; and the fact that the production and reproduction cycles could not be modelled accurately in all situations (Everett, 1984) (i.e. when a drought or other environmental event impact on the population).

2.4 Aim of Research

There were three main aims of this investigation:

- To estimate the genetic gain achievable within the production parameters of a working nucleus flock operation and compare to rates achieved in order to identify areas for improvement.
- To investigate the resulting financial performance and the financial performance of possible system changes in order to identify the effect of management changes on the system.
- To compare the results of lambing-book assigned parentage and DNA-assigned parentage in order to identify the effect of pedigree error on genetic gain, and the financial effect of this error, and to recommend management practices targeting the minimisation of this error.

Chapter 3 Genetic Gain

3.1 Introduction

The following investigation was a case study of the Landcorp Waikite Texel breeding operation. The study was carried out based upon the genetic, phenotypic and production parameters and stock numbers from the ten years 2000 to 2009.

The aim of this study was to compare the actual improvement made in the selection index over the period 2000 – 2009 to trends predicted from flock data in order to identify areas for improvement. To achieve this, the widely discussed methods of calculating genetic gain (ΔG), and the financial implications of this gain, mentioned in Chapter 2 were utilised. The selection processes, flock age structure and financial performance were areas chosen for investigation as these are strongly influenced by on farm management decision and practices.

3.2 Methods

3.2.1 Data

Flock data files included the following information on every animal born between 1993 and 2009:

- Sire and dam current status, current tag, birth year, birth tag and birth flock
- Individual current status, current tag, birth year, birth tag, birth flock, sex, birth date, birth and rearing rank, age of dam, survival, weaning weight, live-weight at 8 and 12 months, ultra sound results, CT scan results, pregnancy scan results and the number of lambs born.
- Disposal information including birth flock, current flock, year born, ear tag, sex, disposal code, disposal month and disposal year.
- Breeding values for the index and individual traits in the index.

For the purpose of analysis, relevant data was extracted using Excel formula and pivot tables. 7195 animals were born between 2000 and 2009 inclusive. Of these, 122 did not have an

identified sire while 22 did not have a dam identified. These records were excluded from the analysis which resulted in 7051 useable records.

From the data provided and subsequent flock parameters (such as lambing percentage (lambs born/ ewes lambing) and survival percentage (lambs weaned/ lambs born)) and mean stock numbers for the studied period, an average flock stock reconciliation was constructed. This detailed the flow of stock in and out of the flock and between age classes in an average financial year. It was assumed in the creation of this stock reconciliation that the opening stock numbers were the same as closing in the average year. Numbers culled in each stock class were adjusted to create this balance. These adjustments may have created some discrepancies with actual system practice.

The mating of ram hoggets in the investigated system is a practice that is expected to continue in the future. The mating of ewe hoggets however, is a practice for which analysis of the cost benefits was desired (Personal communication, Geoff Nicoll 2010). As a result, further reference to hoggets mated and not mated refers specifically to ewe hoggets unless otherwise stated.

3.2.2 Genetic Trend in Index

The actual genetic trend of the flock achieved between 2000 and 2009 was taken as the difference between the mean flock index value of lambs born in each year. The average change in index value (ΔI) for the studied period was then calculated as:

$$\Delta I_n = I_n - I_{n-1}$$

where: n = year and I = mean index value of animals born in year n

A breakdown of the system into the components of ΔG (generation interval, accuracy of selection, variance in the objective and the selection intensity) was carried out in order to evaluate current management practices and to determine their effect on ΔG . Values obtained in this breakdown were compared with those reported in Blair & Garrick (2007) that would maximise the level of gain achieved.

3.2.3 Components of Genetic Gain

Accuracy of Selection (r_{TI}) and Variance in the Objective (σ^2_T)

The accuracy of selection was calculated as a correlation between the true genetic merit and predicted genetic merit in line with the definitions of (Lynch & Walsh, 1998).

Heritabilities, phenotypic and genotypic correlations and phenotypic standard deviations for two indices, the Innervalue Fat index and the Innervalue Lean index, were provided for the traits in the selection indices.

Matrix functions in Excel were utilised to follow the method of Weller (1994) to find index weighting factors, the genetic standard deviation of the index and the correlation between the breeding objective (T) and the selection index (I), which is the accuracy of selection r_{TI} .

- Phenotypic variance-covariance matrix (**P**)
- Genetic variance-covariance matrix (**G**)
- Vector of economic weights in the objective (**a**)
- Vector of index co-efficients (**b**) = $\mathbf{P}^{-1}\mathbf{Ga}$
- Index variance = $\mathbf{b}'\mathbf{Pb} = \sigma_I^2$
- Objective variance = $\mathbf{a}'\mathbf{Ga} = \sigma_T^2$
- Accuracy of selection = $r_{TI} = \sqrt{(\sigma_I^2 / \sigma_T^2)}$

In this calculation of r_{TI} it is assumed that all available records on each individual is used to calculate the BLUP breeding values and maximise the selection accuracy.

Of the two indices involved in the analysis the Fat index was that on which selection was assumed to have been carried out over the studied period while the Lean index was introduced at a later date. Any comparison of the achieved gain, based on the genetic trend, and the estimated gain was with the Fat index. Analysis of the Lean index was included in order to display the benefits of changing index.

Generation Interval (L)

Based upon the definitions of Rendel and Robertson (1950) the Ls for each year were calculated separately for the ewes and rams using the following formula as defined by (Bichard et al., 1973):

$$L = \frac{\sum_{i=1}^x n_i l_{wi}}{\sum_{i=1}^x l_{wi}}$$

Where

n_i = number of ewes or rams of age i to age x (typically $i = 1$ and $x = 6$ or 7 for ewes and 4 or 5 for rams)

l_{wi} = number of lambs weaned to ewes or rams of age i

The overall generation interval ($L_{Overall}$) for each year was then calculated as an average of the ewe and ram Ls using the following formula:

$$L_{Overall} = L_{Ewes} + L_{Rams}$$

Where: L_{Ewes} = Ewe generation interval, L_{Rams} = Ram generation interval

Breakdown of the flock data revealed that hogget mating was carried out for six of the 10 years in the studied period (2003 to 2007 and 2009). Further breakdown of the L was carried out for years in which hoggets were mated (HM) and years in which they were not (HNM). A two sample T-test assuming equal variances was used to analyse the difference between the mean Ls of years hoggets were mated and years they were not.

Generation Interval Based on Replacement Selection (L_{Rep})

During the breakdown of the selection process it was found that significant numbers of animals were removed based on physical performance characteristics and/or died. As with the methods of Bijma & Wooliams (1999) an alternative estimate of the L was calculated to

assess the effect of this on the average parental age of replacements selected. This was calculated using the following formula:

$$L_{Rep} = \frac{\sum_{i=1}^x n_i l_{Ri}}{\sum_{i=1}^x l_{Ri}}$$

Where

n_i = number of ewes or rams of age i

l_{Ri} = number of replacement lambs retained born to ewes or rams of age i

Differences in the proportions of replacements between the parental age groups and between years were first analysed using ANOVA. A two-sample t-test assuming equal variances was then used to analyse the differences between years that hoggets were mated and years they were not for each age group, and between the number of replacements from hoggets and those from dams aged two to five years old. The proportions of rams sold by dam age group was also calculated from the data provided to identify any preference by dam age group.

Selection Intensity (\bar{i})

Selection intensity was calculated using the methods of Dickerson & Hazel (1944). This was achieved using timelines of disposal data for ewes and rams to map the yearly disposals across all age groups. This gave a count of the number of animals removed prior to the application of, and by, index selection each year and allowed for the calculation of the number of animals available before and after index selection events on a month by month basis using the following formula:

First selection event in a year:

$$N_{ti} = A_i - \left(\sum_{i=1}^t DC_i + \sum_{i=1}^t RIS_i \right)$$

Where:

i = Ewe or ram age group

t = round of selection

N_{ti} = Number of ewes or rams of age group i at round t of selection available for selection

A_i = number of animals of age group i available for selection at the start of the year

DC_i = Animals of age group i dead or culled prior to selection

RIS = number removed by index selection

The proportion selected at each selection event in a year for ewes and rams was then calculated using the following formula:

$$p = \frac{(N_i - RIS)}{N_i}$$

Where: p = proportion selected

N_i = Number of ewes or rams of age group i available for selection

RIS = number removed by index selection

The \bar{i} was then found using a reference table from Lynch & Walsh (1998) and the \bar{i} of any multiple selection events in a year and values for each age group were added together to obtain an overall \bar{i} for ewes and rams in each year (Morris, 1980). Truncation selection was not accounted for in these calculations and this is likely to result in upward bias in the calculation of genetic superiorities (Ducroco & Quaas, 1988).

In 2000 there was an unusually large number of ewes (233) disposed based on index. This was significantly more than the mean for 2001 - 2009 of 87 and therefore the year 2000 was excluded from the comparison of hoggets mated (HM) with hoggets not mated (HNM). This exclusion was based on the assumption that such practice was not a usual event and thus would add bias to the analysis of years that hoggets were mated, compared to years that

they were not. A two sample t-test assuming equal variances was used to analyse the difference between years hoggets were mated and years they were not mated.

During this process it was found that the majority of genetic selection was based upon live-weight BVs rather than Index BVs. As a result, calculation of \bar{i} was carried out as though all genetic selection had been based upon Index in order to display the effects of this practice. This was followed by calculation of average genetic superiorities of the top 160 ewe lambs and top eight ram lambs ranked for index value each year from BV data to display the difference in Index values.

The correlation between live-weight and Index value was calculated using the CORREL function in Excel for the BVs of all animals born between 2000 and 2009 inclusive for LW8 against Index and for LW12 against Index.

3.2.4 Estimated Genetic Gain

The estimated ΔG for the system for the years 2000 - 2009 was calculated using the following formula:

$$\Delta G = \frac{(R\bar{i} \times r_{TI} \times \sigma_g) + (E\bar{i} \times r_{TI} \times \sigma_g)}{(RL + EL)}$$

Where: R = Ram values and E = Ewe values

The existence of any difference between ΔI and the estimated ΔG in the Innervalue Fat Index was assumed to indicate that current management practices were resulting in a shortfall of ΔG .

3.2.5 Inbreeding

An estimation of the rate of inbreeding depression (F) of ΔG was calculated using the following formula as used by Everett (1984):

$$\Delta F = \frac{1}{8m} + \frac{1}{8f}$$

Where: ΔF = rate of inbreeding per generation

m = the number of breeding males

And f = the number of breeding females

The finding that flock numbers were sufficient to give a rate of F less than 1¢ per year meant that no further account was made of inbreeding.

3.2.6 Sensitivity of Genetic Gain and Financial Implications

In order to estimate the effects of the current management practices on the financial aspects of the system, and potential alternatives, two base systems were established for both the Fat and the Lean Indices, one mating hoggets and the other not mating hoggets. These alternative practices were both assumed to retain ewes until they weaned a lamb at six years of age and ΔG s and genetic superiorities (taken as the numerator of the ΔG equation ($\bar{i} \times r_{TI} \times \sigma_g$)) were equal to the means for each Index as calculated for the 2000 to 2009 period for ΔG analysis. The genetic contributions of each class of sires and dams to subsequent generations were taken as:

$$CR = \left(\frac{l_{Ri}}{\sum_{i=1}^x l_{Ri}} \right) / 2$$

Where: CR = contribution to replacements

l_{Ri} = number of replacement lambs retained born to ewes or rams of age i

Working expenses for the system were taken from a combination of the 2009 Lincoln financial budget manual (Lincoln University, 2009), AgriData (2010), and the Ministry of Agriculture and Forestry's 2010 National Sheep and Beef Pastoral Monitoring Report (Ministry of Agriculture and Forestry, 2010b) and 2010 Waikato/ Bay of Plenty Intensive Sheep and Beef Monitoring Report (Ministry of Agriculture and Forestry, 2010a) and set at \$37.61 per stock unit. The cost details of the genetic improvement program were provided by Landcorp Farming Limited and included: DNA parentage testing, ultra-sound scanning,

and CT scanning of a subset of ram lambs. The income per head of stock before genetic improvement was taken as: lambs \$80, cull ewes at \$80, and cull rams at \$80.

Gene flow methods as described by Hill (1974) were used following a combination of the methods developed in Hill (1971), Weller (1994), and Wolfova et al. (2011) to calculate the average annual discounted return, cumulative discounted return, cumulative discounted costs, net cumulative return and the number of years from first selection to break even. For the purpose of these calculations the profit horizon was taken as 10 years and the discount value for the period as 7% as reported in Weller (1994). Financial data were presented as costs and returns per stock unit with a total of 1318 stock units in the system as calculated from the Waikite base system stock reconciliation. This value was not assumed to change over the ten years for which financial estimates were completed for.

To follow the spread of genetic improvement through the population a vector $\mathbf{m}_{(t)}$ was defined that was of length $h + k$ where h was the number of male age classes in the population and k was the number of female age classes and t represents the time in yearly intervals. Thus at $t = 0$:

$$\mathbf{m}'_{(0)} = [1\ 0\ 0\ | \ 0\ 0\ 0\ 0\ 0\ 0]$$

and:
$$\mathbf{m}_{(t)1} = \sum_1^n S_{A_n} \mathbf{m}_{(t-1)_n} + \sum_1^n D_{A_n} \mathbf{m}_{(t-1)_n}$$

where: S_{A_n} = contribution of sires of age class n

D_{A_n} = contribution of dams of age class n

n = age class

A vector (\mathbf{s}) of length $h + k$ was defined as the genetic superiorities ($\bar{i} \times r_{T1} \times \sigma_g$) of selected animals at time t in dollars (\$).

The response to selection at time t was defined as:

$$RS_t = (\mathbf{m}_{M(t)} \times \mathbf{s}_S) + (\mathbf{m}_{F(t)} \times \mathbf{s}_D)$$

Where RS_t = response to selection at time t

$\mathbf{m}_{M(t)}$ = proportion of genes in population from males initially selected

$m_{F(t)}$ = proportion of genes in population from females initially selected

s_s = genetic superiorities of selected sires

s_D = genetic superiorities of selected dams

This response was cumulative over the 10 year profit horizon so the total response to selection (TRS) at time t was:

$$TRS_t = \sum_{i=1}^t RS_i$$

A vector \mathbf{w} of length $h + k$ with each element defined as:

$$\mathbf{w}_{(t)SAN} = (X_{SAN} \times \$80) + (X_{SAN} \times \Delta G)$$

Where X_{SAN} = number of animals sold in sex and age class (SA) n at time t

ΔG = genetic gain

$\$80$ = the price received for a cull animal prior to genetic improvement

The discount value of profits at time t was:

$$d_{(t)} = \left(\frac{1}{1+r} \right)^{t/m}$$

Where $d_{(t)}$ = discount value at time t

r = discount rate (7% for the purpose of this study)

m = the number of time period per year (1)

Profit made by one round of selection at time t was taken as:

$$P_t = RS_t \times \sum_{i=SA1}^{SA_n} w_t \times d_t$$

As with response to selection profit was cumulative and thus total profit at time t from single round of selection (TP_t):

$$TP_t = \sum_{i=1}^t P_i$$

Mean annual discounted returns at time t (MP_t) was calculated as:

$$MP_t = \frac{TP_t}{10}$$

Where the profit horizon is 10 years.

Profit made by continuous selection at time t was taken as (PC_t):

$$PC_t = \sum_{i=1}^t RS_i \times \sum_{i=SA1}^{SA_n} w_i \times d_t$$

Cumulative total profit (TP) at time t from continuous selection (TPC_t):

$$TPC_t = \sum_{i=1}^t PC_i$$

The cumulative discounted costs at time t (C_t) were calculated as:

$$C_t = \sum_{i=1}^t d_{(i)} c_{(i)} + c_{(0)}$$

Where: c_t = annual costs at time t

The net return at time t (NR_t) was calculated as:

$$NR_t = PC_t - C_t$$

As selection in this system was based upon the improvement of carcass traits, additional returns from increased wool or lamb production were not accounted for. The returns were thus based upon additional lamb value over \$80/ head, and increases in returns for the sale of cull for age ewes and rams (assuming ewes go to sale and rams are culled) (Conington et al., 2004). This may have underestimated returns from sales if more than an average of \$80 an animal was received over the 2000 – 2009 period.

In order to investigate how various changes in management practices would affect the ΔG and the financial returns and costs over the ten year profit horizon, alternative practices were investigated. These were split into two categories for ease of comparison, those influencing the age structure of the breeding flock (Table 3.1), and effected by farm management practices (Table3.2). These alternatives were calculated for the flock in years that hoggets were mated and years that they were not. The \bar{i} and contributions to the replacements selected each year were assumed to change with these practices, and subsequently the estimated ΔG s. Details of these adjusted values can be found in Appendix B. Also in Appendix B are the altered contributions of each dam age class to replacements for systems changes D, E, M and N (Table3.2).

Resulting ΔG s and financial values for each practice were compared to those of the Waikite base system and presented as the percentage difference from the base in order to identify management practices that would give the optimum levels of ΔG and financial benefit. The cumulative discounted costs were assumed not to change with these changes although it is possible that changes in the numbers of lambs born would have an effect on the cost of the genetic improvement program. Various management practices of the two categories could be combined to optimise the financial and genetic return as the magnitude of changes in each of the two over the base system would be additive.

Table 3.1 Treatment of base system to analyse the effect of changing parent age structure on the financial costs/ benefits of ΔG

System	Description
1	Rams kept until 3 years-old Ewes kept until 6 years-old
2	Rams kept until 3 years-old Ewes kept until 5 years-old
3	Rams kept until 3 years-old Ewes kept until 7 years-old
4	Rams kept until 2 years-old Ewes kept until 5 years-old

Also included in Table 3.2 are the details of systems investigated in Chapter 4 and the estimated effects of the current base system on the commercial clients of this system. In analysing the benefits to the commercial sector it was assumed that: males were the only source of gene transfer, all mating was natural, no male offspring in the commercial male population were retained for breeding, no breeding males were lost and all had equal contributions to the subsequent population of offspring, and that the contributions of commercial females to the replacements selected each year were the same as those in the nucleus operation as with the methods of Amer et al. (2007). The commercial system was assumed to be a breeding and finishing system of equal stock units to the Waikite base. All non replacement stock were assumed to be sold to slaughter at an average price per head of \$80. Further details of the various systems are included in Appendix B.

Table 3.2 Changes to management practices to analyse the sensitivity of the financial costs/ benefits of the base system

Treatment		Treatment Description
Fat Index	Lean Index	
A	J	Base System
B	K	100 ewe hoggets selected as replacements
C	L	250 ewe hoggets selected as replacements
D	M	Increasing contribution of younger age classes of dams to replacements
E	N	Further increasing contribution of younger age classes of dams to replacements
F	O	No DNA parentage testing - costs of selection program reduced (Chapter 2)
G	P	No DNA parentage testing , 20% Lambing-book error reducing genetic gain by 8% (Chapter 2)
H	Q	No DNA parentage testing , 7% Lambing-book error reducing genetic gain by 2% (Chapter 2)
I	R	Gene flow to commercial sector from base system - commercial flock same as base system, 2 rams purchased

3.3 Results

3.3.1 Base System Overview

Over the period 2000 to 2009 it was found that an average of 462 ewes lambed per year at an average lambing percentage of 138% across all age groups (Table 3.3). Lamb survival to weaning was 89%. The disposal file provided gave details of the removal of individual animals from the flock although it was found that the recorded deaths and missing animals for both ewes (289) and rams (304) in 2007 was unusually high and it was assumed that some of these deaths had been recorded incorrectly. Therefore the average death rate was recorded excluding the 2007 deaths and the resulting death rate was 7%. Due to the lack of further detail these "deaths" were not discounted for the purpose of \bar{i} calculation.

The farm working expenses were taken to be \$37.61 per stock unit (SU) and did not include the costs associated directly with the genetic improvement program which were DNA parentage testing, ultrasound scanning and CT scanning of select ram lambs. The income from ram sales and wool was calculated at \$132,828 with wool fetching \$4.20/kg, two year old rams \$850 /head and mixed age (MA) rams \$1250 /head.

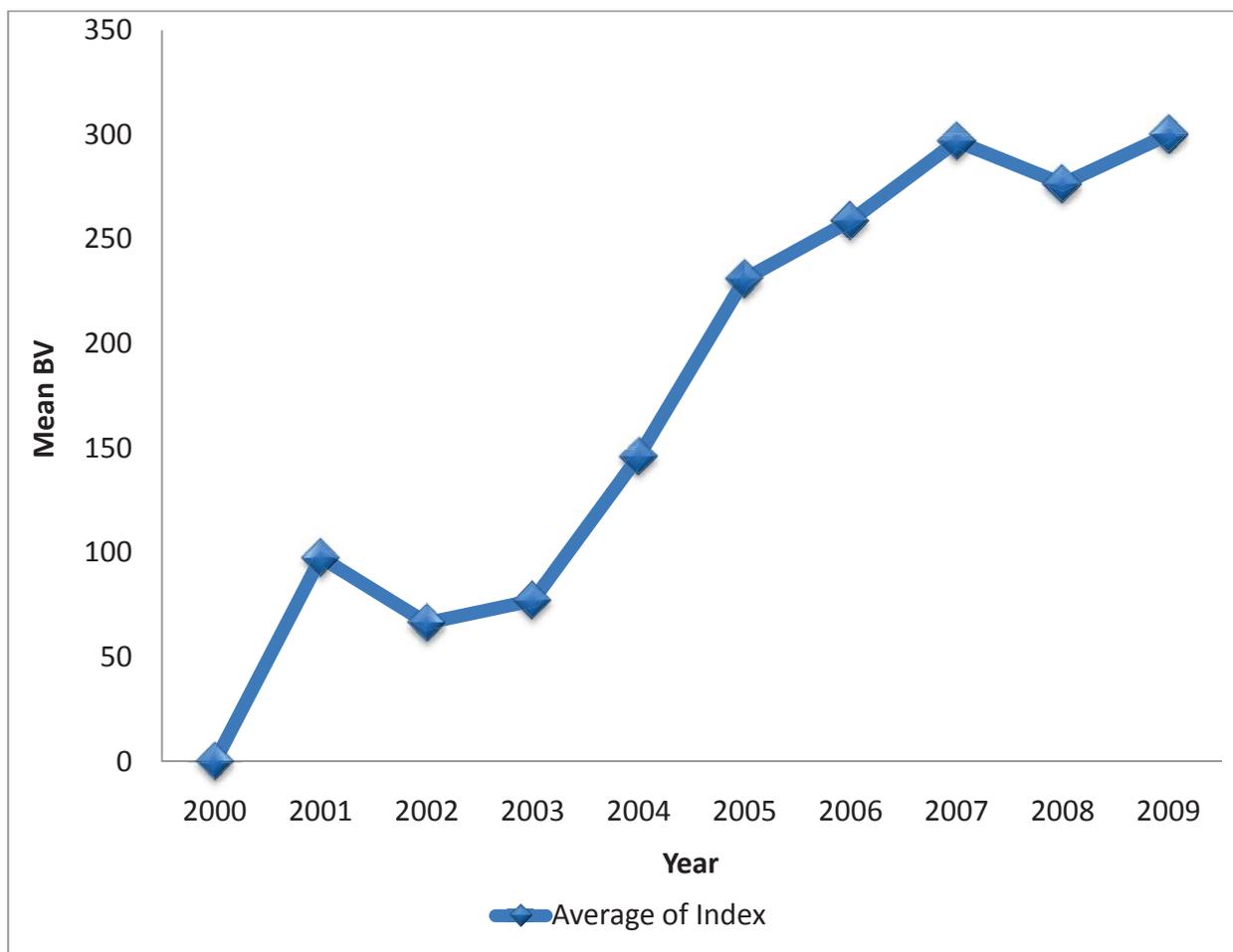
Table 3.3 Stock reconciliation for Landcorp Farming Limited Waikite Texel flock showing average stock numbers and movements between July 1st and June 30th

SHEEP Stock Class	July 1st - June 30th									
	Open	Births	Purchase	TRANSFER		Deaths	Sales	Culls	Closing	
				In	Out					
MA Ewes	266	0	0	223	0	13	0	210	266	
2 Year Old Ewes	268	0	0	268	223	19	0	26	268	
1 Year Old Ewes	340	0	0	344	268	24	0	52	144	
Ewe Lambs	0	386	0	0	344	42	0	14	0	
Ram Lambs	0	333	0	0	288	37	0	8	0	
1 Year Old Rams	259	0	0	288	204	13	0	71	259	
2 Year Old Rams	83	0	0	204	2	4	132	67	82	
MA Rams	24	0	0	2	0	1	1	0	24	
TOTAL	1240	523	0	1133	1133	153	133	448	1240	
Lambing %:	MA Ewes =	164%								
(Lambs born/ Ewes Lambing)	2th Ewes =	153%								
Lamb Survival (weaning) %:	Hoggets =	118%								Average % = 138%
Death (ewes) %:	89%									
	7%									

3.3.2 Genetic Trend in Index

Given that the studied period was from 2000 - 2009, and no prior BV or Index data was provided, lambs born in the year 2000 were assigned a population mean Index value of 0¢. This was in order to study the year by year effects of management practices on ΔG being achieved by the system. As seen in Figure 3.1, there was an increase in mean index value of 300¢ between 2000 and 2009 which gives a ΔI of 33¢/ewe/ year.

Figure 3.1 Mean Index value of lambs born each year between 2000 and 2009 inclusive.



3.3.3 Components of Genetic Gain

Accuracy of Selection and Variation in the Objective

The only difference between the parameters of the two indices investigated were in the values for hind leg, loin and shoulder (Table 3.4 and Table 3.5).

Table 3.4 Genetic and phenotypic co-variances and genetic standard deviations for the Fat index

Trait	Genetic σ	Innervalue Fat										
		WWT	LW8	C	A	B	Fat	Lean	EMA	CTHF	CTLF	CTSF
WWT	1.45		2.54	0.71	0.90	0.70	0.25	0.76	0.41	0.06	0.07	0.13
LW8	2.18	13.23		1.07	1.70	1.15	0.59	1.44	0.94	0.09	0.10	0.20
C	1.23	3.09	5.15		-0.33	0.59	0.41	0.08	0.23	0.09	0.10	0.20
A	2.06	5.18	8.11	0.81		1.68	-0.10	1.07	1.48	0.00	0.00	0.00
B	1.60	4.03	7.12	2.04	5.26		0.08	0.77	1.32	0.02	0.02	0.04
Fat	0.43	1.58	2.46	1.32	1.23	1.08		0.09	0.03	0.04	0.04	0.08
Lean	0.80	3.60	4.88	1.20	2.17	2.62	0.61		0.57	0.02	0.02	0.05
EMA	0.94	2.12	3.67	1.32	2.76	3.12	0.48	1.42		0.01	0.01	0.02
CTHF	0.10	0.36	0.56	0.26	0.31	0.24	0.12	0.15	0.11		0.01	0.02
CTLF	0.12	0.40	0.62	0.28	0.35	0.27	0.13	0.17	0.12	0.03		0.02
CTSF	0.23	0.79	1.23	0.57	0.69	0.54	0.27	0.33	0.25	0.07	0.07	

Genetic co-variances above the diagonal, phenotypic below.

Where WWT = weaning weight, LW8 = live-weight at 8 months, C = eye muscle fat depth, A = eye muscle width, B = eye muscle depth, EMA = eye muscle area, CT = Xray computed tomography, HF = Hind leg fat, LF = loin fat, SF = shoulder fat, HM = hind leg muscle, LM = loin muscle, SM = shoulder muscle

Table 3.5 Genetic and phenotypic co-variances and genetic standard deviations for the Lean index

Trait	Genetic σ	Innervalue Lean										
		WWT	LW8	C	A	B	Fat	Lean	EMA	CTH M	CTL M	CTS M
WWT	1.45		2.54	0.71	0.90	0.70	0.25	0.76	0.41	0.18	0.10	0.14
LW8	2.18	13.23		1.07	1.70	1.15	0.59	1.44	0.94	0.33	0.19	0.26
C	1.23	3.09	5.15		0.33	0.59	0.41	0.08	0.23	0.01	0.01	0.01
A	2.06	5.18	8.11	0.81		1.68	-0.10	1.07	1.48	0.23	0.13	0.18
B	1.60	4.03	7.12	2.04	5.26		0.08	0.77	1.12	0.17	0.09	0.13
Fat	0.43	1.58	2.46	1.32	0.71	1.08		0.09	0.03	0.02	0.01	0.02
Lean	0.80	3.60	4.88	1.20	3.04	2.62	0.61		0.54	0.14	0.08	0.11
EMA	0.94	2.12	3.67	1.32	3.80	3.12	0.48	1.42		0.10	0.06	0.08
CTHM	0.19	0.81	1.14	0.24	0.66	0.56	0.14	0.38	0.30		0.02	0.03
CTLM	0.11	0.48	0.68	0.14	0.39	0.33	0.09	0.23	0.18	0.05		0.01
CTSM	0.15	0.68	0.96	0.20	0.55	0.48	0.12	0.32	0.25	0.08	0.05	

Genetic co-variances above the diagonal, phenotypic below.

Where WWT = weaning weight, LW8 = live-weight at 8 months, C = eye muscle fat depth, A = eye muscle width, B = eye muscle depth, EMA = eye muscle area, CT = Xray computed tomography, HF = Hind leg fat, LF = loin fat, SF = shoulder fat, HM = hind leg muscle, LM = loin muscle, SM = shoulder muscle

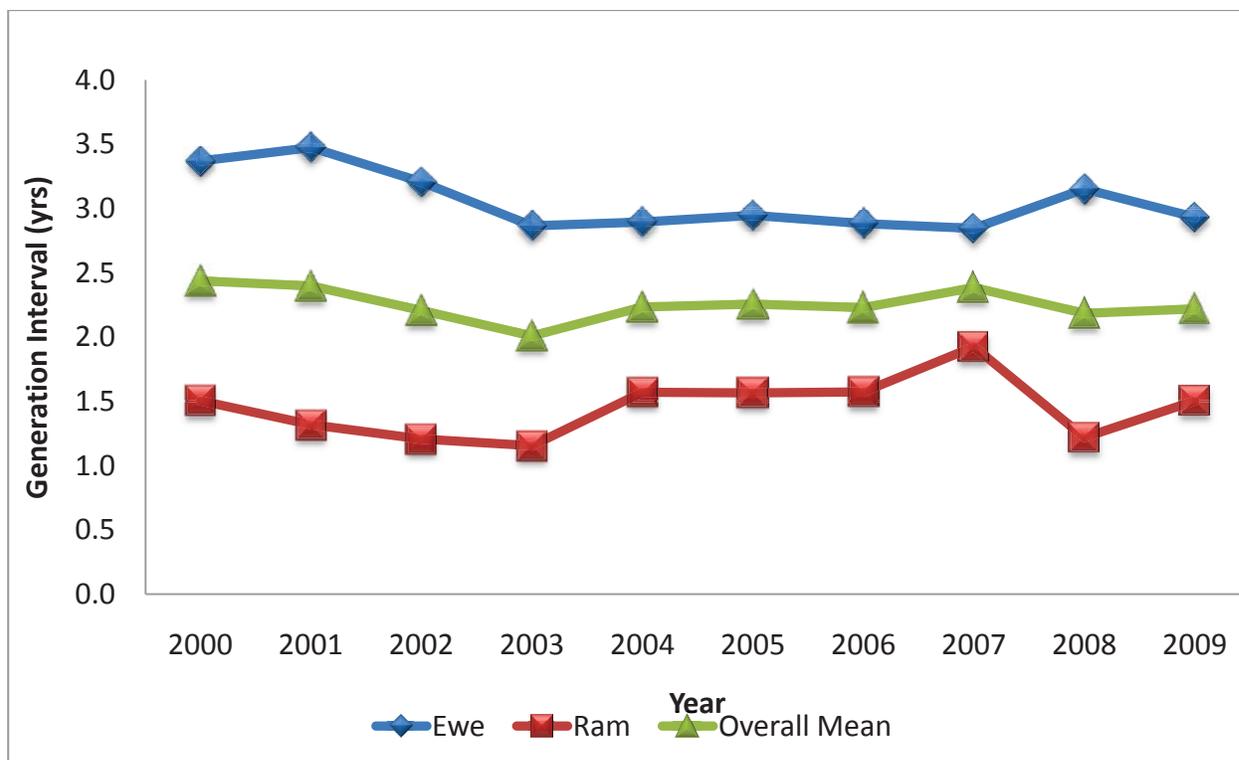
The standard deviation of the objective was 270¢ for the Fat index and 370¢ for the lean index. The correlation between the index and the objective was 0.55 for the Fat index and 0.60 for the Lean index.

It should be noted that the selection indices utilised by the genetic improvement program are not displayed in this report due to their commercially sensitive nature.

Generation Interval

The average ewe L for the period 2000 - 2009 was 3.06 years while the ram L was 1.45 years (Figure 3.2). Further breakdown of the L into HM and HNM found that the mean L for ewes was 2.89 years and 3.28 years respectively. Thus L was less ($P < 0.05$) for HM than HNM but neither value was different from the mean for the studied period. The ram Ls for HM and HNM were 1.55 years and 1.25 ($P > 0.05$) respectively. The overall mean L was 2.44 years.

Figure 3.2 Ewe, ram and average L calculated from parental contribution to lambs weaned



Generation Interval Based on Replacement Selection (L_{Rep})

Alternative calculation of L gave an average ewe L_{Rep} of 3.29 years (Figure 3.3) and an average ram L_{Rep} of 1.44 years (Figure 3.4), neither of which differed ($P>0.05$) from the generation interval calculated as the contribution of each parental age group to the number of lambs weaned.

Figure 3.3 Showing the ewe L_{Rep} and L for the studied period

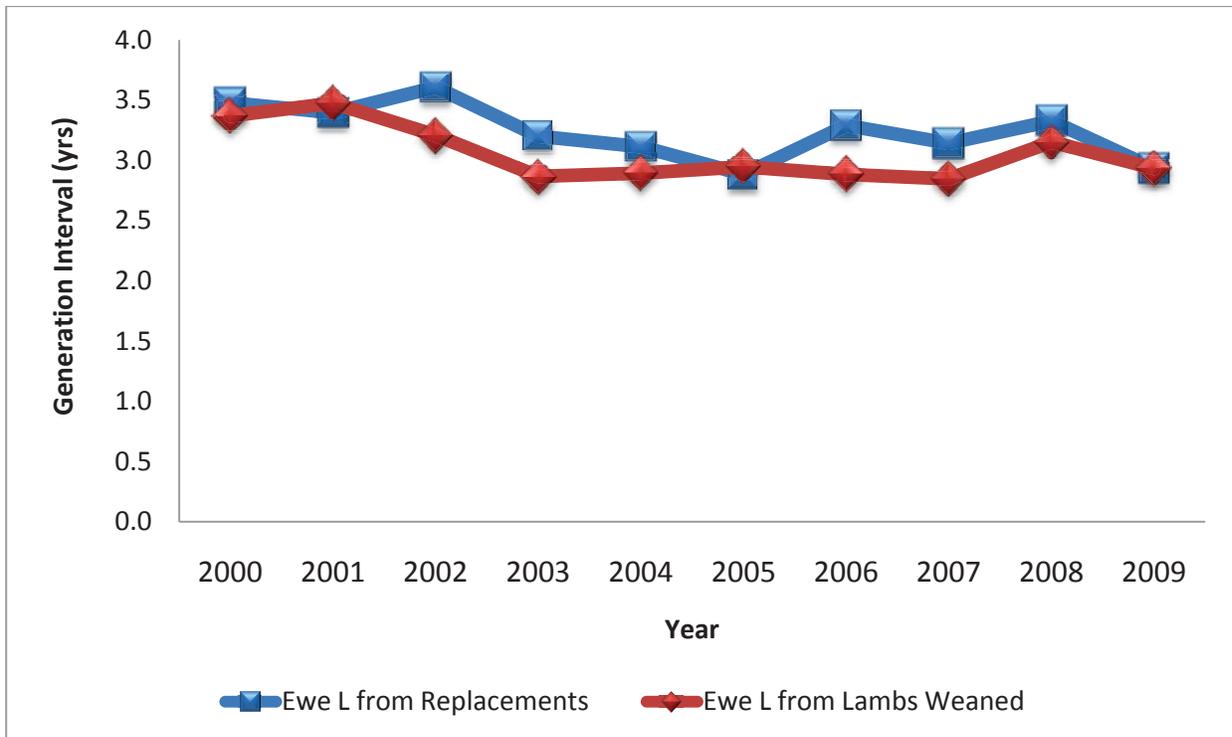


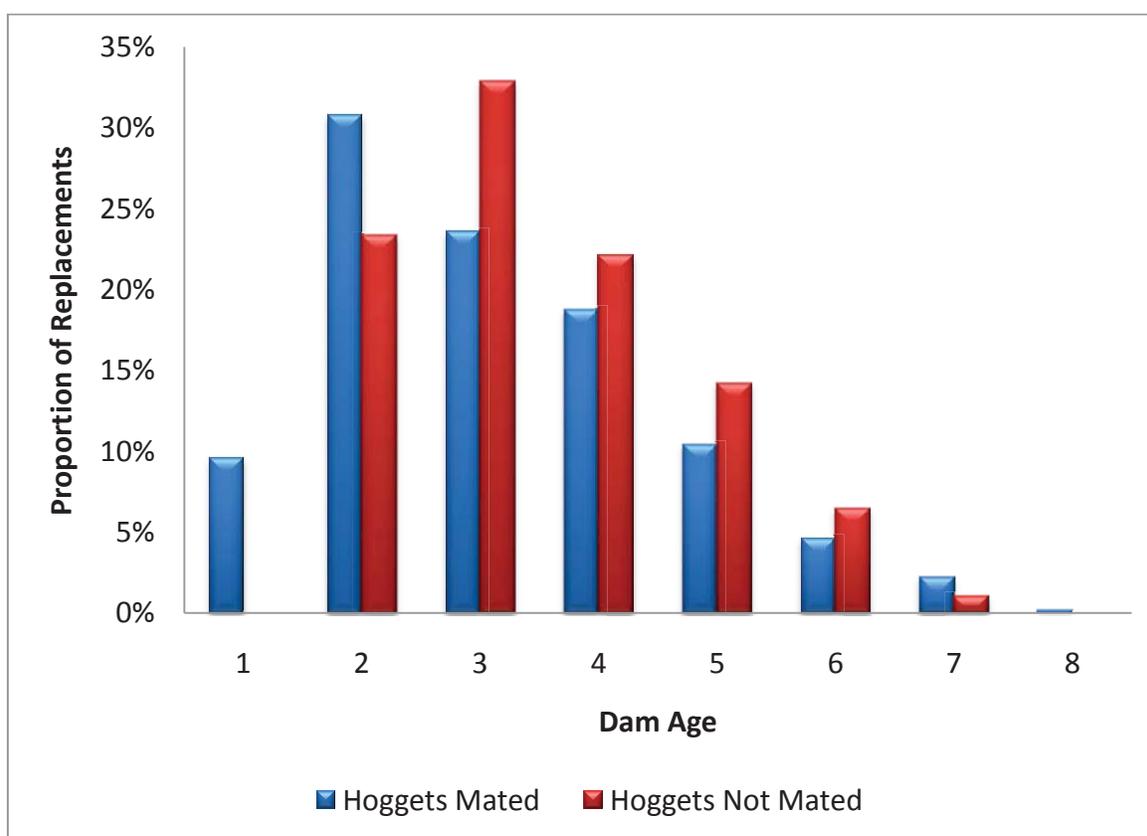
Figure 3.4 Showing the ram L_{Rep} and L for the studied period



The only dam age group that differed in the proportion of replacements selected between HM and HNM was one year old dams ($P < 0.05$). The contribution from all other age groups did not differ between HM and HNM ($P > 0.05$). This resulted in the decrease ($P < 0.05$) in the mean generation interval for HM and HNM. The mean number of replacements selected was 184 and 135 for HM and HNM respectively ($P > 0.05$).

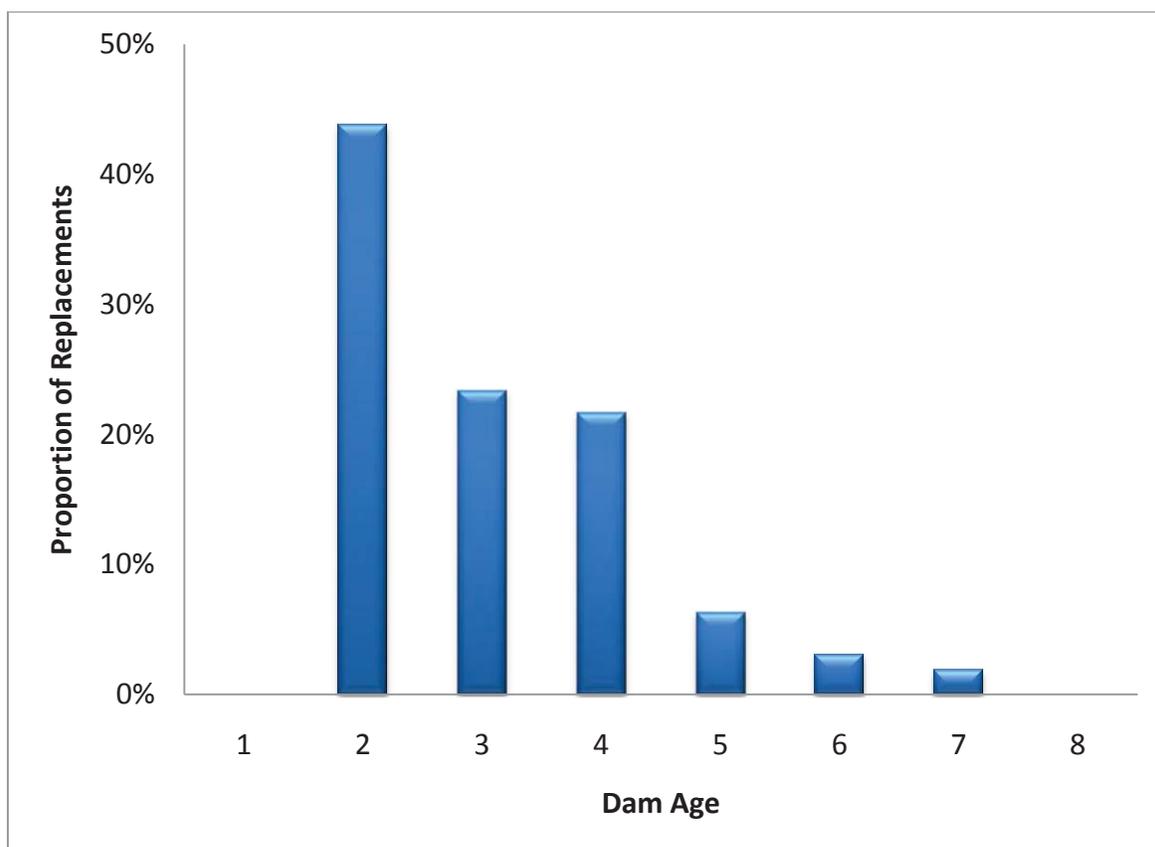
There was a difference ($P < 0.05$) in the mean percentage of lambs kept as replacements between the dam age groups (Figure 3.5). Replacements from ewe hoggets were less ($P < 0.05$) than proportions of replacements retained from two, three and four year old dams but did not differ ($P > 0.05$) from the proportion of replacements born to five year old dams (Figure 3.5). The proportion of replacements born to two year old dams had a mean of 26% while those from three year old dams had a mean of 22% ($P > 0.05$). On average 19% of replacements came from ewes five years or older (Figure 3.5).

Figure 3.5 The proportion of ewe lambs retained as replacements by dam age group



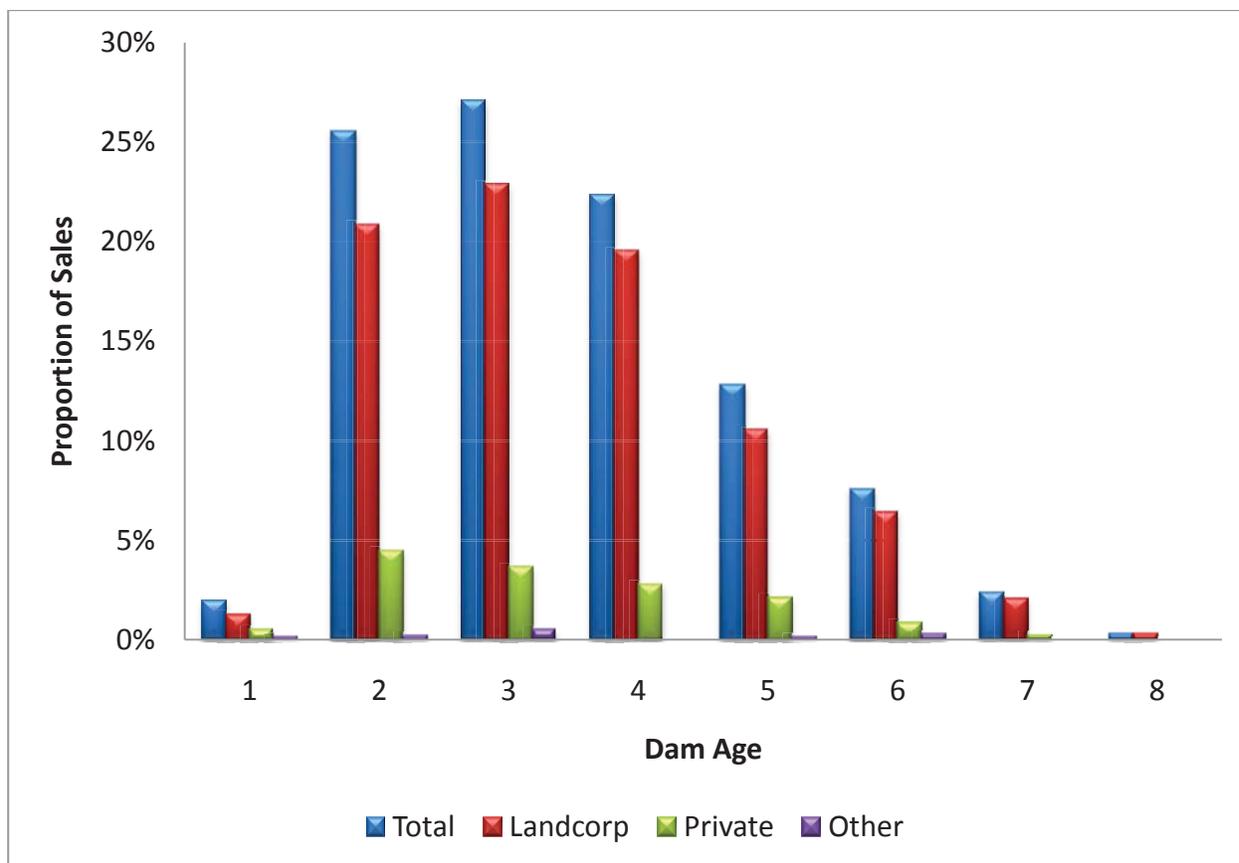
Of the eight ram replacements selected each year an average of four per year were born to two year old dams (Figure 3.6). This was more ($P<0.05$) than any other age group with the remaining four, on average, being born to three and four year old dams. In none of the years of the studied period were replacement rams born to one year old dams.

Figure 3.6 The proportion of rams retained as replacements by dam age group



Of the 1093 ram sales made over the period 2000 - 2009 83% were to other Landcorp farming operations while 15% ($P<0.05$) were sold privately and the remaining 2% were listed as 'Other' sales. Of those sold, 75% were born to dams between the ages of two and four inclusive while just 2% ($P>0.05$) of sold rams were born to one year old dams (Figure 3.7).

Figure 3.7 Average proportion of sales by dam age group



Selection Intensity

It was found during the breakdown of animal disposals each year that 42% of individuals were disposed based on live-weight BVs compared to 7% on Index value (Table 3.6). On average 175 animals across all age groups were culled each year based upon a variety of characteristics. Table 3.6 shows the percentage of those culled for each characteristic.

Table 3.6 Average percentage of animals culled for various traits

Disposal Description	Percentage
Structural	28%
Wool	0%
Pregnancy Diagnosis	16%
LWBV	42%
Index BV	7%
MDU or FDU	7%
Total	100%

NB: MDU & FDU = Male/ Female disposal unknown

Investigation of the BVs provided for all animals born between 2000 and 2009 showed that the BV for live-weight at eight months (LW8BV) had a correlation of 0.69 with Index value, and 12 month live-weight BV (LW12BV) had a correlation with Index of 0.61. A mean shortfall of 13% for ewe lambs (Table 3.7) and 32% for ram lambs (Table 3.8) in the difference between the mean genetic merit of the replacements would have occurred by selecting replacement based on the top LW8BV values. This shortfall based on LW12BV selection would be 16% for ewes and 35% for rams.

Table 3.7 Mean BV of the top 160 ewe lambs born per year based upon selection on Index value, eight month live-weight BV and 12 month live-weight BV

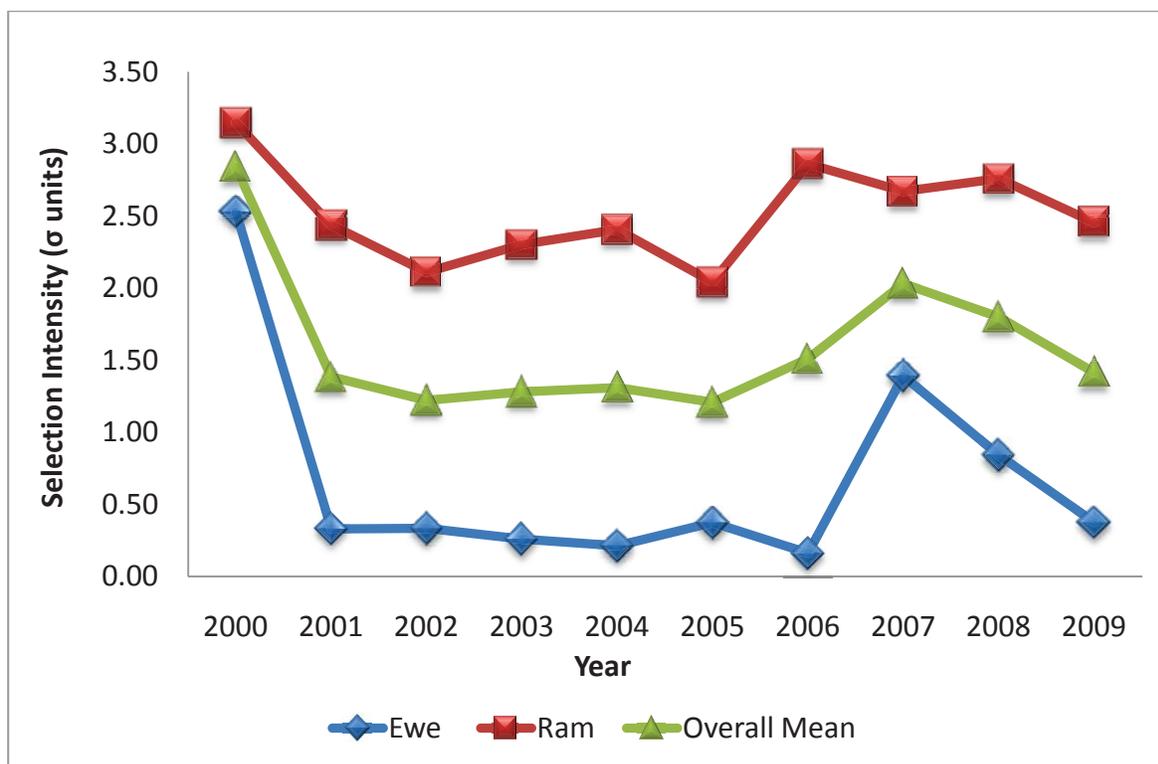
Year	Mean of Ewe Lambs	Based on Index	Based on Live-weight at 8 Months	Percentage Difference From Index Based Selection	Based on Live-weight at 12 Months	Percentage Difference From Index Based Selection
2000	301	452	397	-14%	393	-15%
2001	392	536	453	-18%	438	-22%
2002	358	511	444	-15%	430	-19%
2003	374	539	455	-18%	433	-24%
2004	461	658	578	-14%	556	-18%
2005	524	694	615	-13%	591	-17%
2006	561	729	675	-8%	687	-6%
2007	600	752	691	-9%	659	-14%
2008	567	678	628	-8%	629	-8%
2009	604	732	670	-9%	662	-11%
Average	474	628	561	-13%	548	-16%

Table 3.8 Mean BV of the top eight ram lambs born per year based upon selection on Index value, eight month live-weight BV and 12 month live-weight BV

Year	Mean of Ram Lambs	Based on Index	Based on Live-weight at 8 Months	Percentage Difference From Index Based Selection	Based on Live-weight at 12 Months	Percentage Difference From Index Based Selection
2000	299	831	552	-50%	527	-58%
2001	405	835	560	-49%	487	-72%
2002	376	776	515	-51%	517	-50%
2003	382	832	670	-24%	665	-25%
2004	430	882	652	-35%	639	-38%
2005	540	938	763	-23%	736	-28%
2006	557	1003	736	-36%	795	-26%
2007	594	953	854	-12%	776	-23%
2008	587	878	682	-29%	750	-17%
2009	596	925	813	-14%	787	-17%
Average	477	885	680	-32%	668	-35%

Further breakdown of \bar{i} revealed that the mean of the ewes was 0.68 which was less ($P < 0.05$) than that of the rams which had an mean of 2.52 (Figure 3.8). This gave an overall mean of 1.59 however in HM the mean ewe \bar{i} was 0.46 while the mean ram \bar{i} was 2.45. In HNM the ewe \bar{i} had a mean of 0.50 and the rams 2.43. There was no difference ($P > 0.05$) for both ewes and rams between HM and HNM.

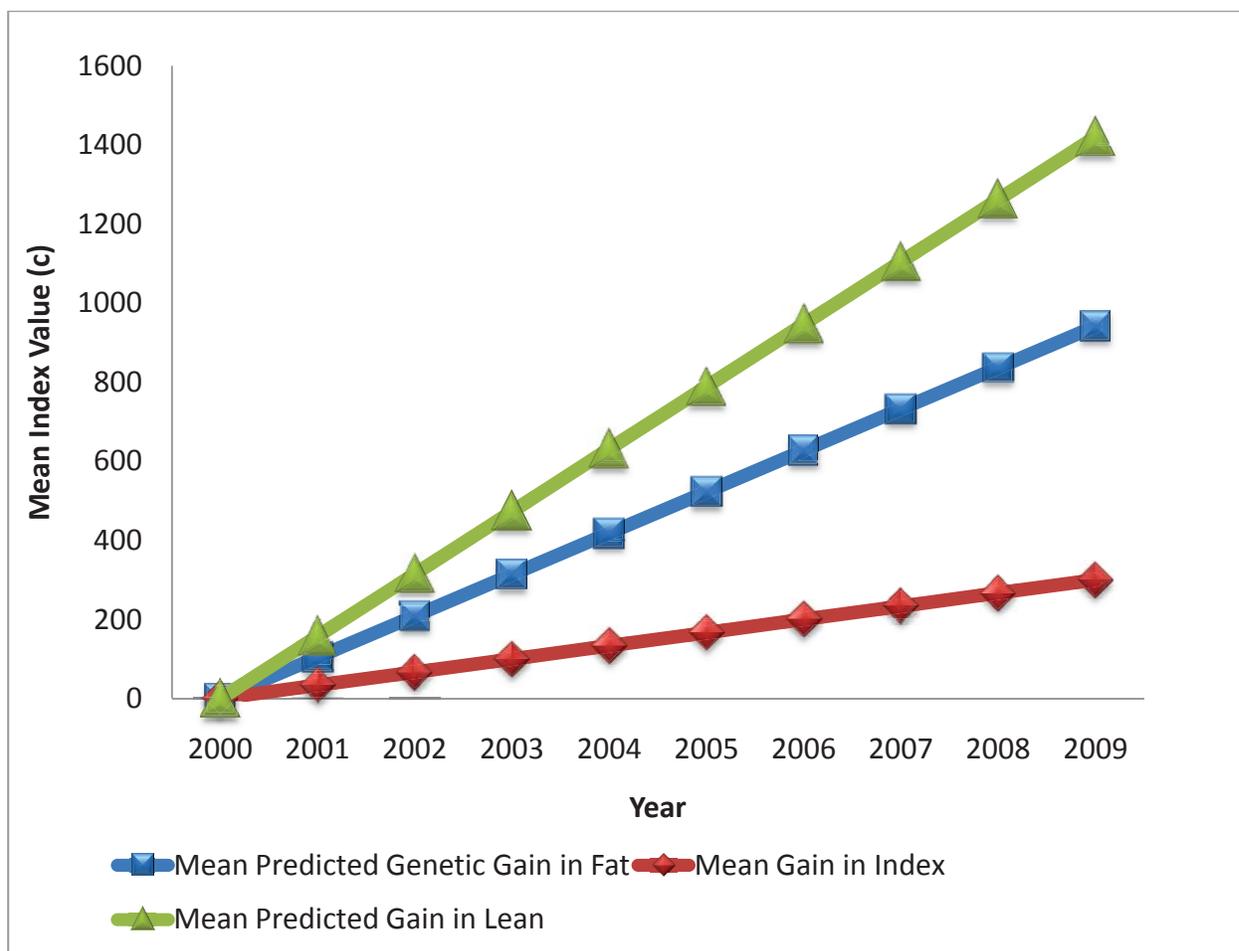
Figure 3.8 Selection intensities for ewes and rams and the overall flock mean for the period 2000 - 2009



3.3.4 Estimated Genetic Gain

The mean gain in the Innervalue Fat index for the period 2000 - 2009 was 97¢/ ewe/ year. The HM mean gain was 97¢/ ewe/ year and HNM mean (excluding 2000) was 96¢/ ewe/ year ($P>0.05$). The Innervalue Lean Index mean gain was estimated at 145¢/ ewe/ year for HM and 145¢/ ewe/ year ($P>0.05$) for HNM. The Lean Index made greater gains than the Fat Index in both HM and HNM ($P<0.05$). The mean gain in this index was estimated at 158¢. Estimated gain for the Fat index was greater ($P<0.05$) than that achieved by the selection Index which had a mean increase of 33¢/ ewe/ year (Figure 3.9).

Figure 3.9 Predicted change in mean index value for the Innervalue Fat and Lean indices and the achieved change in mean index value



3.3.5 Sensitivity of Genetic Gain and Financial Implications

Utilising the specific year by year practices of the system between 2000 and 2009 the achieved gain resulted in a net return of \$128 per SU which was 81% less than that estimated for the Innervalue Fat Index and 89% less than that of the Innervalue Lean Index (Table 3.9).

Table 3.9 Summary of financial implications for actual management practices carried out between 2000 and 2009 inclusive

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Cumulative Discounted Costs (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even	Percentage Difference from Lean
Lean	\$1.71	\$1,393	\$238	\$1,155	5	
Fat	\$1.14	\$926	\$238	\$688	5	-40%
Achieved Index Change	\$0.45	\$366	\$238	\$128	8	-89%

Based on mean figures of ΔG the net financial return from ΔG for HM systems, based on a 10 year profit horizon, was found to be greatest for the Lean Index (Table 3.10). At ΔI the net return for the 10 year period was \$131 per SU, 89% less than that of the Lean Index and 81% less than the Fat Index.

Table 3.10 Summary of financial implications of estimated and achieved ΔG with HM

System	Average Annual Discounted Returns per S.U.	Cumulative Discounted Returns (10 years) per S.U.	Cumulative Discounted Costs (10 years) per S.U.	Net Return from 10 Years of Selection per S.U.	Years From First Selection to Break Even	Percentage Difference From Lean
Lean	\$1.73	\$1,403	\$238	\$1,165	5	
Fat	\$1.15	\$933	\$238	\$695	5	-40%
Achieved Change in Index	\$0.45	\$369	\$238	\$131	8	-89%

ΔI in HNM system resulted in a financial loss of \$61 per SU over the ten year period (Table 3.11). This was 150% less than HM systems, 105% less than the Lean Index and 109% less than the Fat Index. There was no difference between the Lean Index systems mating hoggets and those not. The Fat however showed a \$6 net return per stock unit increase in systems mating hoggets over those not (Table 3.10 and Table 3.11).

Table 3.11 Summary of financial implications of estimated and achieved ΔG with hoggets not mated

System	Average Annual Discounted Returns per S.U.	Cumulative Discounted Returns (10 years) per S.U.	Cumulative Discounted Costs (10 years) per S.U.	Net Return from 10 Years of Selection per S.U.	Years From First Selection to Break Even	Percentage Difference From Lean
Base - Lean	\$1.70	\$1,385	\$220	\$1,165	5	
Base - Fat	\$1.13	\$921	\$220	\$701	8	-40%
Achieved Change in Index	\$0.20	\$159	\$220	-\$61	-	-105%

Application of the figures in tables Table 3.10 and Table 3.11 to whole system gross margins further reflected that the average annual return from ΔI was less than that of the Fat Index. This was both for HM systems (Table 3.12) and HNM systems (Table 3.13). As in Table 3.10 and Table 3.11, there is little difference in whole system gross margins of HM and HNM for the Fat Index.

Table 3.12 Summary of the average annual effects of costs and returns on the gross margin of a system mating hoggets for the Innervalue Fat index and actual gain achieved

	Fat Index	Achieved Gain in Index
Cumulative Discounted Income per S.U.	\$164	\$108
Cumulative Discounted Costs per S.U.	\$50	\$50
Cumulative Discounted Gross Margin per Dollar Invested	\$0.57	\$0.29
Cumulative Discounted Gross Margin per S.U.	\$114	\$57

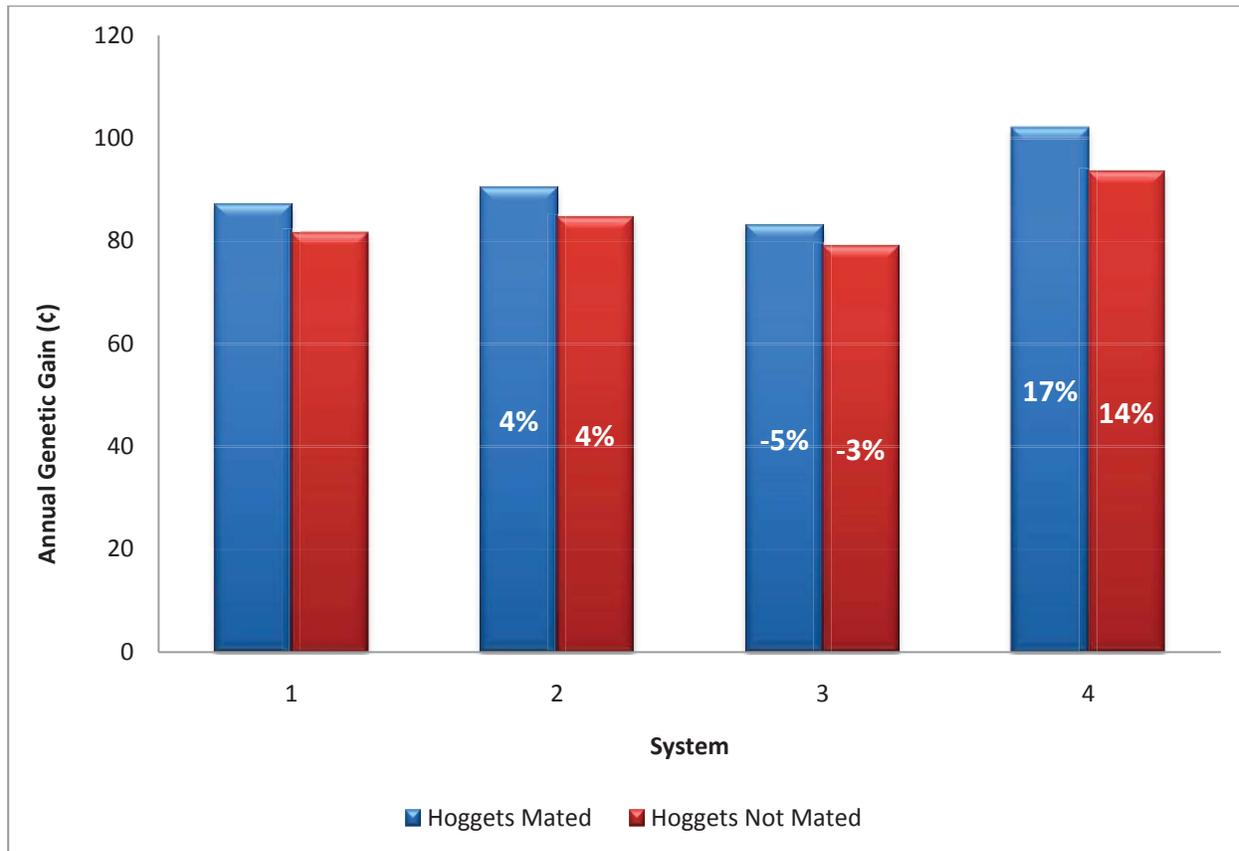
Table 3.13 Summary of the average annual effects of costs and returns on the gross margin of a system not mating hoggets for the Innervalue Fat index and actual gain achieved

	Fat Index	Achieved Gain in Index
Cumulative Discounted Income per S.U.	\$163	\$87
Cumulative Discounted Costs per S.U.	\$48	\$48
Cumulative Discounted Gross Margin per Dollar Invested	\$0.58	\$0.19
Cumulative Discounted Gross Margin per S.U.	\$114	\$38

Changes in Flock Age Structure

Figure 3.10 shows that the largest values of ΔG are made in systems where ewes are retained for breeding until five years of age and rams two. System 3, where ewes are retained until seven years of age and rams three, made the lowest levels of ΔG . Mating ewe hoggets consistently showed greater rates of gain than not mating ewe hoggets although this difference was least in systems where ewes were retained for longer (Figure 3.10).

Figure 3.10 Estimated annual ΔG made under different treatments influencing age structure applied to the base system for the Fat Index (see table in methods). Showing percentage deviation from base system.



1 – Rams kept until 3 years old, ewes kept until 6 years old, 2 - Rams kept until 3 years old, ewes kept until 5 years old, 3 - Rams kept until 3 years old, ewes kept until 7 years old, 4 - Rams kept until 2 years old, ewes kept until 5 years old.

Despite the highest levels of ΔG being made in System 4, the financial returns are the lowest of the three potential alternative systems investigated (Table 3.14 and Table 3.15). The greatest net return was gained from systems retaining rams until three years of age and ewes until five years of age and this system had the second greatest level of gain of the investigated alternatives (Figure 3.10). Keeping ewes until seven years of age gave the lowest ΔG (Figure 3.10) but gave better financial returns than System 4. The costs incurred by these systems remained the same as those of the base system and therefore not displayed below.

Table 3.14 Effects of changing flock age structure on the financial outcomes of 10 years of continuous selection on Fat Index while mating hoggets. Showing the percentage difference from the base systems as in Table 3.10 Summary of financial implications of **estimated** and achieved ΔG with HM

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
2	3%	3%	5%	0
3	-3%	-3%	-3%	0
4	-7%	-7%	-9%	0

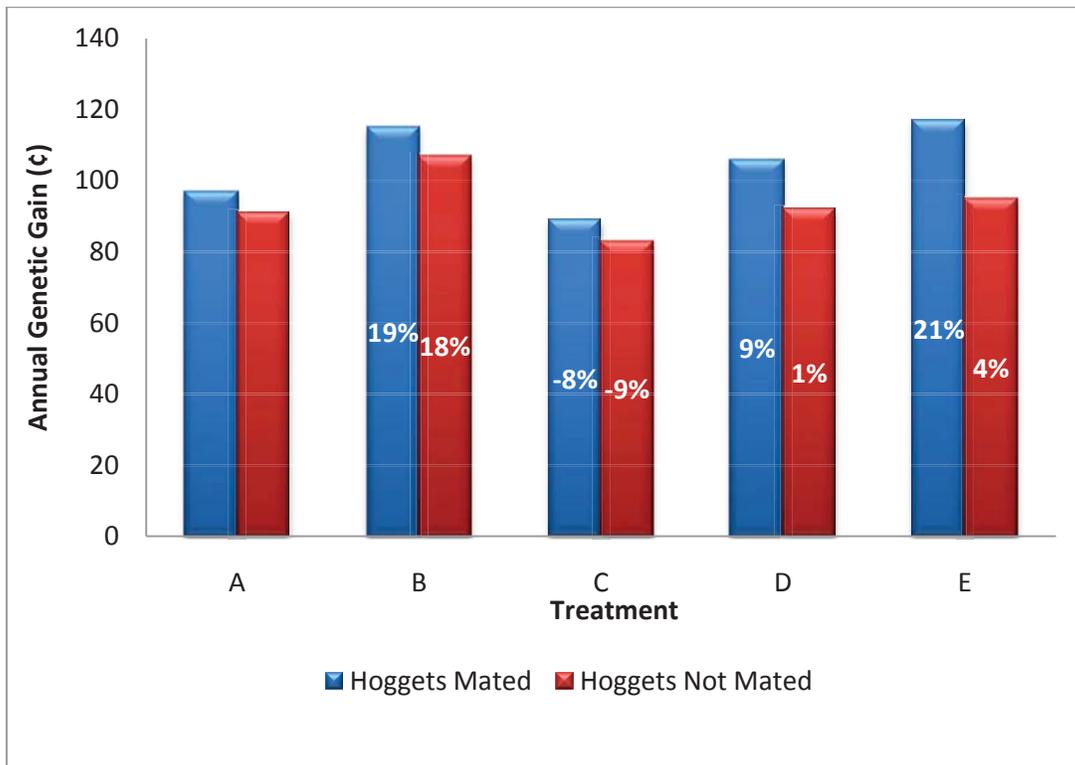
Table 3.15 Effects of changing flock age structure on the financial outcomes of 10 years of continuous selection on Fat Index while not mating hoggets. Showing the percentage difference from the base systems as in Table 3.9 & Table 3.10.

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
2	4%	4%	6%	0
3	-3%	-3%	-4%	0
4	-6%	-6%	-8%	0

Changes in Management

As shown by Figure 3.11 the system selection process that resulted in the greatest level of ΔG per year in HM systems was System E, increasing the number of replacements selected born to primiparous ewes to 40%. This did not hold true for HNM systems which achieved the greatest level of gain in systems selecting 100 hoggets as replacements. Decreasing the selection intensity by increasing the number of replacements selected resulted in the least amount of gain achieved of the five systems investigated.

Figure 3.11 Genetic gain for system changes in the Fat Index. Showing percentage deviation from the base system.



A – Base system, B – 100 ewe hoggets selected as replacements, C – 250 ewe hoggets selected as replacements, D – Increasing the contribution of younger dam age classes to selected replacements, E – Further increasing the contribution of younger dam age classes to selected replacements.

The system giving the most financial return over the ten year profit horizon period was that selecting 100 ewe hoggets as replacements for both HM and HNM (Table 3.16 and Table 3.17). In HM systems the net return was higher than HNM systems when greater proportions of replacements were born to hogget dams. Increasing the number of replacements selected was only financially beneficial in HNM systems.

Table 3.16 Financial effects of changing flock selection practices in systems mating hoggets. Showing the percentage difference from the base system

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
B _{HM}	20%	20%	26%	0
C _{HM}	-8%	-8%	-11%	0
D _{HM}	8%	8%	11%	0
E _{HM}	10%	9%	12%	0

Table 3.17 Financial effects of changing flock selection practices in systems not mating hoggets. Showing the percentage difference from the base system

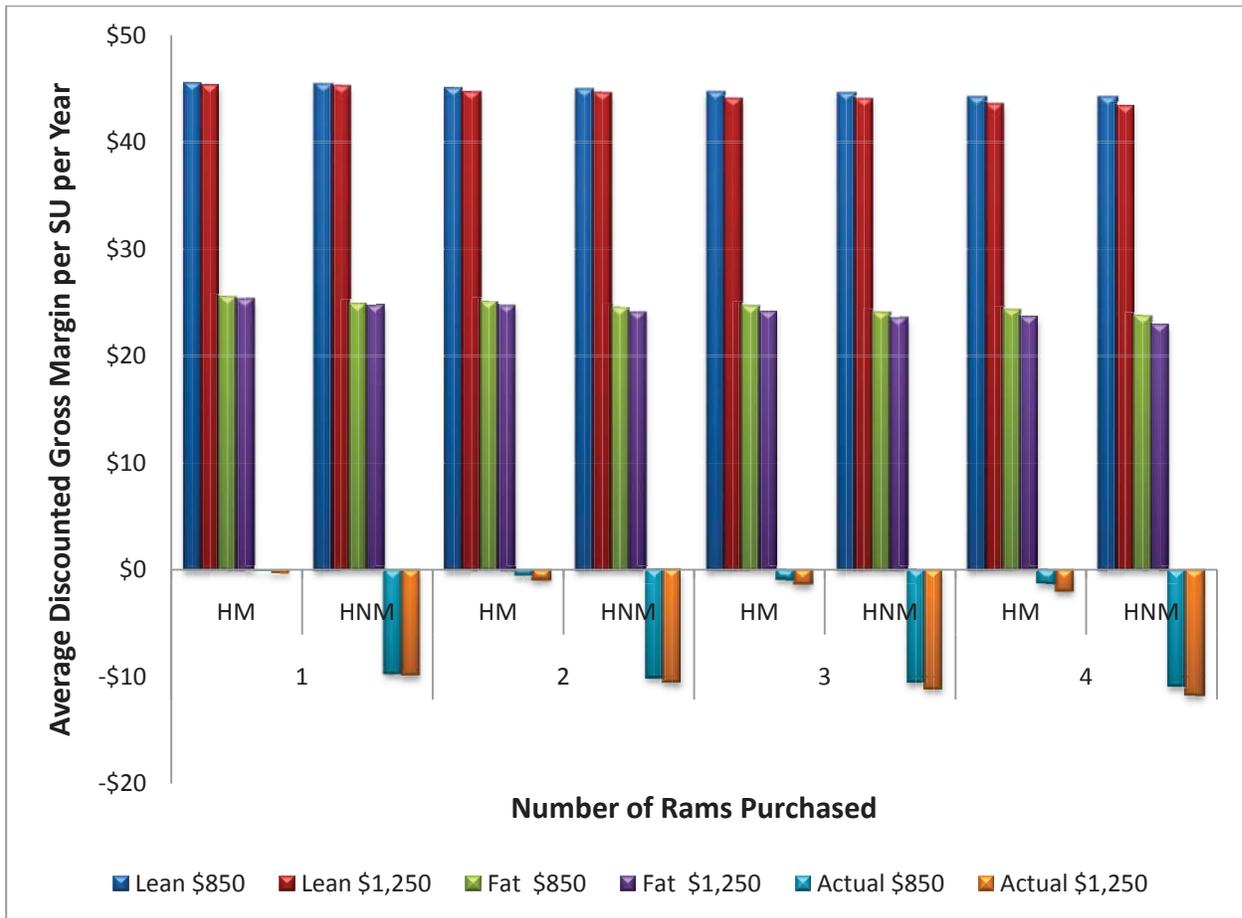
System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
B _{HNM}	18%	18%	24%	0
C _{HNM}	5%	6%	7%	0
D _{HNM}	5%	5%	7%	0
E _{HNM}	6%	7%	9%	0

Implications of Genetic Gain for Commercial Clients

The rate of gain estimated for the Fat and Lean Indices in the nucleus flock would have had subsequent beneficial implications for commercial clients of the operation as shown in Figure 3.12. At ΔI it is estimated that purchasing rams from the system is unlikely to financially benefit a commercial system with similar production parameters to that of the nucleus system. As with ΔG , HM gave a greater net return than did HNM systems with a mean difference of 36¢/ S.U. / year. Under ΔI this difference was \$9.36/ S.U./ year.

An increase in ram price of \$400 resulted in a mean reduction in the gross margin of only \$0.50 per S.U. per year (HM and HNM). This was the result of increasing costs while the percentage contribution of purchased rams to the next generation, and thus the return realised, remained the same.

Figure 3.12 Average discounted gross margin per S.U. per year from ten years of purchasing rams from systems under actual gain, and gain in the Innervalue Fat and Lean Indices. Showing two different ram prices for systems mating hoggets and not mating hoggets.



3.4 Discussion

3.4.1 Genetic Gain

As reported by Kuhlbers & Kennedy (1992), case studies of industries or working farm systems allow for the investigation of specific production parameters and levels of performance. In this case study carried out on the Landcorp Farming Limited Waikite Texel flock it was found that the mean ΔI made in the Index over the ten year period was 81% less than that of the Innervalue Fat index which was estimated as achievable for the system. The estimated ΔG achievable in the Fat Index was 0.36 standard deviations. This is slightly higher than the rate estimated by Blair & Garrick (2007) to be optimal financially.

The main reason for the shortfall of ΔI compared to ΔG in the Fat Index is likely to be due to the majority of genetic selection being based upon live-weight BVs rather than Index values. Over the studied period, selection on live-weight BVs accounted for 42% of all animals disposed compared to just 7% disposed on Index value. Such selection practices would have resulted in a lower than optimal \bar{i} and a loss of genetic improvement efficiency. This is supported by the findings of numerous studies which have shown that, when targeting gain in more than one production trait, Index selection is the most efficient form of genetic improvement (Hazel, 1943; Kuhlbers & Kennedy, 1992; Bijma & Wooliams, 1999).

Because a BLUP selection index utilises the best weightings of traits under selection, selection on a single trait in the index will not necessarily result in the optimum ΔG . While live-weight has a positive genotypic and phenotypic correlation with all carcass traits in the Innervalue Indices used in this system, thus giving an increase in carcass trait BVs along with live weight, the correlation of these live-weight traits with the indices is not 100%. The mean correlation between LW12 BV and LW8 BV and the Index value over the studied period was found to be 0.61 and 0.69 respectively. This reveals that the practice of selecting on live-weight BVs is therefore not giving the optimum improvement on ΔG and consequently not giving the full return on investment into genetic improvement. This shows that, although a financial return was made by the system during the studied period, adoption of management and selection practices targeting increased ΔG will be financially beneficial to the system.

The methods utilised in this study were derived from those discussed in the literature review. Nevertheless, several assumptions had to be made about the nature of the data utilised and the results obtained. These would have had varying effects on the estimates made in this study relating to both the genetic improvement and the financial return made. These are mentioned in the following discussion.

3.4.2 Variance in the Objective and Accuracy of Selection

In the calculation of the accuracy of selection and the variance in the objective, it was assumed that the genetic relationships between individual animals were included in the calculations of the genetic parameters which were thus specific to the system. If this was not the case then both the accuracy and the variance in the objective would differ from that calculated and likely give an incorrect estimation of ΔG . Use of the genetic parameters to calculate the accuracy of selection gives a population average accuracy of selection but the actual accuracies of individual BLUP calculated BVs will be different and continuous across a population (Macbeth, 1994). Although estimates of ΔG in a population can be made based upon the mean accuracy of animals available for selection, doing so does not account for the differences in accuracy between younger and older animals due to the number of records available (Macbeth, 1994) which may result in error in the estimation. Macbeth (1994) carried out a simulation of the selection response using different mean accuracies of the population in order to determine the variation in response. It was found that mean accuracies of 0.3 overestimated response to selection by 25%. Accuracies of 0.5 gave a 2% over estimation at the same variation of population accuracies. This overestimation will increase with an increase in this variance (Macbeth, 1994) and, as a result, will depend on the additional value that further phenotypic records add to the accuracy as individuals in a population age.

The accuracies of 0.55 and 0.6, calculated for the Innervalue Fat and Lean Indices respectively, are higher than those stated by Blair & Garrick (2007) as average for the New Zealand sheep industry.

In terms of the genetic variance, an important feature to note is that it will decrease in a population under selection. Kuhlers & Kennedy (1992) reported that culling based solely

upon BLUP breeding values will result in a greater loss of genetic variation per year, and an increase in the rate of inbreeding, compared to a system selecting based upon phenotype. Nevertheless, these effects were not found to be sufficient to offset the benefits to ΔG (Kuhlers & Kennedy, 1992). If this loss of genetic variation due to genetic selection is not accounted for in estimates of ΔG , selection response can be overestimated by as much as 40% in closed breeding schemes carrying out progeny testing although this will be markedly less in open systems (Christensen, 1994). Loss of genetic variation due to selection was not accounted for in this study, potentially resulting in an over estimation of ΔG and therefore an overestimate in the financial return from this improvement.

3.4.3 Generation Interval

As expected, yearly changes in the flock structure and management resulted in variation in the rates of ΔG achieved through the effects on L and \bar{i} . During the years 2000 to 2003 there was a steady decrease in ewe and ram L which is thought to be the result of active attempts by management to decrease L . The mating of ewe hoggets in 2003 and the subsequent steady ewe L suggests there was little change in management of the ewe flock until 2008. The ram L however, increased from 2004 to 2007, somewhat offsetting the positive effect of the low ewe L . In 2008 the ewe L increased but the ram L decreased which would have, once again, somewhat offset this change. This increase of ewe L occurred as a result of not lambing ewe hoggets and resulted in a decrease in ΔG . A widespread drought in New Zealand in the summer of 2007/ 2008 (Ministry of Agriculture and Forestry, 2008) is thought to contribute to this change in management as restrictions may have been placed upon stock live-weight gain. This would have therefore restricted the ability to breed ewe hoggets.

The average L for ewes is less than that reported by Blair & Garrick (2007) and the lack of change from 2003 to 2007 may indicate that significant further decrease would not be practical given the management and production environment. In this case, management practices focussing on maintaining a low ewe L , including the continued mating of ewe hoggets, will contribute to the optimisation of ΔG . If this is not the case then further attempts to reduce the ewe L offer the potential to increase ΔG .

Mating hoggets is a practice that holds the potential to decrease ewe L (Fogarty, et al., 2007) but this only the case if the resulting offspring are given equal chance of selection (Simm, 2000). In this system the mating of hoggets gives a higher ΔG than not mating hoggets although this difference was not significant over the duration of the studied period. The slight difference is mainly the result of a decrease in the ewe L. However, this was somewhat offset by the decrease in ewe \bar{i} in years hoggets were mated. Investigation of the age groups of dams of selected replacements in this study shows that, when hoggets are mated there is no priority of selection given to their offspring, which under genetic improvement, will have the highest Index values (Bijma & Wooliams, 1999). This is both for replacement ewe lambs and replacement ram lambs. It was found that, lambs of dams in their second parity are the group that contributes the greatest percentage of replacements selected. This may be the result of attempts to optimise the accuracy of selection. Alternatively, it may reflect selection of replacements following phenotypic selection on a trait, this trait may be live-weight as hogget lambs will often be lighter at weaning than lambs from mixed age dams (Kenyon et al., 2006). Because the probability of selection as a replacement should be related to parental age given selection on BLUP BVs, failure to base the majority of selection upon BVs, or to actively select animals from younger dams, is likely to result in the number of ewes of each age group being the main factor controlling L.

The traditional method of calculating L as the contribution of each age class to a generation of offspring is in line with the methods of Rendel & Robertson (1950). Nevertheless, selection on Index BVs including parental information should result in selection preference being given to animals born to younger parents (Bijma & Wooliams, 1999). As a result, calculation of L based upon the contribution to selected replacements is likely to be more representative of the actual system. In this study, the lack of difference between the mean L and L_{Rep} is likely to reflect the large degree of selection pressure being imposed based upon traits other than Index BVs. This reveals that there is some room for improvement on the selection practices that were used in the system.

A point to be noted however is that both of the methods investigated give an L estimate that is potentially different from actual values. Bijma and Wooliams (1999) found that calculating L, both based upon the average parental age of individuals weaned and individuals selected as replacements, was found to consistently overestimate L compared to

a stochastic simulation of a population. Given that genetic merit is partially passed from a parent to its offspring, Bijma and Wooliams (1999) investigated the assumption that L and L_{Rep} were less accurate than that calculated based upon long term genetic contributions. It was found that, for a trait with a heritability of 0.6, L varied depending on the method of calculation used as follows:

- Based on offspring weaned was overestimated by 26%
- Based on replacements selected was overestimated by 8%
- Based on long term genetic contributions overestimated by 9%
- Based on long term genetic contributions and parental sub-groups underestimated L by 1%

The exact magnitude of these differences varied with heritability although the relative difference between L , L_{Rep} and L based on long term genetic contributions remained the same. This shows that the accuracy of the predicted ΔG in this study would have benefited from calculation of L based upon long term genetic contributions and parental sub-groups. This method accounts for the inheritance of “selective advantage” by parental groups and sub-groups which increases its accuracy compared to calculations based on the average parental age of offspring born or replacements selected (Bijma & Wooliams, 1999).

3.4.4 Selection Intensity

As with L , the \bar{i} also reflects variations in management practices between the years for both the ewes and the rams. In 2000, disposal numbers of both ewes and rams were high, and therefore \bar{i} was unusually high compared to the rest of the studied period. These high disposals occurred across all age groups. A similar incidence was observed in the ewe disposal numbers in 2007 although this was not as large as that of 2000. It was reported that such high disposal rates are likely to be the result of a “clean-up” of individuals not physically present in the population but missing disposal details (Personal communication, Geoff Nicoll 2010). Because of these unusually high numbers of animals disposed, 2000 was

excluded from the analysis to give a result that is more representative of average management practices on farm for the entire system.

In the conduction of \bar{i} calculation, accounting was not made for truncation selection which, due to the disposals identified as “low” BVs for live weight and Index and genetic selection across age groups, is likely to have occurred. Truncation selection occurs when a threshold genetic value is set for selection and any animals, regardless of age, above this threshold are selected as replacements (Ducroco & Quaas, 1988). When populations under selection have overlapping generations the genetic merit of an individual will be related to its age as each age group will have different genetic variances and means (Ducroco & Quaas, 1988). This means that, under truncation selection, the probability of an individual being selected will be related to its age (Ducroco & Quaas, 1988). Neglecting to account for this in estimates of ΔG is likely to result in underestimates of the ΔG predicted as achievable by as much as 12% (Bichard et al., 1973). This is likely to be the most efficient form of selection in a genetic improvement operation (Kuhlers & Kennedy, 1992).

While the overall \bar{i} (averaged over the ewes and rams) of the system was within the range reported by Blair & Garrick (2007) that of the ewes was less than that reported to be possible when there are 1.3 lambs available at selection per ewe mated. This was the case for when hoggets were mated and were not mated. However, during years hoggets were mated, ewe \bar{i} was less than when they were not. If accounting of truncation selection was made then this predicted value may fall in the range reported by Blair & Garrick (2007). However, with 42% of individuals disposed based upon pregnancy diagnosis and structural faults, there is potential to increase the percentage disposed based on genetic merit. Although traditional selection of breeding stock in livestock industries worldwide was based upon physical characteristics rather than genetic merit (Harris & Newman, 1994) genetic selection is the most efficient form improvement (Kuhlers & Kennedy, 1992).

The ram \bar{i} was slightly less than the value reported by Blair & Garrick (2007) as achievable when the top 1% of candidates available for selection are selected. This is likely to be due to the use of ram hoggets as sires as this practice requires fewer ewes per ram than the use of rams 18 months or older for breeding (Smith & Knight, 1998). Nevertheless, this difference

is small and thus, without the adoption of artificial breeding technologies such as artificial insemination, it is not expected that there is much room for improvement.

Despite the potential of the methods utilised to give sub-optimal estimates of different ΔG components Bijma and Wooliams (1999) reported that, when predicting the ΔG being made by a system it is the ratio of genetic superiorities ($\bar{i} \times r_{TI} \times \sigma_T$) over L which is the most important factor rather than the separate definitions of both. As a result, L_{Rep} and \bar{i} as the deviation of the parents from the population mean gives acceptable results (Bijma & Wooliams, 1999).

Increasing the number of replacements available for selection presents a way to decrease L or increase \bar{i} however, increased lamb production targeting greater genetic improvement should be assessed to evaluate the associated costs and the benefits to the production system. An important point to note when attempting to increase ΔG is that reducing L and increasing \bar{i} by selecting fewer replacements, especially for the males of which there are fewer, will quite possibly result in increases in the rate of inbreeding and decreases in the genetic variance (Kuhlers & Kennedy, 1992). The degree of these changes will vary with population size and be most prominent in smaller populations unless genetics from outside the flock are introduced (Kuhlers & Kennedy, 1992). In light of this, systems carrying out BLUP selection should monitor rates of inbreeding and genetic variance along with any changes to the system.

3.4.5 Financial and Industry Implications

In the calculation of the financial benefit of genetic improvement to the system the estimated farm working expenses may differ from those actually incurred by the system but unless this is by a large amount, the financial results are unlikely to be greatly affected. It is also possible that the estimated average lamb price over the studied period was not \$80 as estimated and this may create some degree of error in the financial estimations. Despite this, the proportional differences due to different management practices are not likely to be affected by this. Another point to note about the methods utilised in the financial analysis is that accounting was not made of separate maternal traits in the calculation of gene flow.

Wolfova et al. (2011) stated that the inclusion of these traits are important in the development of gene flow algorithms. Their exclusion may have underestimated the genetic value of the female replacements selected and therefore underestimated the financial outcome of selection. A factor that may over-estimate the financial return of the system is the lack of accounting for depreciation. Hill (1971) stated that no accounting of depreciation is necessary only when the assumption is made that any assets are sold at the end of the time horizon. Such a sale is thought to be unlikely in this system.

During the financial calculations the assumption was made that the parameters used in the calculation of financial return such as lambing percentages, lamb prices, stock numbers and numbers sold had remained at constant at levels. These were set as means for the system that occurred over the 10 year profit horizon 2000 to 2009. In an actual operating environment, these values would have shown seasonal and/ or annual variation which reinforces the fact that the financial figures provided by this analysis are estimates only.

When the financial costs and returns of genetic selection were investigated it was found that, at ΔI , a financial return was made. Nevertheless, this was less than what was predicted to be achievable given the supplied genetic, phenotypic and production parameters. Using the mean production parameters of years hoggets were mated and years they were not, the expected net return after ten years of selection for both was calculated. It was found that ΔI resulted in a financial loss in systems not mating hoggets but a return when hogget mating was carried out.

Investigation of the Innervalue Fat and Lean Indices revealed that the Lean Index showed no difference in net return after ten years of selection between HM and HNM, however there was a slight difference in the Fat Index with HM returning slightly less per S.U. than HNM. This shows that the additional costs of mating hoggets, such as DNA testing more lambs were not returned by the additional benefits of ΔG and additional lamb sales and thus, the flock structure and selection practices during the time period studied did not allow for the realisation of the full benefits of hogget mating.

When different flock age structures were simulated using the base system production parameters the maximum ΔG was made by restricting the maximum breeding age of the ewes to five years of age and the rams to two years. Nevertheless this is also the flock

structure that gives the least financial benefit over ten years of selection. That which gave the most financial return was a system restricting maximum breeding age in the ewes to five years and rams to three years. This shows that, although high rates of ΔG are desirable, they are not always practical within the current system and/ or industry environment (Blair & Garrick, 2007). Nor are the highest rates of ΔG always the most cost effective (Blair & Garrick, 2007). Most farming systems are profit driven and therefore it is not feasible to maximise ΔG . Instead the financial and management investments must be balanced with the financial return received. This also indicates that there are optimum lengths of time animals should be retained in the population in order for the genetic contributions to generations of offspring to become established in the population .

Financially, the greatest benefit from the investigated changes in management practices resulted from increasing the ewe \bar{i} through a reduction in the number selected. Although some adjustment to L was made to allow for the immediate reduction in flock size, the continued use of this practice would soon surpass the ability of retaining ewes for longer to maintain the number of breeding ewes in the system. This would result in the need to either purchase additional ewes or significantly decrease the ewe \bar{i} . Alternatively, an increase in ewe \bar{i} could be achieved by increasing the number of lambs weaned per ewe.

In the investigated systems, increasing the contribution of primiparous two year old ewes to a generation of replacements had a lesser impact on ΔG and financial return than did increasing the contribution of primiparous ewe hoggets by the same amount. This shows that when ewes first lamb at two years of age, proportionally more focus must target restricting the maximum ewe breeding age, and that, in order for the full benefits of hogget mating to be realised, ewe hogget offspring must have equal or greater chance of being selected as replacements as those of older ewes.

At ΔI , commercial farming clients purchasing rams were estimated to not make any financial improvement in their systems. A loss was estimated to be made when both hoggets were mated and when they were not, despite the fact that HM gave a greater return than HNM. As would be expected, increasing the number of rams purchased by a commercial system only had the effect of increasing the costs incurred. In order for the returns to a system to be increased with the purchase of additional rams, it would be necessary to increase the

genetic contribution of these rams to a generation of lambs. At the higher rates of ΔG that were calculated for the Fat and Lean Indices, commercial systems were estimated to make a financial return, even when as many as four rams were purchased per year. This shows that, not only should a nucleus system focus on achieving the desired balance between genetic improvement and financial return, but that the ΔG achieved should be sufficient to financially benefit commercial farming clients purchasing breeding stock.

Rae (1964) predicted that, in order for a commercial farmer to purchase a ram which is genetically superior to those already in his flock, the nucleus flock rams are purchased from should be at least 0.75 standard deviations superior in any trait in the objective or in overall index value than the commercial flock. Nevertheless, this value does not take into consideration the long term financial costs and returns of the nucleus and commercial systems. Investigations, such as that carried out in this study, which provide such information are not only important for the continued benefit of ΔG to be realised on an industry scale, but also for the potential for investment in additional genetic improvement technologies to be realised.

Investment in new technologies that will benefit the sheep industry first requires that these technologies are profitable to individual nucleus systems (Everett, 1984). To achieve this, the technology has to either directly increase the returns of a system or reduce the costs without substantially increasing the labour requirement (Everett, 1984). Currently, the high cost of some tools to aid in genetic improvement (such as DNA parentage testing and CT scanning to measure meat yield) means that not all nucleus systems can afford to utilise them (Blair & Garrick, 2007).

Another way a nucleus system can increase financial return is to increase the price of breeding stock for sale. Harris & Newman (1994) stated that the pricing of genetically superior rams for sale should reflect their genetic, and therefore financial, value to the commercial sector. Receiving a return from ram sales which is reflective of the ΔG being achieved in the nucleus system would give more incentive, and more ability, for nucleus breeders to invest in genetic improvement systems and uptake new technologies in order to increase genetic improvement. If it was determined the current ram prices are not at such levels then it is possible for a nucleus breeding system to increase the financial return by

increasing ram price. If this was to occur then evidence of the returns that can be expected from ram purchases should subsequently be provided to clients (Harris & Newman, 1994). As a result, unless the purchased rams are of sufficient genetic superiority to give a financially beneficial increase in production to commercial systems over the current mean, then such changes would be difficult to justify.

In light of these findings it is recommended that steps be taken to increase the rate of genetic improvement. These steps include:

- Shifting the genetic merit selection pressure from live-weight BVs to Index values.
- Maintaining the ewe and ram L.
- Imposing more pressure on genetic selection and less on structural selection.
- Mating ewe hoggets where possible and ensuring lambs born to these dams have equal chance of selection.

Carrying out these recommendations will increase the ΔG being achieved and result in a greater genetic and financial benefit to both this nucleus system and commercial clients purchasing breeding stock from the system.

3.5 Conclusions and Recommendations

In conclusion, the ΔI was less than what could have been achieved as predicted from the flock production, genetic and phenotypic parameters. It was found that most of the genetic selection pressure is imposed upon live-weight BVs rather than Index BVs which contributed significantly to the shortfall in ΔG .

The L of both the ewes and rams was less than that reported by Blair & Garrick (2007) as average for New Zealand sheep industry nucleus breeders. It is possible that further decrease is not practical under the current operational environment of the system, however, continued selection on BVs will ensure that the L of both the ewes and rams remains low. Mating ewe hoggets is another practice that can be utilised to achieve this when practical. Nevertheless, this practice is only effective when the offspring of ewe hoggets are given

equal opportunity to be selected as replacements, which increased selection on BVs is likely to ensure.

The ewe and ram \bar{i} was less than that of Blair & Garrick (2007). The \bar{i} of the rams was only slightly less and this is attributed to the mating of ram hoggets and the need for fewer ewes per ram, and thus more rams for breeding, when utilising this practice. The cause of the low ewe \bar{i} was mainly the result of culling a large number of individuals based upon structural faults.

Investigation of the financial implications of ΔI and ΔG revealed that, although a financial gain was made in the system, there was a shortfall over that which could have been achieved. Mating hoggets gave a greater net return than not mating hoggets in ΔI but, at the higher levels of ΔG , the current management practices would not be sufficient to allow for hogget mating to benefit the system financially. This could be achieved by decreasing the ewe L or increasing ewe \bar{i} in order to further increase ΔG and the net financial return.

Not only was the shortfall in ΔG achieved restricting the financial return of the system but it is also resulted in an estimated loss being achieved by commercial farming clients purchasing rams from the system.

As a result of these findings it is recommended that steps be taken to increase the level of ΔG being achieved by the system. Such changes will increase both ΔG and financial return and have will also benefit commercial systems purchasing breeding stock from this nucleus system.

Chapter 4 Parentage Identification

4.1 Introduction

When estimating genetic merit prior to the availability of DNA parentage testing, it was assumed that offspring were accurately assigned to correct parents (Banos et al., 2001). Nevertheless, any errors in the assignment of parents to a generation of offspring will have an adverse affect on the ΔG , mainly through a decrease in the accuracy of selection (Long et al., 1990; Crawford, et al., 1993). The percentage of pedigree errors present will depend on several factors including the method used to determine parentage and how this method was carried out.

The aims of this study were to compare the results of lambing-book recorded parentage and DNA-assigned parentage, and to investigate the effects of lambing-book error on ΔG . Practices that should minimise pedigree error rates and potentially the cost of parentage recording, were identified.

4.2 Methods

4.2.1 Data

Two databases were received in the form of Microsoft Excel spreadsheets; the lambing-book database and the DNA parentage database.

The lambing-book database came from a study carried out by a previous study (unpublished data) on the effect of live-weight and live-weight gain in 950 mixed-age Romney ewes on the live-weight and survival of lambs. Ewes were assigned to paddocks based on scanning results for lambing and the 1779 lambs born were all matched to dams and tagged within 24 hours of birth. The records included: dam identification and age; lamb identification, birth rank, birth date and weaning date and weight.

The DNA parentage testing was carried out by Pfizer Animal Genetics (www.pfizeranimalgenetics.co.nz) on blood samples taken from individual lambs at docking. As

a result, any lamb that was not present at docking was not DNA tested. Lambs that were also not present at weaning were considered to have died between tagging at birth and docking and were eliminated from the analyses of DNA parentage. Lambs present at weaning but not DNA tested were also removed from the analysis. Three quintuplet litters, one sextuplet litter and one septuplet litter were recorded in the lambing-book. It was assumed that these large litter sizes were recording errors or rare events and the lambs associated with each litter were removed from the data prior to analysis. After editing, there were 1410 lambs with both lambing-book assigned dam and a DNA-assigned dam.

The DNA file included: lamb identification, birth date and birth rank; DNA match status and the P_prob; dam identification (including birth year) and sire identification (parental DNA information was assumed to be acquired from an existing database for the flock). In the identification of the parents of each lamb by DNA-assignment it is common that more than one parent can be listed however, in this analysis, only the best match dam and sire were provided. The "P_prob" was a value calculated by Pfizer and is "the probability that the pedigree combination is correct from the potential combinations tested" (Sharl Liebergreen, Pfizer Genetics, personal communication). Values ranged from 0.0 to 1.0. No lambing book records of sire identification were provided therefore, under the assumption that ewes were single-sire mated, and detailed records of this kept, investigation was only made of the identified dams and this value was therefore called the P_dam.

4.2.2 Analysis

The following parameters for each litter size were calculated:

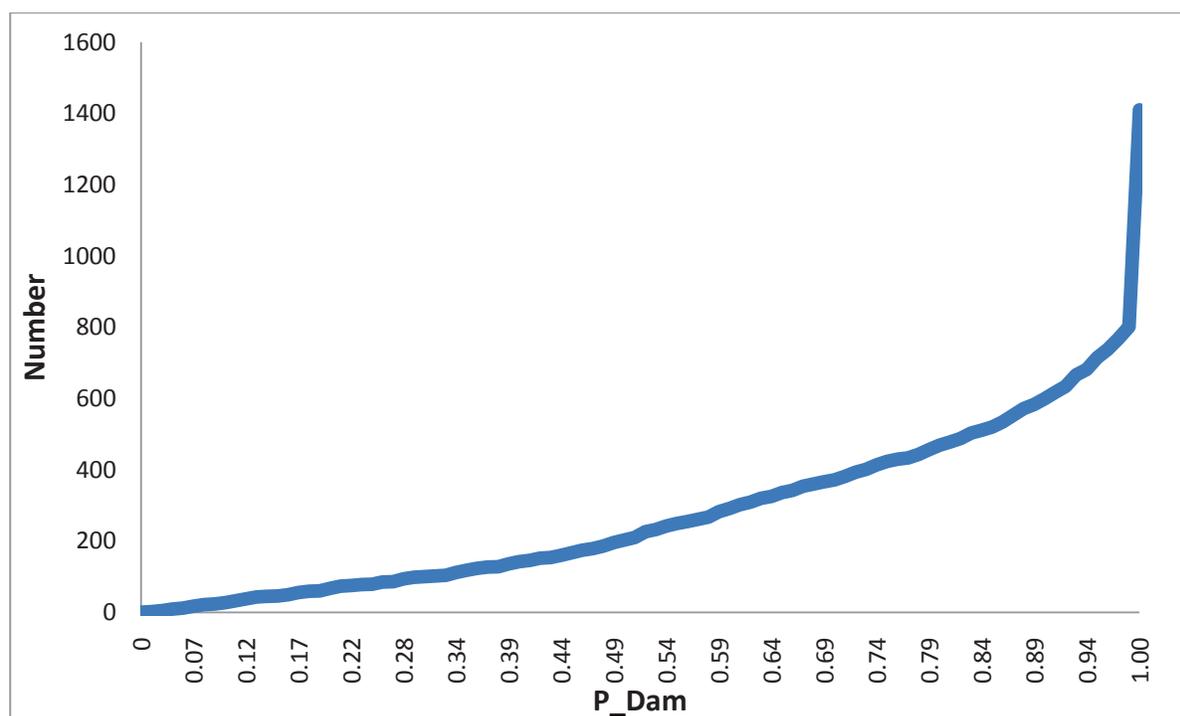
- The survival percentage of lambs - the number of lambs recorded as weaned in the lambing-book file divided by the total number of lambs born recorded in the lambing-book.
- The percentage of lambs born present in the DNA file - the number of lambs in the DNA file divided by the number of lambs born recorded in the lambing-book litter.

- Lambs with lambing-book and DNA dams matched as a percentage of those tested - the number of lambs in the DNA file with lambing-book dams matching the DNA-assigned dams divided by the total number of lambs in the DNA file.
- Lambs with lambing-book and DNA-assigned dams matching as a percentage of all lambs born - the number of DNA lambs with the correct dam divided by the total number of lambs born.
- The mean P_dam is the probability that the DNA selected dams are correct by lambing-book birth rank.

The lambing-book dam of each lamb was compared to the DNA-assigned dam to give a yes (1) or no (0) match. The mean P_dam of each litter size (1, 2, and 3) for those with the correct dam was calculated.

Due to the continuous nature of the P_dam values, and the non-normal distribution (Figure 4.1) lambs were divided into one of three P_dam groups: those with a P_dam of 1, those with P_dams between 0.5 and 0.99, and those with P_dams between 0 and 0.49 and were labelled P_dam 100, P_dam 50 – 99 and P_dam 0 - 49, respectively.

Figure 4.1 The cumulative frequency of P_dam values for all lambs DNA tested.



Data were analysed using a generalised model (GENMOD procedure) in SAS version 9.2 (SAS Institute Inc., 2008). Generalised models with binomial distributions were used to calculate the least square means. The data was first logit transformed for analysis and the logit means then back transformed to present the means. This analysis was completed for: the survival percentage (lambs weaned/ lambs born) and the percentage of lambs weaned (lambs born/ lambs docked), all with lambing-book birth rank as a fixed effect; lambing-book and DNA dam matching with dam age, lambing-book birth rank, P_dam group and birth rank by P_dam group as fixed effects. Differences with a P-value of greater than 0.05 were considered not significant.

To calculate implications of lambing-book error on long term ΔG and the financial costs and benefits, error was introduced into the Innervalue Fat and Lean indices of the Waikite Base system from Chapter One. The first pedigree error rate of 7% was equal to that found in the lambing-book and the second was set at 20%. The effect on ΔG was estimated based on estimates of Crawford, et al. (1993) and Long et al. (1990). The genetic superiority of the sires and dams was calculated by using the average Ls for ewes and rams for the base system and introducing ΔG reductions of 2% and 8% respectively.

In calculating the financial implications of DNA parentage and lambing-book error, the cost of DNA parentage (\$19.50 per head) was removed from the base system breeding program costs to display its effect on:

- The average annual discounted returns from a single round of selection.
- The cumulative discounted returns after ten years.
- The cumulative discounted costs after ten years.
- The net return after ten years.
- The difference from the base system.
- The percentage change from the base system.
- The number of years of selection required to break even.

Then the two rates of lambing-book error were introduced, in the absence of DNA parentage testing costs, to find the change in the same financial parameters.

4.3 Results

Table 4.1 shows the number of lambs of each litter size as were recorded in the lambing-book.

Table 4.1 Numbers of lambs recorded in lambing-book and DNA file

Birth Ranked	Lambs Present as in Lambing-book
1	218
2	1144
3	417
Total	1779

Ewes in Lambing-book = 950

Of these 1779 lambs present in the lambing-book, 346 were absent from the DNA file and were excluded from analysis. 304 of these missing lambs were not present at weaning and therefore assumed to have died before docking. This gave a lamb loss of 17% (lambs docked/ lambs born) of lambs born. 42 lambs that were not in the DNA file were weaned and thus considered to have been missed at docking. A further 23 lambs recorded as large litters in the lambing-book were excluded. Of the remaining 1410, 42% were assigned the P_dam 100, 43% to the P_dam 50 - 99 and the remaining 14% P_dam 0 - 49. In total 82% of lambs in the DNA file had the same dam as the lambing-book and the remaining 18% had different dams identified. In total 215 ewes gave birth to single born lambs, 630 to twins and 105 to triplet lambs.

Lamb survival was higher ($P < 0.05$) for both single- and twin-born lambs compared to triplets, although there was no difference ($P > 0.05$) between singles and twins (Table 4.2). Single- and twin-born lambs also had more ($P < 0.05$) lambs matching as a percentage of those present in the DNA file and those born than did the triplet lambs.

Table 4.2 Average litter born, weaned and DNA tested statistics for singles, twins and triplets

Lambing- book Litter Size	Lamb Survival (Lambs weaned/ Lambs Born)	Percentage of Lambs DNA Tested and Matched
Singles	183 (86% ^A)	151 (79% ^A)
Twins	931 (86% ^A)	811 (85% ^A)
Triplets	258 (64% ^B)	199 (75% ^B)
Average	1439 (81%)	1161 (82%)

^{ABC} Values with different superscripts are significantly ($P>0.05$) different

The mean P_dam values of twins and triplets DNA tested was greater ($P<0.05$) than that of the singles (Table 4.3).

Table 4.3 Mean P_dam values of all lambs DNA tested by litter size.

Litter Size	Mean P_Dam
Singles	76% ^A
Twins	81% ^B
Triplets	84% ^B

^{ABC} Values with different superscripts are significantly ($P>0.05$) different

The mean P_dam of those tested with matching dams varied between all three litter sizes. Triplets had a smaller mean, at 61% ($P<0.05$) than the singles and twins. Twins had a mean P_dam of 66% which was not different ($P<0.05$) from the single born lambs which had a mean of 65% ($P<0.05$).

Table 4.4 shows that the proportions of dams correctly matched varied between the three P_dam groups with P_dam 100 having the most and P_dam 0 - 49 the least. If the DNA identified dams in the P_dam 100 group are 100% correct then the lambing-book has an error rate of 7%. If this error rate is consistent across the other two P_dam groups then the choice of best match dam in P_Dam 50 - 99 will have a DNA error rate of 11% (given 82% correctly matched) and P_Dam 0 - 49 an error rate of 36% (given 50% correctly matched). Of those lambs that were DNA tested there was a greater proportion of twins matched to dam than triplets ($P<0.05$) (Table 4.4). In contrast singles did not differ from either twins or triplets in the proportion matched ($P>0.05$). The ratio of lambs in each of the P_dam groups did not differ ($P>0.05$) between singles, twins and triplets.

Table 4.4 Numbers and percentages of identified dams matched by litter size between the lambing-book and the DNA-assigned parentage. Across P_dam groups and totals.

Litter size	P_Dam 100		P_Dam 50 - 99		P_Dam 0 - 49		Total	
	Number	Dam matched ¹	Number	Dam matched ¹	Number	Dam matched ¹	Number	Dam matched ¹
1	71	65 (91%) ^A	89	73 (82%) ^A	31	16 (53%) ^A	191	151 (79%) ^{AB}
2	404	388 (96%) ^B	409	352 (86%) ^A	141	78 (55%) ^A	954	664 (85%) ^A
3	122	111 (91%) ^A	113	87 (77%) ^A	30	13 (43%) ^A	265	199 (75%) ^B
Overall	597	93%	611	82%	202	50%	1410	80%

¹ Number of dams matched with percentage of group matched in brackets.

with different superscript letters differ significantly at the 0.05 level

^{ABC}Values

It was found that, of the 861 ewe lambs and the 917 ram lambs in the lambing-book, 84% of ewe lambs and 79% of ram lambs had a matched dam ($P>0.05$) (Table 4.5) with mean P_dam values of 76% and 72% respectively ($P>0.05$).

Table 4.5 Numbers and percentages of identified dams matched by sex of lamb between the lambing-book and the DNA-assigned parentage. Across P_dam groups and totals.

Sex	P_Dam 100		P_Dam 50 - 99		P_Dam 0 - 49		Total	
	Number	Dam matched ¹	Number	Dam matched ¹	Number	Dam matched ¹	Number	Dam matched ¹
Ram	268	255 (95%) ^A	329	286 (87%) ^A	109	63 (58%) ^A	706	593 (84%) ^A
Ewe	329	309 (94%) ^A	282	226 (80%) ^A	93	42 (45%) ^B	704	556 (79%) ^A
Overall	597	95%	611	84%	202	52%	1410	82%

¹ Number of dams matched with percentage of group matched in brackets.

^{ABC}Values with different superscript letters differ significantly at the 0.05 level

Table 4.6 shows that as dam age increased, the percentage of lambs within each dam age group correctly matched decreases. No difference ($P>0.05$) in the average P_dam value or the percentage of lambs DNA tested of each birth rank ((Single/ twin/ triplet lambs)/ total lambs DNA tested) for each dam age group was found (data not shown).

Table 4.6 Numbers and percentages of identified dams matched by lambing-book dam age between the lambing-book assigned parentage and the DNA-assigned parentage. Across P_dam groups and totals.

Dam Age	P_Dam 100		P_Dam 50 - 99		P_Dam 0 - 49		Total	
	Number	Dam matched ¹	Number	Dam matched ¹	Number	Dam matched ¹	Number	Dam matched ¹
3	237	225 (95%) ^A	275	237 (86%) ^A	94	56 (60%) ^A	606	515 (85%) ^A
4	189	178 (94%) ^A	158	130 (82%) ^A	45	25 (56%) ^{AB}	392	318 (81%) ^{AB}
5	77	71 (92%) ^A	93	69 (74%) ^A	26	11 (42%) ^B	196	153 (78%) ^B
6	52	50 (96%) ^A	52	39 (75%) ^A	24	9 (38%) ^{AB}	128	100 (78%) ^C
7	42	40 (96%) ^A	33	28 (84%) ^A	13	4 (33%) ^{AB}	88	70 (79%) ^C
Overall	597	95%	611	80%	202	46%	1410	80%

¹ Number of dams matched with percentage of group matched in brackets.

^{ABC} Values with different superscript letters differ significantly at the 0.05 level

Over a period of ten years of selection, an error rate of 7% in the lambing-book resulted in a shortfall of index value of 6% for the fat index (Figure 4.2). An error rate of 20% resulted in a shortfall of 12% in the ΔG.

Figure 4.2 The effect of lambing-book error on the change in mean index value over a period of ten years for the Innervalue Fat index

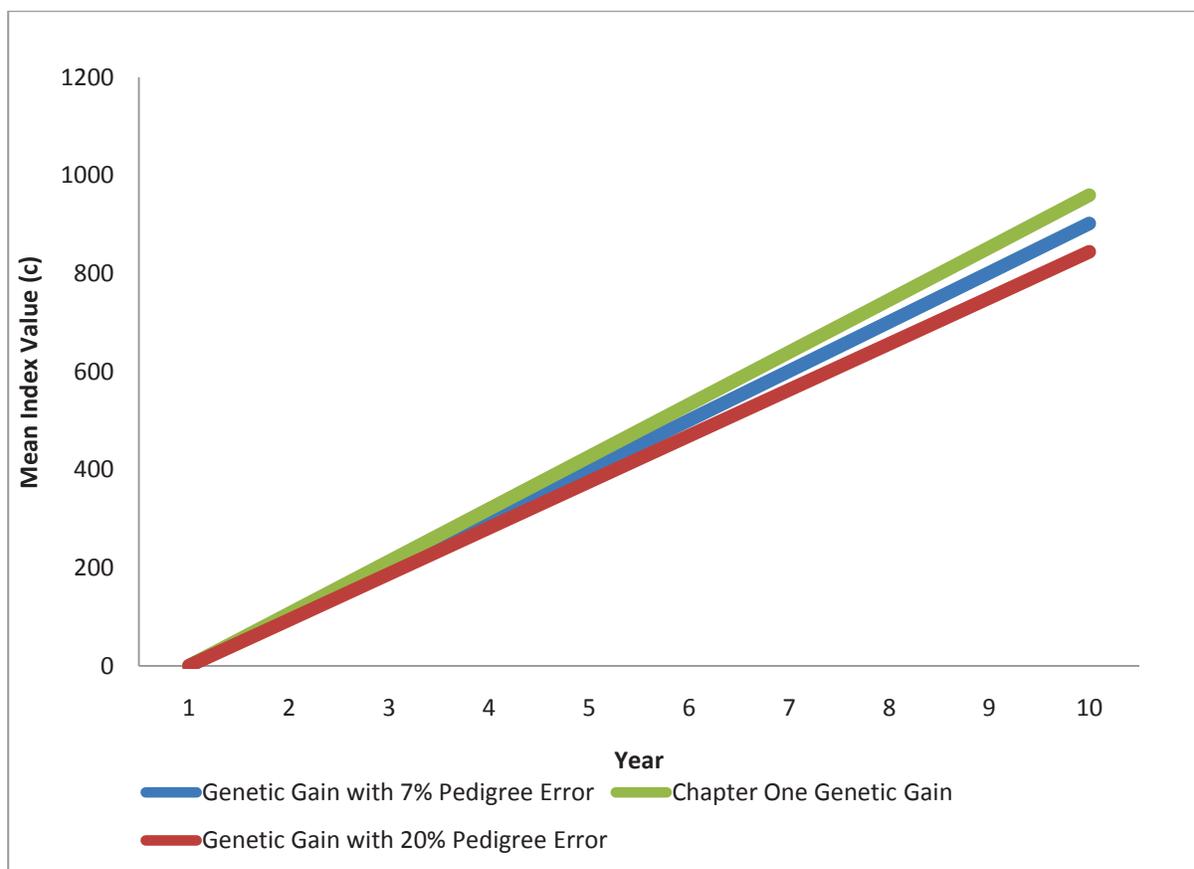


Table 4.7 and Table 4.8 show the cumulative financial effects of these error rates on the performance of the Waikite base system, when hoggets are mated and when they are not, for the Innervalue Fat Index over a period of ten years. These tables show that, at the current cost of DNA parentage testing incurred in the flock, the practice is generally only financially beneficial when hoggets are not mated and a 20% pedigree error rate would be incurred.

Table 4.7 Comparison of the financial performance per S.U. of the base system for the Innervalue Fat Index mating hoggets (presented in Chapter One) with no DNA parentage testing costs, assuming no lambing-book pedigree error, a 7% lambing-book error and a 20% lambing-book error

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Cumulative Discounted Costs (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even	Percentage Difference From Base
Base System	\$1.15	\$933	\$238	\$695	5	
Without DNA Parentage	\$1.15	\$933	\$148	\$785	5	13%
20% Lambing-book Error, No DNA Parentage	\$1.06	\$856	\$148	\$709	5	2%
7% Lambing-book Error, No DNA Parentage	\$1.13	\$925	\$148	\$777	5	12%

Table 4.8 Comparison of the financial performance of the base system for the Innervalue Fat Index not mating hoggets (presented in Chapter One) with no DNA parentage testing costs, assuming no lambing-book pedigree error, a 7% lambing-book error and a 20% lambing-book error

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Cumulative Discounted Costs (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even	Percentage Difference From Base
Base System	\$1.13	\$921	\$220	\$701	5	
Without DNA Parentage	\$1.32	\$1,076	\$143	\$933	4	34%
20% Lambing-book Error, No DNA Parentage	\$1.03	\$830	\$143	\$687	5	-1%
7% Lambing-book Error, No DNA Parentage	\$1.11	\$904	\$143	\$762	5	10%

4.4 Discussion

Ewes were randomly allocated across feeding levels prior to breeding and managed as one mob prior to lambing. As a result, feed levels were assumed to have no effect on the outcomes of this investigation. It was also assumed that, by the separation of ewes into mobs by scanning birth rank for lambing, there was no significant variation in the treatment between mobs that would have affected the results. This may create error if pasture cover was lower some paddocks as this could increase the incidence of mis-mothering due to ewes moving away from the birth site earlier to feed (Everett-Hinks & Dodds, 2008). A factor that may overestimate the financial return of systems not carrying out DNA parentage testing is the omission of potential additional labour costs associated with an increase in the number of lambing checks per day. This was due to the assumption that lambing checks are also carried out when DNA testing in order to record traits such as number of lambs born and birth weight. No details of other studies which investigated the relationship between lambing-book data and DNA parentage data were found to compare the results of this study to.

It is widely reported that triplets can display lower survival rates than singles and twins (Kerlake et al., 2005; Everett-Hinks & Dodds, 2008). This is reflected in this dataset with a lower percentage of triplet born lambs present in the DNA file than singles and twins due to a lower survival rate.

A potential drawback of DNA parentage assignment is the negative effect that missing data will have on the validity of the DNA database. Lambs not present in the DNA file due to being missed at docking will have an adverse effect on the validity of the DNA database should they be retained as flock replacements later in life (Bolormaa et al., 2008). In the case of such occurrences, animals should be tested after docking and entered into the database. Failure to do so would possibly lead to the assignment of close relatives (full or half siblings) as the dams of these lambs born to these animals given a "best fit" assignment of parentage.

This "best fit" assignment of parentage refers to the process of DNA parentage assignment that eliminates potential parents to find those that are the most likely matches (Banos et al., 2001). As a result, there is the possibility that, in systems where one or both parents have close

relatives also in the parent population, a large number of potential parents may be identified (Banos et al., 2001). In this DNA dataset just the best match dam was assigned for each lamb but at lower P_{dam} values there would have been several possible dams and thus a greater chance of error in the prediction. With a lambing-book error rate of 7% the error above this in the P_{dam} 50 – 99 and 0 – 49 groups is likely to be what results from the selection of more than one individual as a potential sire or dam and the selected "best match" parent being incorrect. This is a deficiency of the use of DNA parentage that will be especially prominent in a system that contains closely related animals (Sherman, et al., 2004) and reveals the need for this tool to be used in conjunction with a degree of on farm recording of stock identification and management.

If it was assumed that this 7% of lambs with dams not matching found in the lambing-book in the P_{dam} 100 group was a result of mis-mothering then this rate falls into the range reported by Blair & Garrick (2007). The lambing of all 950 ewes in this study took place over the space of 33 days between September 1st and October 3rd. This gives an average number of ewes lambing per day of 29. Based on the rates of mis-mothering reported by Alexander et al. (1983) and Blair & Garrick (2007) this means that anywhere between 2 and 4 lambs per day were mis-mothered and potentially recorded to the wrong dam. Checking lambing ewes just once a day, as was done in this study, gives limited opportunity to detect this so checking ewes on a more regular basis presents the chance to reduce error due to mis-mothering (Dodds et al., 2005) although this will result in an increase in labour costs.

Dam age had no effect on mean P_{dam} or litter size. In regards to the percentage of lambs DNA-tested only seven year-old ewes had fewer than the other dam age groups. Table 4.6 however, shows a clear downward trend in the number of lambs with dams matched as dam age increases. This potentially indicates a higher rate of mis-mothering in older ewes and, a possible decrease in expression of maternal behaviour as ewes age. Alternatively, maternal behaviour may have improved, and therefore tendency to steal lambs pre-parturition, increased with dam age. If poor maternal behaviour is the cause of this relationship then, in a system not accounting for pedigree accuracy during selection, the pedigree error rate will increase with an increase in the number of triplets born, which are reported by Everett-Hinks et al. (2005) to start replacing singles above 1.7 lambs born per ewe. An increase in the L of a flock will have a similar effect, subsequently decreasing ΔG .

Grandinson (2005) reported that, as litter size increases, dams must increase the time spent bonding with their lambs. The most important aspects of maternal behaviour were listed by this author as: behaviour that allows proper bonding of dam to offspring, nursing behaviour, attention paid to offspring, reaction to needs of offspring, and protectiveness. Such behaviours are important factors in lamb survival (Everett-Hinks et al., 2005; Grandinson, 2005; Everett-Hinks & Dodds, 2008). Thus there is a possibility that, as the number of lambs born increases above 1.7 lambs per ewe, triplet lamb mortality rates will increase in older ewes.

It has been found that there is a small genetic component to maternal behaviour as a trait of the ewe with the heritability being reported as 0.09 by Everett-Hinks et al. (2005). As a trait on the lamb, lamb survival had a heritability of 0.14 while the value for maternal effects was 0.11 (Everett-Hinks et al., 2005). Thus, selective breeding for the rearing ability of dams shows the potential to improve the survival rate of lambs. If this trait has been under selection in the flock in this study it is possible that genetic improvement contributes to the differences in the lambs match status as the younger ewes would have a higher genetic value for mothering ability. However it is also possible, and unobservable with the available data, that the trend results from unobserved factors in the DNA data set for this flock.

As was expected, given that the P_{dam} was a measure of the probability of the DNA matched dam being correct, the P_{dam} was directly related to the likelihood of the DNA dam matching the lambing-book dam. The separation of ewes at lambing by scanning rank means that, in a given paddock, there were fewer potential dams as litter size increased. This is an effect explained by Sise et al. (2001) and explains why the mean P_{dam} of each litter increased as litter size increased. This was despite the fact that the proportions of each birth rank in each of the three P_{dam} groups did not differ. The percentage of single lambs with matching dams was not different from the twins or triplets but this effect of lower P_{dam} indicates that there is room for improvement in the number correctly matched.

ΔG is greatest with a high degree of pedigree accuracy. The DNA output that was obtained from Landcorp Farming Limited did have a system to estimate the effect pedigree errors would have upon the breeding values of individuals. This system is called Fitted Pedigree Reliability and gives each individual a score (A, B, C or D) based on the effect of any alternative parentage on the breeding value/s. It is assumed that these are considered when making selection

decisions and that DNA error would have minimal impact on the ΔG of the Waikite base system. In this study, no investigation of the average birth rank of replacement lambs selected in the base system was made but, if a triplet born lambs were a significant proportion of these, then it is likely that the error in ΔG would be greater than that reported in this study. This is something that would affect the financial performance of the operation and warrants further investigation.

The findings of simulating the Waikite base system with no DNA parentage testing used and then with the introduction of lambing-book errors on the ΔG show that, despite the shortfall of up 6% in the ΔG experienced at a 7% pedigree error rate, maximum financial benefit is found in systems not DNA parentage testing and having minimal error in their pedigree records. When pedigree error rates of around 20% were experienced, resulting in a 12% shortfall in ΔG , a financial loss was made in comparison to the base system. This shows that the utilisation of DNA parentage is only financially beneficial when pedigree error rates would otherwise be high.

The financial loss from 20% pedigree error rates was greater in the Lean index which shows that, the greater the ΔG , the greater the cumulative shortfall of genetic merit, and therefore financial benefits, over the long term. Because the loss in gain is cumulative the approach taken towards DNA parentage testing will be unique to each system. If ΔG is a priority then DNA parentage should be utilised to reduce the risk of pedigree error. If financial input is restricted, the focus of DNA parentage analysis can be on groups identified as having high rates of mis-mothering or, alternatively, on farm management practices should be utilised that will minimise the chance of errors occurring in lambing-book records.

These findings have implications for any nucleus farm carrying out, or considering of adopting practices targeting genetic improvement. A 2003 report to New Zealand's Ministry of Agriculture and Forestry (MAF) titled *Shepherding Intensity and Ewe and Lamb Survival* (Brock et al., 2003) stated that, of 400 surveyed farmers running a combination of prime, store and stud operations, the majority had one shepherd to 1500 ewes while some had over 3500 ewes per shepherd. Nucleus breeding operations made up just 5% of farms surveyed (20 farms which, based on the New Zealand nucleus flock estimate of 1000 flocks by Garrick et al. (2000), is just 1.3% of nucleus flocks), 12 of these on hill country and the 8 remaining on flat to rolling

topography. Table 4.9 shows the frequency of checks made on the ewe flock during lambing in these flocks.

Table 4.9 The frequency of shepherding during the lambing period carried out on stud farms in a survey of 400 New Zealand Sheep farms by Brock et al. (2003)

	Frequency of Shepherding During Lambing					
	Never	Up to 1/week	Up to 2/week	Up to 1/day	Up to 2/day	More
Hill country (12)	18%	18%	9%	45%	9%	0%
Flat/ rolling (8)	0%	0%	0%	33%	44%	22%
Weighted Average	7%	7%	4%	38%	30%	13%

Although the numbers of nucleus schemes carrying out DNA parentage testing in New Zealand presented by Crawford et al. (2007) gave the approximate number of tests carried out in the nucleus of the sheep industry, the number, or percentage, of nucleus flocks that this represents was not given. Nevertheless, it is stated that those using this technology were more likely to be larger breeders for whom the benefits of reduced labour input outweigh the cost of testing. If the data from studs checking lambing ewes at least once a day from Brock et al. (2003) was representative of all stud flocks in the nucleus sector carrying out pedigree recording but not DNA testing in 2003, then 40% of pedigree flocks could have significant pedigree error rates similar to the 7% found in the studied flock if DNA parentage is not in use. This was estimated to reduce ΔG by 2% a year, an effect which is cumulative over time and this represents a shortfall in potential production both for individual systems and the industry.

The adoption of DNA parentage testing, and/ or the extent and manner of its use in nucleus breeding systems, will have implications for the financial and ΔG aspects of a system. Depending on the levels of investment cost and return and ΔG deemed acceptable there are precautions that can be taken to increase the chance of assigned parentage being correct using DNA parentage and/ or lambing recorded parentage. These include:

- More markers can be used in the DNA parentage assignment for all lambs born or just for select groups of those identified as being at risk of incorrect dam identification.
- Ewes can be single sire mated and lambled in mobs of approximately equal proportions of ewes from each sire group (Sise et al. 2001).

- Lambing can also be carried out in mobs based on the number of lambs identified at pregnancy scanning.
- The number of lambing checks per day can be increased, especially during the peak of lambing to increase the chances of observing lambs with the correct dam.
- If doubt exists around litter size and the placenta can be matched to the ewe the umbilical vessels can be counted (Alexander et al., 1983; Crawford, et al., 1993).
- The recording of information can also be double checked for duplicate or missing values on a daily basis (Crawford, et al., 1993).

The costs and returns of these practices were not investigated as the particular use of one or several of these will depend on the specific production environment, management practices and goals of a system. As a result, there are several factors to consider when investigating the potential uptake of DNA parentage testing including: the immediate and long term effect of DNA inaccuracies on ΔG ; the financial cost of DNA parentage testing; the potential management costs and benefits; the long term financial costs and benefits that will be incurred; and the management and production environment of a system. Thus, decisions on the usage of this technology are dependent on the individual/s involved in performance recording systems.

4.5 Conclusions

This investigation comparing lambing-book assigned parentage with DNA-assigned parentage found that the lambing-book had an estimated error rate of 7%. This falls within the average estimated by (Crawford et al., 1993). It is thought that this error could be reduced by increasing the number of lambing checks per day from the once per day in this study.

The number of lambs with dams matched between the lambing-book and the DNA-parentage decreased as P_Dam decreased. Singles had a mean P_Dam less than that of the twins and triplets. This is thought to be the result of a greater number of potential dams per paddock than were present for the twins and triplets. As a result, single born lambs were identified as a group that may benefit from practices targeting a reduction in pedigree error rates.

Triplet lambs had fewer dams matched than twins and had the lowest percentage of correct matches of the three litter sizes. The cause of this was thought to be a change in maternal

behaviour of dams with triplet litters compared to that of single and twin dams. As a result, this is another group that could benefit from increased focus on pedigree accuracy.

The percentage of dams matched also decreased as dam age increased, potentially indicating that maternal behaviour expression changes as ewes age in such a way that leads to more mis-mothering. Steps to minimise pedigree error rates in older ewes should be taken.

An error rate of 7% in pedigree identification in a system carrying out genetic improvement is estimated to result in a shortfall in ΔG of 6% over ten years of selection. However, the cost of DNA parentage was such that this shortfall, occurring in a system not utilising DNA parentage, did not result in a financial loss over the ten year period. If this error rate is increased to 20% then the shortfall in ΔG was estimated to be around 12% and the net return after ten years of selection is only slightly greater than that of a system carrying out DNA parentage testing. It is concluded that the use of DNA parentage assignment in a genetic improvement system will thus be for the main purpose of genetic improvement rather than financial return.

Chapter 5 Summary and Recommendations

5.1 Genetic Gain and Financial Implications in the Waikite Texel Flock

New Zealand has long been recognised as a world leader in pastoral agriculture (Morris, 2008), but for this reputation to be upheld continued improvement in farm management and performance is necessary. Genetic improvement has been, and can continue to be, used to achieve this and is a tool in which efficient and accurate use should be targeted.

Using flock genetic, phenotypic and production parameters and performance information from the years 2000 to 2009 inclusive for the Waikite Texel flock of Landcorp Farming Limited, an assessment of genetic gain (ΔG) and the associated financial implications was carried out. It was found that a mean Index change (ΔI) of 33¢/ewe/year was made over the studied period while it was estimated that a ΔG of 97¢/ewe/year was achievable in the Innervalue Fat Index, and 145¢/ewe/year in the Innervalue Lean Index.

The mean generation interval (L_{Rep}) of the investigated system, estimated at 2.44 years, was less than the three to four years stated by Blair & Garrick (2007) as typical for the New Zealand sheep industry. This was a result of both the ram and ewe L_{Rep} s being close to the minimum values possible in a sheep breeding operation as reported by Blair & Garrick (2007). In years ewe hoggets were mated (HM), the ewe L_{Rep} was less than years that they were not (HNM). These values were obtained by defining L_{Rep} as the average age of the dams of lambs selected as replacements.

In a genetic improvement system selecting mainly on BLUP derived BVs, younger animals will generally be of higher genetic merit than older individuals, as will animals born to younger dams compared to those born to older dams (Bijma & Wooliams, 1999). In such systems it would be expected that individuals born to younger dams therefore have a greater probability of being selected as replacements than those from older dams (Bijma & Wooliams, 1999). Investigations of L calculated as the average age of the parents of selected replacements (L_{Rep}) found no change compared to the traditional method used of the contribution of parental age groups to offspring weaned. Thus it was found that the majority of selection pressure is not on BVs and that the full benefits of ewe hogget mating to ΔG were not being realised.

Attempts to further decrease L_{Rep} may not be practical in the current operating environment so it is simply recommended that maintenance of these low values be a focus of the management of L.

The selection intensity (\bar{i}) of the ewes and the rams was less than that reported by Blair & Garrick (2007) as possible when 1.3 lambs are weaned per ewe mated, although the overall value did fall within the range reported as typical for the New Zealand sheep industry. The ram \bar{i} was thought to be lower due to the mating of ram hoggets and the need to have fewer ewes per ram when utilising this practice (Smith & Knight, 1998). The low ewe \bar{i} was attributed to selection on phenotypic traits prior to genetic selection. Some of this selection was on pregnancy diagnosis (16% of individuals disposed) while the majority (28%) was based on structural faults. In order to increase ewe \bar{i} , selection pressure should be imposed more on genetic value and less on phenotypic faults.

It was further found that, rather than imposing the majority of genetic selection upon Index value, 42% of individuals disposed were removed due to live-weight BVs while just 7% were removed based on Index value. Selection on a single trait is less efficient than selection on Index (Hazel, 1943), and it was this factor that was thought to contribute most to the shortfall in ΔG made by the system during the studied period.

Due to the shortfall in ΔI compared to ΔG , a shortfall in the financial return was also made over the studied period. At the mean ΔI of years hoggets were mated a greater net financial return was estimated over ten years of selection compared to a net financial loss estimated when hoggets were not mated. Despite this, at the ΔG or the Innervalue Fat Index not mating hoggets made a greater return than mating hoggets while the two practices made the same return in the Lean Index. The difference in the Fat Index was only small and may be the result of rounding error.

The difference between the predicted values for the Innervalue Indices and the values calculated from the actual Index change show that, at higher rates of gain, the full benefit of hogget mating is not being realised financially. This was supported by simulations in which the contribution of hoggets to a generation of replacements was increased, the maximum breeding age of ewes was restricted and the \bar{i} of the ewe flock was increased. All three practices resulted in an increase in ΔG and the net financial return after ten years of selection.

Commercial systems achieving an average lamb price of \$80 a head were not found to achieve any financial benefit from purchasing rams from the nucleus system at the levels of gain achieved. At the potential levels of gain achievable in the Lean and Fat indices however, a net return was achieved from ten years of purchasing rams from the system. These findings show that, not only should a nucleus system focus on achieving the desired balance between genetic improvement and financial return, but that the ΔG achieved should be sufficient to financially benefit commercial farming clients purchasing breeding stock.

In light of these findings it is recommended that steps be taken to increase the rate of genetic improvement and therefore net financial return. These steps include:

- Shifting the genetic merit selection pressure from live-weight BVs to Index values.
- Maintaining the ewe and ram L.
- Imposing more pressure on genetic selection and less on structural selection.
- Shifting the focus of genetic selection from live-weight BVs to Index BVs.
- Mating ewe hoggets where possible and ensuring lambs born to these dams have equal chance of selection.

5.2 Comparison of Lambing-book Records and DNA-Assigned Parentage to Minimise Pedigree Error

Before the introduction of DNA parentage testing to agricultural systems it was assumed that offspring were accurately assigned to correct parents in nucleus breeding operations (Banos et al., 2001). Nevertheless, if there are errors present in the assignment of parents to a generation of offspring the ΔG will be negatively affected, mainly through a decrease in the accuracy of selection (Long et al., 1990; Crawford, et al., 1993). The percentage of error that is present in pedigree records will depend on several factors including the method used to determine parentage and how this procedure was carried out.

The common method of parentage identification in the New Zealand sheep industry is to identify and match lambs at birth to the correct dam. This is commonly achieved by checks on lambing ewes one or more times a day and single sire mating of ewes to identify the sire (Dodds et al., 2005). A negative aspect of this method is that lambs may be mis-mothered

before they can be observed with the correct dam (Alexander et al., 1983; Dodds et al. 2005). This can result in pedigree error rates of up to 15% (Crawford, et al., 1993).

DNA testing offers an additional method of parentage testing however, testing a large number of individuals to a high level of accuracy can be expensive (Dodds et al., 2005). As a result, the identification of parentage in a sheep breeding system is likely to be most effective when a combination of methods are used.

A comparison of DNA-assigned parentage and lambing-book data found that the lambing-book dam identification records had an error rate of 7%. These records had been taken once a day over the course of the lambing period and with an estimated number of ewes lambing per day of 29. Blair & Garrick (2007) estimated that between 6% and 18% of lambs are mis-mothered during the lambing period which was between 2 and 4 lambs per day in this study. Checking ewes just once a day gives limited opportunity to identify lambs to the correct dam therefore it is likely to be more beneficial to check lambing ewes at least twice a day.

Singles had a lower mean probability of the DNA identified dam being correct (P_{Dam}) than did twins or triplets. This was attributed to the greater number of potential dams per paddock as ewes were lambed in mobs based on scanning rank. This reveals that single bearing ewes are a group that could potentially benefit more from additional checks during lambing.

Triplet lambs were a group found to have a lower percentage of dams matched between the lambing-book and the DNA-assigned parentage than the single and twin born lambs. The percentage of dams matching also decreased with dam age. Both of these findings were attributed to a change in maternal behaviour as litter size increased from twins to triplets and as ewes aged, however, if genetic selection for maternal behaviour has occurred in this flock this may explain the trend associated with ewe age. A change in maternal behaviour could either be an increase, with ewes being more active in stealing newborn lambs pre-parturition, or a decrease, with lambs more likely to follow other ewes. This suggests that lambs from these groups would also benefit most from an increase number of checks per day during the lambing period.

There are other methods that can be utilised in conjunction with additional lambing checks in order to minimise pedigree error. Single sire mating is a common practice in systems where

pedigree records are utilised and this should be used in conjunction with detailed records of each ewe and ram mated. Sise et al. (2001) suggested that lambing ewe in mobs of equal, or near equal, proportions of ewes from each sire group. When utilised with accurate mating records, this reduces the number of potential parentage combinations per paddock. Lambing of ewes can be carried out in mobs based upon scanning rank and, if doubt exists over the number of lambs in the litter, it is possible to count the umbilical vessels on the placenta given it can be matched to the correct ewe. The utilisation of more DNA markers will increase the accuracy of a DNA parentage test however, as the cost of testing will increase with the number of markers used it may be more beneficial to only increase the number of markers in groups more likely to have dams incorrectly matched in lambing-book records.

It was estimated that a pedigree error rate of 7% in a system carrying out genetic improvement would result in a 6% shortfall in ΔG over ten years of selection. If this error rate is increased to 20%, then this shortfall increases to 12% over ten years. Assuming that such errors occurred in systems not carrying out DNA parentage testing, this does not result in a financial loss compared to a system with no pedigree error and carrying out DNA-parentage testing. Thus, the use of this technology will mainly be for the benefit to ΔG rather than financial benefit.

As a result of these findings several practices were identified which offer the potential to minimise pedigree error in a genetic improvement system. These include:

- The use of more markers in DNA parentage assignment.
- Single sire mating of ewes
- Lambing ewes in mobs of equal, or near equal, proportions of ewes from each sire group (Sise et al. 2001).
- Lambing in mobs based on the number of lambs identified at pregnancy scanning.
- Carrying out two or more checks per day on lambing ewes.
- If the litter size of a ewe is in doubt, and the placenta can be matched to the ewe then the umbilical vessels can be counted to work out the number of lambs (Alexander et al., 1983; Crawford, et al., 1993).
- The recording of information can also be double checked for duplicate or missing values on a daily basis (Crawford, et al., 1993).

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Appendices

Appendix A

Table A1 Genetic and Phenotypic Parameters of Fat and Lean Indices respectively

Trait	Phenotypic σ	Innervalue Fat										
		WWT	LW8	C	A	B	Fat	Lean	EMA	CTHF	CTLF	CTSf
WWT	4.2	0.12	0.80	0.40	0.30	0.30	0.40	0.65	0.30	0.40	0.40	0.40
LW8	4.2	0.75	0.27	0.40	0.38	0.33	0.63	0.82	0.46	0.60	0.60	0.60
C	2.45	0.30	0.50	0.25	-0.13	0.30	0.77	0.08	0.20	0.70	0.70	0.70
A	4.11	0.30	0.47	0.08	0.25	0.51	-0.11	0.65	0.77	0.00	0.00	0.00
B	3.2	0.30	0.53	0.26	0.40	0.25	0.11	0.60	0.88	0.10	0.10	0.10
Fat	0.75	0.50	0.78	0.72	0.23	0.45	0.33	0.25	0.07	0.85	0.85	0.85
Lean	1.32	0.65	0.88	0.37	0.56	0.62	0.62	0.37	0.76	0.25	0.25	0.25
EMA	1.68	0.30	0.52	0.32	0.55	0.58	0.38	0.64	0.31	0.10	0.10	0.10
CTHF	0.19	0.45	0.70	0.55	0.20	0.40	0.85	0.60	0.35	0.30	0.85	0.85
CTLF	0.21	0.45	0.70	0.55	0.20	0.40	0.85	0.60	0.35	0.30	0.85	0.85
CTSf	0.42	0.45	0.70	0.55	0.20	0.40	0.85	0.60	0.35	0.85	0.85	0.30

Trait	Phenotypic	Innervalue Lean										
		WWT	LW8	C	A	B	Fat	Lean	EMA	CTHM	CTLM	CTSM
WWT	4.2	0.12	0.80	0.40	0.30	0.30	0.40	0.65	0.30	0.65	0.65	0.65
LW8	4.2	0.75	0.27	0.40	0.38	0.33	0.63	0.82	0.46	0.80	0.80	0.80
C	2.45	0.30	0.50	0.25	-0.13	0.30	0.77	0.08	0.20	0.05	0.05	0.05
A	4.11	0.30	0.47	0.08	0.25	0.51	-0.11	0.65	0.77	0.60	0.60	0.60
B	3.2	0.30	0.53	0.26	0.40	0.25	0.11	0.60	0.75	0.55	0.55	0.55
Fat	0.75	0.50	0.78	0.72	0.23	0.45	0.33	0.25	0.07	0.25	0.25	0.25
Lean	1.32	0.65	0.88	0.37	0.56	0.62	0.62	0.37	0.72	0.90	0.90	0.90
EMA	1.68	0.30	0.52	0.32	0.55	0.58	0.38	0.64	0.31	0.55	0.55	0.55
CTHM	0.32	0.60	0.85	0.30	0.50	0.55	0.60	0.90	0.55	0.35	0.90	0.90
CTLM	0.19	0.60	0.85	0.30	0.50	0.55	0.60	0.90	0.55	0.90	0.32	0.90
CTSM	0.27	0.60	0.85	0.30	0.50	0.55	0.60	0.90	0.55	0.90	0.90	0.30

Genetic correlations above the diagonal, phenotypic below. Heritability on the diagonal

Where WWT = weaning weight, LW8 = live weight at 8 months, C = eye muscle fat depth, A = eye muscle width, B = eye muscle depth, EMA = eye muscle area, CT = Xray computed tomography, HF = Hind leg fat, LF = loin fat, SF = shoulder fat, HM = hind leg muscle, LM = loin muscle, SM = shoulder muscle

Table A1 shows the genetic and phenotypic parameters used in calculations of accuracy of selection for both the Fat and Lean indices. Table A2 shows the genetic gain made during the studied period in each trait for which BVs were provided.

Table A2 Improvement in Selection Criteria Traits between 2000 and 2009

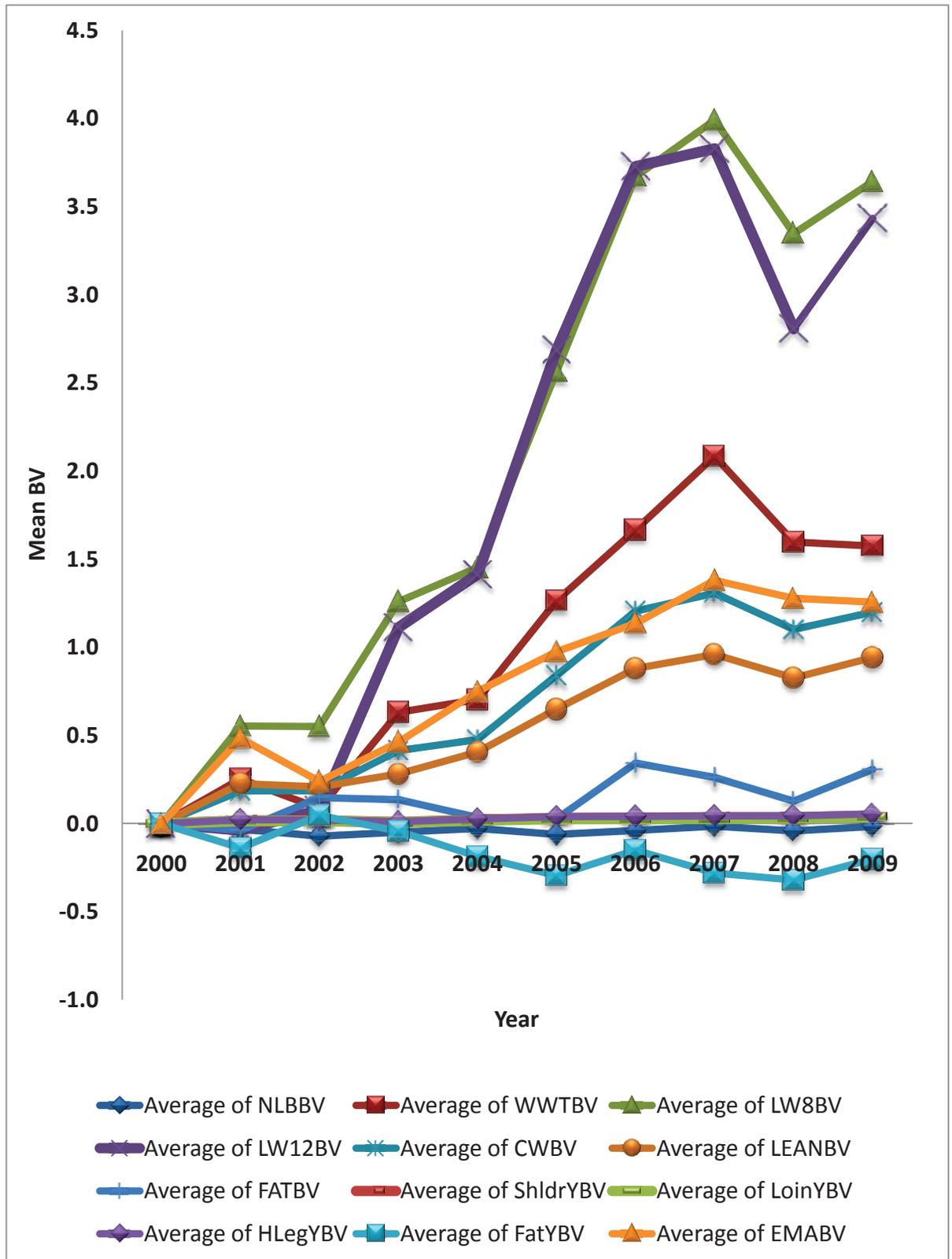


Table B1 Genetic superiorities and rates of gain in the Fat Index used in financial analysis of alternate systems.

Fat Index			
Treatment	Genetic Superiority of Offspring With Each Unit of Genetic Gain		Genetic Gain (cents per ewe per year)
	Males	Females	
A _{HM}	3.74	0.68	97
A _{HNM}	3.74	0.74	91
B _{HM}	3.74	1.54	115
B _{HNM}	3.74	1.54	107
C _{HM}	3.74	0.31	89
C _{HNM}	3.74	0.31	83
D _{HM}	3.74	0.68	106
D _{HNM}	3.74	0.74	92
E _{HM}	3.40	0.68	117
E _{HNM}	3.47	0.74	95
F _{HM}	3.67	0.68	97
F _{HNM}	3.67	0.74	91
G _{HM}	3.47	0.63	89
G _{HNM}	3.40	0.68	83
H _{HM}	3.67	0.67	94
H _{HNM}	3.67	0.73	89

Subscripts denote hoggets mated (HM) and hoggets not mated (HNM)

Table B2 Genetic superiorities and rates of gain in the Lean Index used in financial analysis of alternate systems.

Lean Index			
Treatment	Genetic Superiority of Offspring With Each Unit of Genetic Gain		Genetic Gain (cents per ewe per year)
	Males	Females	
J _{HM}	5.59	1.02	144
J _{HNM}	5.59	1.11	136
K _{HM}	5.59	2.30	173
K _{HNM}	5.59	2.30	161
L _{HM}	5.59	0.47	132
L _{HNM}	5.59	0.47	124
M _{HM}	5.59	1.02	159
M _{HNM}	5.59	1.11	138
N _{HM}	5.12	1.02	174
N _{HNM}	5.12	1.11	141
O _{HM}	5.59	1.02	144
O _{HNM}	5.59	1.11	136
P _{HM}	5.12	0.94	133
P _{HNM}	5.12	1.02	125
Q _{HM}	5.49	1.00	142
Q _{HNM}	5.50	1.09	134
Subscripts denote hoggets mated (HM) and hoggets not mated (HNM)			

Tables B1, B2 and B3 all show various parameters utilised in the calculation of financial benefits of current and alternative systems.

Table B3 Percentage contribution of each dam age class to a generation of replacements as used in financial calculations.

	Maximum Ewe Age	Hoggets Mated or Not	Ewe Age						
			1	2	3	4	5	6	7
Contribution to Lambs Weaned	5	HM	0.100	0.150	0.150	0.050	0.050	0.000	0.000
		HNM	0.000	0.150	0.150	0.100	0.100	0.000	0.000
	6*	HM	0.064	0.153	0.119	0.083	0.046	0.040	0.000
		HNM	0.000	0.157	0.138	0.108	0.061	0.040	0.000
	7	HM	0.050	0.150	0.100	0.050	0.050	0.050	0.050
		HNM	0.000	0.150	0.100	0.100	0.050	0.050	0.050
Contribution to Replacements	5	HM	0.050	0.150	0.150	0.100	0.050	0.000	0.000
		HNM	0.000	0.150	0.150	0.100	0.100	0.000	0.000
	6*	HM	0.048	0.154	0.118	0.094	0.052	0.033	0.000
		HNM	0.000	0.117	0.164	0.111	0.071	0.037	0.000
	7	HM	0.050	0.150	0.120	0.080	0.050	0.030	0.030
		HNM	0.000	0.150	0.120	0.080	0.070	0.050	0.030
Increase in Hogget Contribution to Replacements	5	HM	0.100	0.200	0.150	0.025	0.025	0.000	0.000
		HNM	0.000	0.200	0.150	0.075	0.075	0.000	0.000
	6	HM	0.100	0.200	0.130	0.025	0.025	0.025	0.000
		HNM	0.000	0.200	0.130	0.060	0.060	0.050	0.000
	7	HM	0.100	0.200	0.100	0.025	0.025	0.025	0.025
		HNM	0.000	0.200	0.100	0.080	0.070	0.030	0.030
2nd Increase in Hogget Contribution to Replacements	5	HM	0.200	0.250	0.020	0.015	0.015	0.000	0.000
		HNM	0.000	0.250	0.100	0.100	0.050	0.000	0.000
	6	HM	0.200	0.200	0.070	0.010	0.010	0.010	0.000
		HNM	0.000	0.200	0.150	0.050	0.050	0.050	0.000
	7	HM	0.200	0.200	0.025	0.025	0.020	0.015	0.015
		HNM	0.000	0.200	0.100	0.050	0.050	0.050	0.050

*For the base system the maximum ewe age was taken to be 6 years old and the values in these rows for HM and HNM are those actually achieved by the system

Appendix C

Lean Results

Sensitivity of Genetic Gain and Financial Implications

Selection on the Lean index (Table C1) was shown to give greater return and the same cost as the Fat index.

Table C1 Summary of the effects of costs and returns on the gross margin of a system under gain estimated in the Innervalue Lean index

	Hoggets Not Mated	Hoggets Mated
Cumulative Discounted Income per S.U.	\$209	\$211
Cumulative Discounted Costs per S.U.	\$48	\$50
Cumulative Discounted Gross Margin per Dollar Invested	\$0.81	\$0.81
Cumulative Discounted Gross Margin per S.U.	\$161	\$161

Sensitivity of Genetic Gain and Financial Outcomes To Changes in Management

Changes in Flock Age Structure

Figure C1 shows that the largest values of ΔG are made in systems where ewes are retained for breeding until five years of age and rams two. System 3 where ewes are retained until seven years of age and rams three made the lowest levels of ΔG .

Figure C1 Estimated annual ΔG made under different treatments influencing age structure applied to the base system for the Lean Index (see table in methods). Showing percentage deviation from base system.

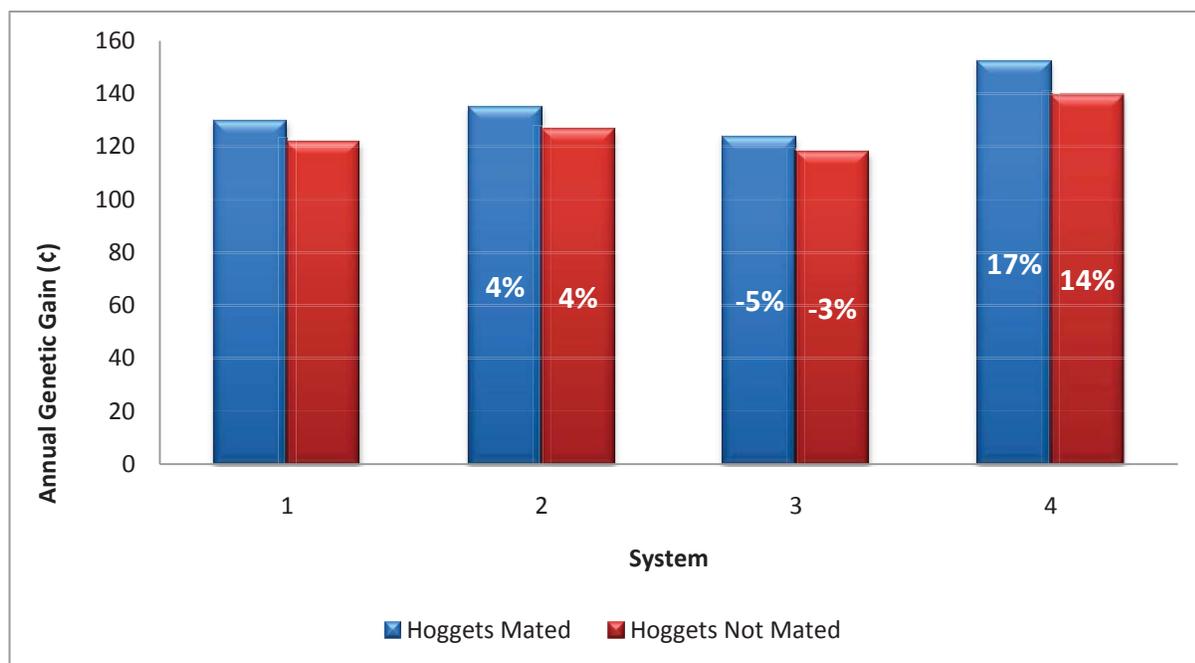
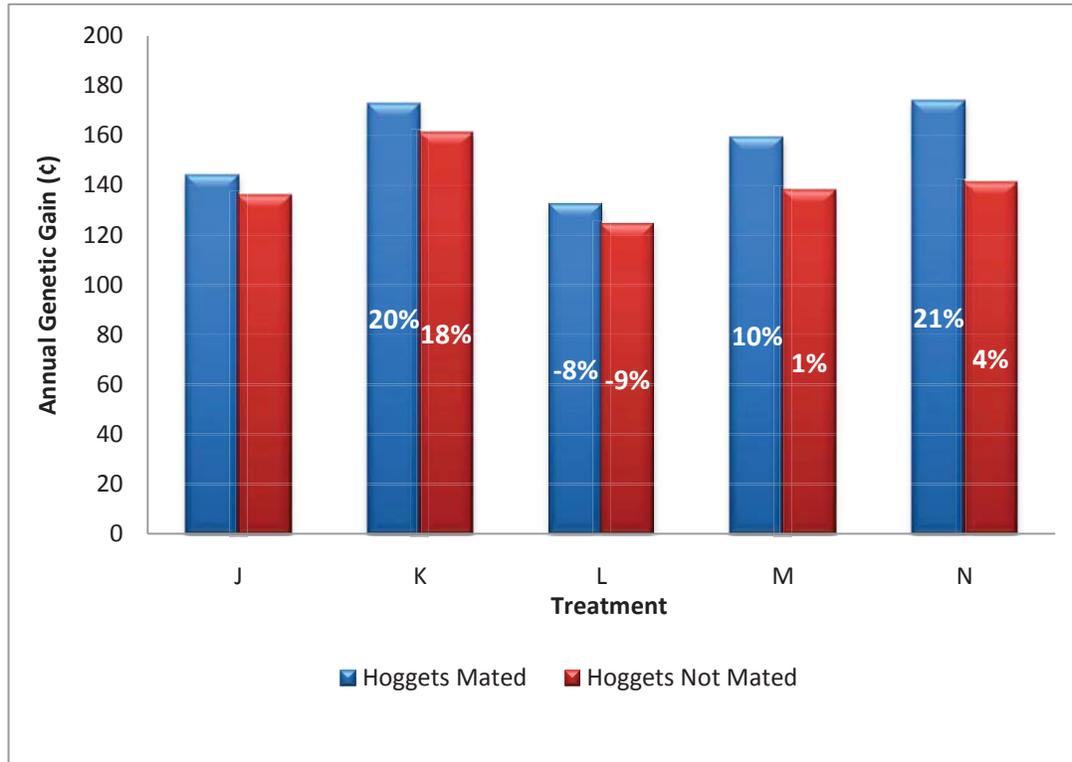


Table C2 Effects of changing flock age structure on the financial outcomes of 10 years of continuous selection on Lean index. Showing the percentage difference from the base system.

Hoggets Mated				
System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
2	3%	3%	4%	0
3	-3%	-3%	-3%	0
4	-7%	-7%	-8%	0

Hoggets Not Mated				
System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
2	4%	4%	5%	0
3	-3%	-3%	-3%	0
4	-6%	-6%	-7%	0

Figure C2 Effects of changing flock selection practices on ΔG in the Lean index. Showing percentage deviation from the base system.



J – Base system, K – 100 ewe hoggets selected as replacements, L– 250 ewe hoggets selected as replacements, M – Increasing the contribution of younger dam age classes to selected replacements, N – Further increasing the contribution of younger dam age classes to selected replacements.

The effects revealed in changes in the Lean index (Table C2, Table C3 & Figure C2) with selection changes to the base system were similar to those observed in the Fat index except for systems selecting 250 ewe hoggets as replacements and not mating hoggets which, compared to the increase in net return over the base system for the Fat index, experienced a decrease in net return over the base system.

Table C3 Financial effects of changing flock selection practices. Showing the percentage difference from the base system.

Contribution to Replacements - Hoggets Mated

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
K _{HM}	20%	20%	24%	0
L _{HM}	-8%	-8%	-10%	0
M _{HM}	8%	8%	10%	0
N _{HM}	10%	9%	11%	0

Contribution to Replacements - Hoggets Not Mated

System	Average Annual Discounted Returns from a Single Round of Selection	Cumulative Discounted Returns (10 years)	Net Return from 10 Years of Selection	Years From First Selection to Break Even
K _{HNM}	18%	18%	22%	0
L _{HNM}	-10%	-10%	-12%	0
M _{HNM}	5%	5%	6%	0
N _{HNM}	6%	7%	8%	0