Genetic evaluation of milk traits, live weight, somatic cell score, and litter size at birth, and development of a selection index for dairy sheep

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Abstract

There is interest in building alternative dairy production systems in New Zealand involving sheep. However, there is currently no national breeding scheme to ensure that genetic change will occur in the right direction. The objective of this study was to develop a prototype genetic evaluation of milk traits, live weight, somatic cell score, and litter size at birth, and a selection index for dairy sheep. The flock consisted of 123 crossbred ewes with a mixture of East Friesian, Highlander, Polled-Dorset and Poltex breeds. A total of 479 monthly flock tests for milk volume and percentages of fat, protein and lactose, and somatic cell count were obtained during the production season 2015-16. Corresponding first let-down time (FLDT) and yields (FLDY) were recorded at afternoon milkings. Ewes were weighed four times during the production season and litter size was recorded at birth (LS). Lactation curves for each ewe were derived using a random regression model with an orthogonal polynomial of 3rd order for fat and lactose daily yields, and an orthogonal polynomial of 4th order for milk and protein daily yields. Average ± SE for lactation length (LL) was 126±4.32 days and averages of accumulated yields were 234±9.10 litres milk, 16.5±0.65 kg fat, 13.0±0.56 kg protein and 12.6±0.48 kg lactose. Average FLDT and FLDY were 79±2.02 seconds and 0.5±0.01 litres, respectively. Averages were 17.5±0.16 for somatic cell score (SCS), 75.9±0.88 kg for live weight (LWT) and LS 2.0±0.06 lambs born per ewe. The coefficient of variation was 38% for lactation length and between 42 and 47% for yields. Breeding values for the different traits were estimated from a multiple-trait animal model using heritability and genetic correlations published in the literature and phenotypic standard deviations obtained from the data set. Economic values (EV) were derived from relative economic weights desired by the famer and genetic standard deviations of the traits. The economic values were $0.516/day for LL, $2.00/kg milk, $6.73/kg fat, $8.37/kg protein, -$0.81/kg LWT, -$46.80/unit of SCS, -$1.80/s of FLDT, $332.30/kg FLDY and $44.00/lamb of LS. It is recommended that the Gunsons use these EVs to calculate a selection index for the ranking of ewes and rams to be selected as parents of the next generation. This will achieve genetic gain for each of the traits in the right direction, in the right proportion as well as producing progeny with improved milk yield, milk quality, milking speed and overall efficiency.

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Table of Abbreviations

AI	Artificial insemination
BLUP	Best linear unbiased prediction
BO	Breeding objective
BV	Breeding value
DFREML	Derivative-free restricted maximum likelihood estimation
dsEBI	Dairy sheep economic breeding index
EBV	Estimated breeding values
EV	Economic value
FLDY	First let-down milk yield
FLDT	First let-down time
FY	Fat yield
GBV	Genomic breeding values
GLS	Generalized least squares
HYE	High-yielding ewe
LL	Lactation length
LS	Litter size
LWT	Live weight
LY	Lactose yield
LYE	Low-yielding ewe
MME	Mixed-model equations
MOET	Multiple ovulation and embryo transfer
MY	Milk yield
PY	Protein yield
REML	Restricted maximum likelihood estimation
REW	Relative economic weight
REV	Relative economic value
r_{TI}	Correlation between breeding objective and selection index
SAS	Statistical analysis software
SI	Selection index
SCS	Somatic-cell score
SNP	Single-nucleotide polymorphism
T	Breeding objective
TBV	True breeding value

Chapter 1

General introduction

There is interest in building alternative dairy production systems in New Zealand involving sheep (Peterson and Prichard, 2015). Poll Dorset used to be the main sheep breed milked in New Zealand, due to its greater milk production over other meat and wool breeds (Geenty, 1979) but, the milk yields of Poll Dorset are significantly less than those of dairy sheep breeds around the world such as the Lacaune, Chios, Awassi, East Friesian and the Sarde (Newman and Stieffel, 1999). The main reasons for introducing East Friesians to New Zealand in 1992 was their high milk production (Allison, 1995) and prolificacy (Meyer et al., 1977). Crossbreeding was implemented to produce more sheep with East Friesian genes as well as progeny with hybrid vigour. This was achieved when the East Friesian was crossed with Poll Dorset and Romney ewes, resulting in progeny with higher milk production (Newman and Stieffel, 1999; Hunter et al., 2015), and crossed with Coopworths, which resulted in additional improvements in growth (Jopson et al., 2000).

In 2014 there were ten dairy sheep production systems operating in New Zealand, with milking flocks consisting of either purebred East Friesian (King et al., 2014) or East Friesian crossed with Dorset (McMillan et al., 2014a). Milk was exported to Australia, as powder to China and Indonesia, used for local yoghurt production, sold to local cheese and yoghurt producers, or remained on site for cheese manufacture (Peterson and Prichard, 2015). Growth of the New Zealand sheep dairy industry was projected to reach two million sheep (New Zealand Parliament, 2013) with the potential to be a billion dollar industry in 10 years' time (Griffiths, 2015). A goal for the sheep dairy industry as a whole, is to export over $200 million of sheep dairy products by 2030 (McMillan et al., 2014b). One approach to achieving this goal is to improve the genetic merit of dairy sheep in New Zealand. This will require the development of a genetic evaluation system and selection scheme, to enable the identification of superior parents for future generations.

Up until 2014, culling policies based on milk production of ewes in New Zealand had been minimal. Progeny tests had been used for East Friesian rams, however, there had been no selection for milking performance (McMillan et al., 2014b). A genetic evaluation was conducted on the Blue River Dairy (BRD) flock of East Friesian crosses, which provided an early estimate of genetic merit (McMillian et al., 2014b). The results from this study demonstrated early genetic progress in rams for milk yield at 180 days in milk with breeding values exceeding +100 litres. Further developments for the dairy sheep industry would require the determination of an appropriate breeding objective and an economic index, as there are none currently published.

The breeding objective is defined as the gene complex targeted for improvement via selection (Charfeddine, 2000). Determining traits to be considered in the breeding objective is a crucial step in designing a breeding program as it determines the direction of genetic improvement (Lopez-Villalobos and Garrick, 2005). Hazel (1943) first demonstrated the inclusion of economic values into a breeding objective to generate phenotypic selection indices and estimate breeding values of livestock. This idea was extended into different selection pathways such as, ewe to ewe, ewe to ram, ram to ewe and ram to ram (Rendel and Robertson, 1950). Mixed-model equations can be used to derive best linear unbiased predictions (BLUP – further explanation in section 2.3.2.1) of these estimated breeding values for traits considered in the breeding objective (Henderson, 1963). Progeny testing East Friesian rams was the first selection scheme implemented for dairy sheep in New Zealand (McMillan et al., 2014b). Then, with the estimation of genetic merit achieved, the challenge for the industry is how to disseminate, quickly, the genes from these superior animals into the population.

The participation of Blue River Diary in the initial genetic evaluation program has created the potential for such improvement programs, however, there is currently no breeding program to ensure that genetic gains will occur in the right direction, to produce milking ewes required for future production systems. Therefore, this research is aimed at extending the genetic evaluation to include estimated breeding values and the development of an economic index. This will allow selection of superior animals to breed from, and rapidly increase the rate of genetic gain within the already evolving industry. Based on the current stage of the sheep dairy industry, the objectives of this thesis are to;

- Define the most important traits to be considered in the breeding objective.
- Determine the economic values for the traits considered in the breeding objective.
- Develop a genetic evaluation system to estimate breeding values for the traits considered in the breeding objective or to be included in a selection index.
- Construct a selection index to rank animals for profit.

For any industry to become more efficient, the implementation of a genetic improvement program is required. Therefore, the objective of this literature review was to review the breeding objectives, selection indices, selection schemes and dissemination systems for genetic improvement in dairy sheep around the world and identify what is required to implement a successful genetic improvement program for the New Zealand dairy sheep industry.

Chapter 2

Literature review: Aspects of genetic improvement of dairy sheep

2.1 Sheep production systems worldwide

Worldwide production of fresh sheep milk was 10,137,749 t/year in 2013, a minimal amount compared to a total of 635,575,895 t/year produced by dairy cattle (FAO, 2013). Europe and Africa contribute 29.8% and 22.2% respectively. In regards to countries, Turkey produces the largest volume of sheep's milk (1,101,013 t/year), followed by Greece (705,000 t/year) and Spain (600,620 t/year). These values can be seen in Table 2.1, which also shows milk production and the total number of animals milked in different countries.

Table 2.1. Sheep milk production and number of milking animals in different countries (FAO, 2013).

Country	Milk production (t/year)	Milking sheep	Milk production per sheep (kg/year)
Turkey	1,101,013	14,280,000	77
Greece	705,000	7,198,000	98
Spain	600,620	2,950,000	204
Iran	472,500	12,600,000	38
Italy	383,837	4,848,000	79
France	259,083	1,238,433	209

For centuries, dairy sheep have been farmed in the Mediterranean basin, central Europe and Near-East countries, such as Iran (Carta et al., 2009). The production systems practiced vary greatly depending on environmental conditions and access to resources (Todaro et al., 2015). The traditional pastoral management systems for dairy sheep include transhumance, intensive, semi-intensive and semi-extensive systems (Wolfova et al., 2009a; Carta et al., 2009). Within these systems, it is common for the dairy sheep to be bred and raised for dual purposes, such as meat and milk (Gandini et al., 2014). For dual-purpose breeding, a mix of maternal and paternal sires is required as the replacement ewes are primarily bred for milk production and reproductive performance, while lambs are bred for milking replacements, or meat.

The traditional transhumance system includes the seasonal movement between fixed summer and winter pastures (Groen, 2000). This type of system is commonly found in the

Mediterranean countries (Groen, 2000; Pollot and Gootwine, 2001), where small mountain breeds are farmed. In comparison, intensive systems in Greece generally involve high-yielding indigenous breeds as well as foreign breeds.

Intensive systems entail sheep housed all year round, with no access to pasture (EFSA, 2014). Animals are generally improved local breeds or crosses, and milk production is either seasonal, or continuous (Carta et al., 2009). Sheep are fed hard feeds such as concentrates, as well as silage and other roughages (Folman et al., 1996). Dairy ewes start breeding at one year of age and an accelerated lambing regime is implemented with several mating/insemination periods throughout the year (Todaro et al., 2015). Lambs are either removed immediately after lambing, or kept on dams for two to four weeks before being separated and changed to an artificial rearing system (Todaro et al., 2015). Ewes are machine-milked twice daily. Awassi is the common breed of sheep intensively farmed in the Middle East (Folman et al., 1966; Hossamo et al., 1985) and generally selected for milk yield (EFSA, 2014). Other breeds of sheep intensively selected for milk yield and milk quality are Lacaune, Awassi, Asaf, Comisana and the French Sarda (EFSA, 2014).

Semi-intensive farming systems involve keeping the animals inside for the entire night and part of the day, and outside on pasture for the remainder of the day. The animals are generally fed a mixed diet of concentrates, roughage and silage, and graze either improved or unimproved pastures (Cappio-Borlino et al., 1997). Common breeds of dairy sheep include the, Churra, Lacaune, Castellana, Latxa, Awassi, Chios, Sarda and the Comisana, and are selected for both production traits as well as adaptability to the local environment (EFSA, 2014). As with intensive systems, animals are bred at one year of age, either naturally or by artificial insemination. During the pre-weaning period, lambs are kept indoors while their dams graze outside. These lambs remain with their dams for a few weeks before being removed for artificial rearing and then ewes are milked twice-daily. Semi-intensive production systems are common in France, Greece, Israel and Spain (EFSA, 2014). Sheep in Sicily are also semi-intensively farmed, however, due to small scale (100-200 ewes per flock), animals are hand-milked and the milk is used for on-farm cheese production (Tolone et al., 2011).

Semi-extensive production systems enable animals to be continually grazed on pastures for several days/weeks and then brought under housing for lambing. Animals are moved between paddocks (including rotational grazing) and, in some cases, provided with supplementary feed (EFSA, 2014). Indoor lambing during the winter, and grazing mountain/hill pastures during the summer, is common practice for both the Improved Valachian and Tsigai breeds in Slovakia (Krupova et al., 2009). These dairy breeds are not high milk producers, as they are also selected for meat and wool production (Wolfova et al., 2009b).

2.2 Husbandry systems

In addition to the range of production systems described above, husbandry systems regarding weaning strategy also vary. Until recently, it was commonly accepted to raise lambs on the dams for two months (Folman et al., 1996; Komprej et al., 2009). However, in France, the husbandry systems for dairy sheep support a dual-purpose production system of both meat and milk, involving a suckling period of at least one month before milking commences. This month can be pure suckling, or a combination of suckling and milking (David et al., 2008). In Spain, lambs are also traditionally suckled for up to one month before weaning (Fuertes et al., 1998; Todaro et al., 2015). In stark contrast, the Israeli and German breeding systems ensure lambs are removed from the ewe very soon after birth and reared on a lamb nursing bar with milk replacer. This enables the entire lactation period to be exploited by milking (Carta et al., 2009).

A “mixed” husbandry system which includes one morning milking, while enabling lambs to suckle during the day is common practice in Sardinia (Rassu et al., 2015) for the first 30 days of lactation (Papachristoforou, 1990; Gargouri et al., 1993; Folman et al., 1996). For dual-purpose production systems, this mixed husbandry system is economically superior to both the 30 days of lamb suckling followed by twice-daily machine milking, and removing and weaning the lambs 24 hours after lambing followed by twice-daily machine milking (McKusick et al., 2002). However, a potential drawback of a mixed husbandry system is the low fat content in the commercial milk obtained in the first 30 days of lactation (period of partial lamb contact) (Rassu et al., 2015). Similar results have been observed in other breeds and partial suckling systems (Gargouri et al., 1993 Fuertes et al., 1998; Jaeggi et al., 2008). From these studies it is suggested that the low fat content is due to the inhibition of milk ejection, thus, failing to collect alveolar milk, which has a higher fat concentration

(Labussiere, 1988). However, when lambs are permanently removed, milk fat concentration returns to normal values (McKusick et al., 2001; Jaeggi et al., 2008; Rassu et al., 2015).

Examples of levels of milk production reported in the literature in different countries and different breeds are presented in Table 2.2.

Table 2.2. Production levels of dairy sheep in different countries and breeds.

Study	Country	Breed	Lactation length (days)	Milk yield (L)	Fat yield (kg)	Protein yield (kg)
Geenty (1979)	New Zealand	Romney		106[a]		
		Romney-Dorset		120 [a]		
		Dorset		163 [a]		
Gosling et al. (1997)	New Zealand	Dorset	147	116		
Newman and Stieffel (1999)	New Zealand	Polled Dorset and Polled Dorset-East Frisian crosses	102	100		
McMillan et al. (2014a)	New Zealand	East Friesian cross	160	365		
McKusick et al. (2001)	United States	East Friesian	183	260	13.2	13.7
Morgan et al. (2006)	Australia	East Friesian	128	107		
Legarra and Ugarte (2001)	Spain	Latxa	120	127	6.6	6.3
Ramon et al. (2010)	Spain	Manchega		148	9.9	8.4
Pelmus et al. (2014)	Romania	Teleorman Black Head	172	103	6.8	5.9
Barillet (2007)	France	Lacaune	152	242	21.1	16.7
		Average	145	174	11.5	10.2

[a] Means of accumulated milk production up to week 9 of lactation.

2.3 Breeding program

A genetic improvement programme should be designed to improve successive generations of animals to become more efficient producers under future farm ecologic, economic and social circumstances, than the present generation of animals. To achieve this type of improvement and sustainability in a commercial environment, requires the careful design and decision making involved in a breeding scheme (Groen, 2000). Harris et al. (1984) suggested an array of choices, decisions and other relevant information to design a breeding program with seven steps. These steps were schematically summarised by Lopes-Villalobos and Garrick (2005) who also discussed the design and ability to enhance a breeding program in any livestock enterprise Figure 2.1. These steps are synergistically related and all systematically organised to achieve the farmer's goal.

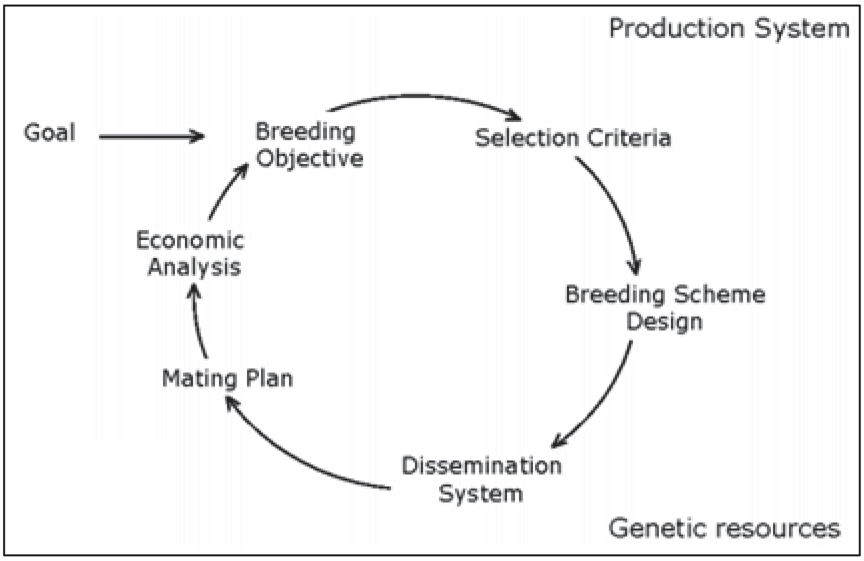


Figure 2.1. A systematic approach to design breeding programs (Lopez-Villalobos and Garrick, 2005).

Step 1 - Breeding goal

The first step of any breeding program is to define a breeding goal (Groen, 2000; Lopez-Villalobos and Garrick, 2005). This is a statement of direction in animal breeding programs for the genetic improvement of future generations. In the agricultural industry, animal productivity is generally measured by the income generated from the enterprise. Because of this, the farmers breeding goal for selection include animal traits aimed at improving the profitability of the farm. Common breeding goals include, profit per milking ewe, profit per hectare or, in regards to efficiency, profit per kg of dry matter consumed (Lopez-Villalobos and Garrick, 2005).

Step 2 - Breeding objective

This desired change is then formalised in the breeding objective, a mathematical equation representing important traits which affect overall farm profit (Newman, 1992; Charfeddine, 2000). This breeding objective can be described in two steps (Harris et al., 1984). First, the animal traits which influence the breeding goal are identified and second, the relative weight of each trait is quantified (Lopez-Villalobos and Garrick, 2005). The relative economic weights can be determined using different methods, including budgeting with bio-economic models, first partial derivative of profit equations and preference-based approaches (Byrne et al., 2012). The selection of animals based on a well-defined breeding objective will increase the frequency of the favourable genes influencing the expression of the breeding objective traits (Groen, 2000).

Step 3 – Selection criteria

The third step in designing a breeding program is to define the selection criteria. This step will enable the selection of individuals of the greatest genetic merit for the breeding objective (Lopez-Villalobos and Garrick, 2005). Very often the breeding objective traits are difficult and expensive to measure, for example, sex-limited traits like milk yield is only measured in cows and ewes but not in bulls and rams, feed conversion efficiency that requires dry matter intake in individual animals, and longevity, which is not measured until the animal leaves the production system. Hazel (1943) described this step as the selection of traits which are measureable on the individual and relatives, and used as predictors of the traits included in the breeding objective.

Step 4 – Breeding scheme design

The fourth step in designing a breeding program is to define the breeding scheme to maximise the rate of genetic gain (Rendell and Robertson, 1950). A decision must be made as to how to select the genetically superior individuals (Harris et al., 1984). These individuals will have the highest estimated genetic merit for the breeding objective described. Care must be taken when designing the scheme, as to how many, and which, animals should be selected as parents for the next generation (Van der Werf, 2014). These decisions may influence the selection intensity, the accuracy of selection and the interval between generations. The breeding scheme determines the potential rate of genetic gain that could be achieved in the breeding objective and has a large influence on the financial benefit of the overall breeding program (Lopez-Villalobos and Garrick, 2005). For example designing a progeny test scheme to find the optimum number of rams to be tested and the optimum number of progeny per ram.

Step 5 – Dissemination system

Deciding on the dissemination system is the fifth step in designing a breeding program, and involves designing an appropriate system for the transfer of genes from the genetically superior individuals already included in the breeding scheme, into the commercial population (Harris et al., 1984). This decision is largely determined by the size of the commercial population, and the cost and efficacy of the biotechnologies available (e.g., AI, MOET, trans vaginal recovery and in vitro production, and sexed semen) (Lopez-Villalobos and Garrick, 2005).

Step 6 – Mating plan

The sixth step in designing a breeding program is the design of a mating plan of the superior animals in the commercial populations. There are numerous approaches to potential mating systems, such as, crossbreeding, inbreeding, assortative or random mating strategies (Harris et al., 1984). The use of reproductive technologies play an important role in the design of mating plans, for example, using artificial insemination, a ram of high genetic merit for the breeding objective will be used more extensively than a ram of lower genetic merit. Thus, preferential mating will occur and some ram lambs will be selected and used more than others.

Step 7 – Economic analysis

The final and perhaps the most important step in designing a breeding program is the economic analysis of the breeding program (Lopez-Villalobos and Garrick, 2005). This step evaluates the effectiveness of the selection program. It is a very complex process and requires whole-system modelling including the costs of the selection scheme (Harris et al., 1984). This step also defines who will profit from the breeding program, whether it be farmers, or breeding companies. In a breeding program controlled by a governmental body, a compromise among breeding companies is achieved in such a way that breeding companies will provide superior animals to the farmers, which ensure that the farmers will make genetic progress in the right direction (Lopez-Villalobos and Garrick, 2005). In a free market, forces of supply-demand operate and farmers will choose superior animals from all available breeding companies that not necessarily ensure the maximum rate of genetic gain for the whole population.

2.3.1 Breeding objectives

A breeding objective (BO) which is very specific and has a clear desired direction for improvement will produce rapid genetic improvement (Ponzoni, 1986). The breeding objective for the French Lacaune breed was to "improve milk yield" (Barillet et al., 2001a). This is very precise in respect of the desired direction of change and from 1960 to 1986 the Lacaune breed more than doubled milk production (Barillet et al., 2001a). During the same period as the implementation of the breeding program in the French Lacaune, sheep farmers in Australia attempted to improve wool production in Merino sheep. However, a poorly defined breeding objective led to minimal genetic progress (Lindsay and Skerritt, 2003). These examples show that, even though goals are made and traits identified, if the breeding objective is not clearly defined, animals may be unintentionally selected for undesirable traits and thus, minimal progress is achieved.

The original selection goal for Lacaune dairy ewes was limited to milk yield, however, inclusion of milk components in the breeding objective is also important. The reason that milk yield was the only selection criterion included was that measuring other characteristics such as milk composition was expensive at that time (Barillet and Boichard, 1987). As sheep milk is most commonly processed into cheese, in the 1980s selection schemes began to include milk composition as well as milk yield (Othmane et al., 2002). Therefore, the breeding objective and selection index should include traits which are desirable for cheese manufacture if milk is to be used for that purpose.

Early studies of the New Zealand Romney breed suggested that culling ewes with low milk yield, to ensure that high-milk-producing ewes were retained for breeding purposes, would achieve greater lamb growth (Barnicoat et al., 1956). This type of method has been adopted by one sheep farmer, who milks sheep in order to identify which are high producers for selection and breeding (Peterson and Prichard, 2015), with 2/3 of the selection criteria for milk volume and 1/3 for lamb weaning weight (Macdonald, 2015). Another method used in New Zealand is to select replacements based on temperament, lactation length and general ewe health (King et al., 2013). Furthermore, breeding programs for East Friesian ewes have achieved milk yields in excess of 200 L/ewe/year (McMillan, 2014b). With this said, other traits for consideration in future breeding objectives include; live weight, milk components, somatic cell count, and udder traits (Peterson and Prichard, 2015).

As discussed, the first step in designing a breeding program is to determine the breeding goal, which, for a commercial farm, tends to be profit. In order to achieve this goal, a breeding objective has to be determined (Ponzoni, 1986; Lopez-Villalobos and Garrick, 2005). The breeding objective is defined as the gene complex targeted for improvement via selection, which describes the genetic merit of an individual (Charfeddine, 2000). This was first defined by Hazel (1984) as a linear function of breeding values for economically important traits. The traits included in the breeding objective should be of economic importance, and traits which the farmer wants to improve (James, 1982; Groen, 2000).

2.3.1.1 Determination of traits

Defining a breeding objective is a crucial process in determining the direction of genetic change (Fuerst-Waltl and Baumung, 2009). Accurate definition of the breeding objective will enable genetic change to occur in the right direction (Bradford and Meyer, 1986), while an inaccurate definition of a breeding objective could result in minimal genetic gain, or could possibly lead to economic deterioration of the population (James, 1982; Ponzoni, 1986). For example, in the 1990s, the breeding objective for dairy cattle in Ireland, New Zealand and Australia was to increase milk production through upgrading of local cows (Walsh et al., 2011), however, due to the unfavourable genetic correlation between milk yield and fertility, the increased milk yield led to decreased fertility (Oltenacu and Broom, 2010). Traits included in the breeding objective should have a positive influence on farm profitability in order to meet the defined breeding goal. Therefore, traits included in the breeding objective are commonly based upon production and reproduction traits, as these tend to have a large effect on farm profitability. However, functional traits such as ease of milking are becoming increasingly popular (Casu et al., 2006). Although the economic importance of functional traits is a key reason for including traits in the breeding objective, other reasons such as ethical and consumer concerns are becoming considerably important (Bytyqi et al., 2015).

According to Groen (2000), when analysing sheep-production systems, economic considerations should be included when defining a new breeding objective. As mentioned, great understanding of each trait's contribution in a breeding objective is crucial when designing a suitable breeding program for dairy sheep. In addition to their economic importance, other aspects should be explained and understood. For example, ensuring farmers understand and are aware of the production and breeding decisions which take place regarding nutrition, body condition and welfare of animals, appropriate reasons for culling, and support for future selection and breeding decisions (Bytyqi et al., 2015). Furthermore, including too many traits in the breeding goal may distract from selection of the more important traits (Santos et al., 2015) and reduce the rate of genetic gain for the most important traits.

Note-worthy milk-production traits used in well-established breeding programs for dairy sheep include; milk yield, fat yield, protein yield as well as fat content and protein content (Kominakis et al., 1997; Lindsay and Skerritt, 2003; Macciotta et al., 2005). The dry matter content (fat plus protein content) indicates predicted cheese yield while the linear combination of total fat and protein yields represent the best predictor of total cheese output (Barillet, 2007). Thus, the inclusion of such traits will improve production of milk suitable for cheese manufacture, provided there are no negative correlations with milk yield.

Inclusion of functional traits related to reducing production costs could also be considered in the breeding objective and selection index. Functional traits define how a species interacts with the environment. Some functional traits, such as disease resistance, are difficult to measure and require quantitative genetics or molecular mapping for selection (Barillet, 2007). In addition, improving the ability of animals to adapt to the local environment would mitigate the potential limitations caused by the importation of new genetic material, and enable greater performance (Kominakis et al., 1997). Ewes selected for milk production in European farming conditions cannot be expected to perform well in New Zealand conditions. For example, East Friesian ewes are considered “soft” by many New Zealand farmers and thus, are unsuitable for hill country conditions. For these reasons, the inclusion of functional traits in a breeding objective and selection index could help reduce animal losses and improve the rate of genetic gain in imported sheep.

2.3.1.2 Calculation of economic values

As the traits in the breeding objective have different economic values, Hazel designed an approach which combined the important traits with their individual relative economic values (Smith et al., 1986). The economic values for each trait are derived by partial differentiation of the profit equation (James, 1982). Thus, the combined genotype (breeding objective) that describes the net genetic merit of an individual takes the form;

$$T = \sum EV_i TBV_i \qquad (2.1)$$

where T is the breeding objective, EV_i is the economic value of a trait and TBV_i is the true breeding value for an economically important trait of the individual (Hazel, 1943). However, the true breeding value is impossible to calculate and has to be estimated. This estimation is calculated with the aid of a selection index which becomes the predictor of the true breeding value.

Profit equation

Defining a breeding objective requires critical analysis of income and expenses associated with the production system. A profit equation can be used to identify and evaluate such costs. According to Ponzoni (1986) the profit equation is a suitable technique for estimating economic values in the short term (e.g., 10 years), when the costs associated with production are fixed. However, if the time scale was longer (say, 25 years) then there would be no fixed costs, and thus, there is freedom to vary the scale of the enterprise. The latter method was defined by Dickerson (1970) as the ratio of costs and returns ($Q = C/R$). James (1982) demonstrated that the resulting relative economic values derived from both profit equations could be very different and, in some cases, may require restrictions on either the inputs or outputs.

The profit equation includes the most relevant animal traits which affect the goal and their economic values (Groen, 2000). In order to design the profit equation, it is crucial to identify the traits which best express the breeding goal. In most cases, the breeding goal for a farm is profit per hectare and, thus, the profit equation will produce the value of profit per hectare. With this said, the breeding goal for the European Sardinian breed is not based on area (ha), but to “increase milk yield for a standardized milking period of 162 days” (Casu et al., 2006). This difference is due to labour being the limiting factor, rather than land price, and thus, breeders of Sardinian sheep are interested in improving the machine milkability of the ewe.

Economic values

Economic values (EV) represent a change in profit caused by a change (either up or down) in one unit of the trait, while holding other traits in the breeding objective constant (Hazel, 1943; VanRaden, 2002). When discussing animal breeding programs, there are three different ways of expressing economic values. The first expression was previously defined by Hazel (1943) as the expected increase in profit caused by the improvement in one unit of the trait, holding all other traits constant. Second, is the relative economic value (REV), which is the percentage of the economic value expressed in relation to the economic value for other traits in the breeding objective (Krupova et al., 2009), and the third function is the relative economic weight (REW), which is equivalent to the relative economic value, but expressed as a genetic standard deviation (Ramon et al., 2010).

$$\text{EVtrait} = \text{change in profit} \,/\, \text{change in trait (holding other traits constant)}$$

Economic values are generated using economic evaluations that reflect stable current conditions and avoid seasonal cyclical irregularities in marketing and purchasing. As mentioned, the cost of milk production relative to milk prices and consumer demand has led to the inclusion of functional traits in the design of an efficient breeding program (Carta et al., 2009). There is an increasing number of studies which include the estimation of economic values of such functional traits (Fuerst-Waltl and Baumung, 2009; Wolfova et al., 2011), as well as the milk production traits (Bytyqi et al., 2015).

Depending on the farm system, economic values for traits within a selection index may differ considerably. This is due to the differing productivity and physical constraints of the farms themselves (McManus et al., 2011). The economic values generated for each trait are partial, rather than simple derivatives of profit (VanRaden, 2002; Ramon et al., 2010). For example, a breeder could be inclined to breed large sheep for greater milk production. However, in practice, the larger animal may produce more milk but also incur additional feed costs. Thus, live weight should not automatically receive a positive selection in an index that aims for increased milk production.

Economic values have already been published for the Spanish breeds, Latxa and Manchega (Legarra et al., 2007), Austrian dairy sheep (Fuerst-Waltl and Baumung, 2009), Slovakian dairy breeds (Wolfova et al., 2009) and, more recently for dual purpose breeds in Kosovo

(Bytyqi et al., 2015). However, there is no such data for dairy sheep in New Zealand. To achieve the breeding objective, the New Zealand industry must develop economic values and a selection index.

2.3.2 Development of a selection index

The selection index (SI) is the step in a breeding program which amalgamates information about several desirable traits into a single estimate of estimated genetic merit. This is designed as an appropriately weighted mathematical function of both direct and indirect traits of individuals and their relatives. The selection index comprises of genetic and phenotypic information on traits which are known to be included, or genetically correlated with, the traits identified in the breeding objective. The traits to include in the index are based on a number of factors; availability of phenotypes, cost of data collection, and genetic correlations among the traits, to name a few (James, 1986). A salient characteristic of the selection criteria is that the correlation between the breeding objective (T) and selection index (I) is maximised (Hazel, 1943).

$$r_{TI} = \text{maximised} \tag{2.2}$$

Hazel (1943) defined an index, based on this correlation, as;

$$I = \sum b_i P_i \tag{2.3}$$

where I is the selection index, b_i is the regression factor which correlates the phenotypic values with the breeding objective, and P_i is the phenotypic information on a trait. Ideally, P will be the phenotypes of the traits included in the breeding objective, but, sometimes these phenotypes are not easy to measure. For example, feed conversion efficiency is a difficult trait to measure, as well as those traits which cannot be expressed in both sexes, such as milk production. Although the phenotypes can’t be calculated, the estimated breeding values (EBV) can, therefore, model selection indices are used instead of the phenotypes;

$$I = \sum b_i EBV_i \tag{2.4}$$

and, in this process, the selection index derived by Hazel (2.3), where b_i is the regression factor that maximises the correlation between T and I (i.e., r_{TI}), however, instead of using phenotypes, this index can be derived with estimated breeding values from best linear unbiased predictors. In addition, the regression factor (b_i), which is a type of weighting, can be replaced with economic values to produce the following index (Hazel, 1943);

$$I = \sum EV_i \; EBV_i \tag{2.5}$$

From this, the weights are applied and used for genetic evaluation of the traits of each individual, to create a single value or ‘selection index’ (Moioli and Pilla, 1994; Serrano et al., 2002; Marie-Etancelin et al., 2005; Marie-Etancelin et al., 2006; Portolano et al., 2006; Barillet, 2007; McMillan et al., 2014b). This selection index is then used to rank the animals for selection.

Confusion when distinguishing between the selection index and the breeding objective could be detrimental to genetic improvement and must be avoided (Ponzoni, 1986). The breeding objective is the combination of traits we want to improve, and is based on economic importance. The ability or difficulty in measuring these traits is irrelevant, whereas, such considerations are largely relevant when deciding on the selection criteria, as the breeder makes their decisions based on these traits (James, 1986).

2.3.2.1 Estimation of breeding values using best linear unbiased prediction

Henderson (1950) developed mixed model equations (MME) to derive best linear unbiased predictions (BLUP) of breeding values. Best linear unbiased prediction is a common method used for estimating random effects of a mixed model. This method was originally designed for estimating the breeding values in animal breeding programs, however, is now widely used across many areas of research (Piepho et al., 2008). These mixed linear models are used in the majority of animal breeding programs, with best linear unbiased estimates used for estimating the linear functions of the fixed effects, and the best linear unbiased predictor for estimating the random elements of the model.

Linear regression models occur when data variables are multivariate and normally distributed (Mulder et al., 2007) and can be used when genetically evaluating dairy ewes. A simple mathematical equation which can be used to generate breeding values for dairy ewes for a single trait includes;

$$y_{ijk} = h_i + u_j + e_{ijk} \tag{2.6}$$

where

y_{ijk} is the k^th^ observation from the j^th^ animal in the i^th^ subclass,

h_i is the mean level of performance for the i^th^ subclass,

u_j is the additive genetic component relating to the performance record (breeding value),

e_{ijk} is the residual effect (including random environmental and non-additive genetic effects, corresponding to the y_{ijk} record).

Subclass effects are generally referred to as fixed effects, while the additive genetic effects are regarded as random effects. Statistical models which contain fixed and random effects are mixed models. The above model equation can be rewritten in matrix notation as follows;

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zu} + \mathbf{e} \tag{2.7}$$

where

y is the vector of all observations,

X is the incidence matrix associating effects in **β** to **y**,

β is the vector containing subclass effects,

Z is the known matrix associating genetic effects in **u** to **y**,

u is the vector containing genetic effects,

e is the vector of residual effects, one effect corresponding to each observation in **y**.

Before completion, the distributional properties of the effects in the model equation must first be specified. The general definitions for this equation involve the following expectations and variances.

The expectation of **y**, **u** and **e** are assumed to be

$$E\begin{bmatrix}\mathbf{y}\\\mathbf{u}\\\mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{X}\beta\\0\\0\end{bmatrix}$$

with the variance-covariance matrices

$$\mathrm{var}\begin{bmatrix}\mathbf{u}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{G} & \mathbf{0}\\ \mathbf{0} & \mathbf{R}\end{bmatrix}$$

$$\text{and } \mathrm{var}(\mathbf{y}) = \mathbf{V} = \mathbf{ZGZ}' + \mathbf{R} \qquad (2.8)$$

When the random effects are in common, then the covariances among the **y**, **ZGZ**', are included. In animal breeding, the application for a single trait analysis is **G** = $\sigma_a^2\mathbf{A}$, and **R** = $\sigma_e^2\mathbf{I}$, therefore;

$$\mathrm{var}\begin{bmatrix}\mathbf{u}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\alpha^{-1}\mathbf{A} & \mathbf{0}\\ \mathbf{0} & \mathbf{I}\end{bmatrix}\sigma_e^2 \qquad \text{with } \alpha^{-1} = \frac{\sigma_a^2}{\sigma_e^2}$$

where

A is the numerator relationship matrix between individuals in **u**,
σ_a^2 is the additive genetic variance for the trait,
I is an identity matrix,
σ_e^2 is the residual variance.

The above assumptions lead to the following implications;

(i) All genetic values are from the same distribution and have common genetic variance, in the absence of inbreeding.
(ii) All residual effects have the same variance and are independent.
(iii) Random effects **u** and **e** are assumed to have zero covariance, equivalent to assuming no genotype-environment interaction.

From the simple matrix model (2.7), Henderson (1963; 1975; 1984) identified various desirable criteria for predicting breeding values. Thus, it is possible, given **G** and **R** from equation (2.8) are known, to formulate a method of predicting **u**, with the following properties;

(i) Method is unbiased as in the predictor $\hat{\mathbf{u}}$ has the same expectation as the unknown variable **u**, i.e.,

$$E(\hat{\mathbf{u}}) = E(\mathbf{u}).$$

(ii) Minimises the variances of the prediction error in the class of unbiased linear predictors, i.e.,

$$\text{Predictor error variance} = \mathrm{var}(\hat{\mathbf{u}} - \mathbf{u}) = \text{min}.$$

(iii) Maximises the correlation between the predicted and the actual breeding values, i.e.,

$$r_{\hat{\mathbf{u}}\mathbf{u}} = \max$$

(iv) When the distribution is multivariate normal,

a. Yields the maximum likelihood and best linear unbiased estimator of the conditional mean of the actual breeding values.

b. In the class of linear, unbiased predictor maximises probability of a correct pairwise ranking.

In 1963, Henderson published a theory which combined the selection index theory with the least squares method, to find the best linear unbiased estimators of **β**, and to use these estimators, **β**° in predicting **u** satisfying the above criteria. This method, therefore, requires a predictor **a'y** of **m'u**, such that;

$$E(\mathbf{m'u} - \mathbf{a'}\,\mathbf{y})^2 = \min$$

When applying these restrictions to the simple matrix model (2.7), the best linear unbiased estimator of **β** can be derived from the generalised least squares equations;

$$\mathbf{X'V}^{-1}\mathbf{X}\,\boldsymbol{\beta}^\circ = \mathbf{X'V}^{-1}\mathbf{y}$$

where

$\mathbf{X'V}^{-1}\mathbf{X}$ is generally not of full rank. Instead, a solution denoted by **β**° instead of $\hat{\boldsymbol{\beta}}$ to indicate that **β** has many solutions, can be obtained from;

$$\boldsymbol{\beta}^\circ = (\mathbf{X'V}^{-1}\mathbf{X})^{-}\,\mathbf{X'V}^{-1}\mathbf{y} \qquad (2.9)$$

$(\mathbf{X'V}^{-1}\mathbf{X})^{-}$ being a generalised inverse of $(\mathbf{X'V}^{-1}\mathbf{X})$.

The best linear unbiased predictors of **u** can be obtained from (**y** - **X β**°) as;

$$\hat{\mathbf{u}}=\mathbf{GZ'V}^{-1}(\mathbf{y} - \mathbf{X}\,\boldsymbol{\beta}^\circ) \qquad (2.10)$$

This expression is essentially the regression of **u** on **y**, after adjustment of **y** for fixed effects (**y**-**X β**°). However with this method, the **V** is regularly a matrix, and thus, so very large that its inversion is very expensive. With this in mind, Henderson (1950) suggested an alternative process which simultaneously solves $\boldsymbol{\beta}°$ and $\hat{\mathbf{u}}$ without computing $\mathbf{V}^{-1}$. The same best linear unbiased estimator of $\boldsymbol{\beta}$ in (2.9) and best linear unbiased predictor in (2.10) can be obtained by maximising the variation in $\boldsymbol{\beta}$ and $\mathbf{u}$, the joint density function of $\mathbf{y}$ and $\mathbf{u}$. Thus, differentiating with respect to $\boldsymbol{\beta}$ and $\mathbf{G}$ and equating to zero gives the following equations;

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta}° \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix} \tag{2.11}$$

Henderson (1959) proved that $\boldsymbol{\beta}°$ of (2.11) is best linear unbiased estimations of the generalised least square (GLS) equations, and that $\hat{\mathbf{u}}$ is the best linear unbiased predictions (Henderson, 1963). These equations are advantageous for numerous applications as $\mathbf{R}^{-1}$ and $\mathbf{G}^{-1}$ are of simple structure (as previously mentioned, generally $\mathbf{R}$ is $\sigma_e^2\mathbf{I}$ and $\mathbf{G}$ is $\sigma_a^2\mathbf{A}$), and thus, feasible to compute.

Henderson's mixed-model equations correspond to a very general matrix model in which $\mathbf{u}$ can comprise of several random factors. Given the assumptions explained in the definition of the model (2.7), the mixed-model equations reduce to;

$$\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \alpha\mathbf{A}^{-1} \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta}° \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{bmatrix} \tag{2.12}$$

with

$$\alpha = \frac{\sigma_e^2}{\sigma_a^2}$$

where

$\mathbf{X}$ is the incidence matrix indicating for each observation, the fixed effects by which it is influenced.

$\mathbf{Z}$ is the known matrix indicating for each observation, the random effects by which it is influenced.

$\mathbf{A}^{-1}$ is the inverse of the relationship matrix between individuals in $\mathbf{u}$.

$\boldsymbol{\beta}°$ is the vector of solutions for fixed effects,

$\hat{\mathbf{u}}$ is the vector of animal solutions, which are the estimated breeding values,

$\mathbf{y}$ is the vector of observations.

These mixed-model equations can also be extended to multi-trait analysis, however this will be discussed further in the methods section.

This best linear unbiased predictor methodology has been applied in dairy sheep in Australia (Fogarty and Gilmour, 1993), Spain (Gabina et al., 1993; Ugarte et al., 1996), Italy (Sanna et al., 2002; Casu et al., 2006; Carta et al., 2009), Croatia (Dzidic et al., 2004), France (Marie-Etancelin et al., 2005), Morocco (Boujenane et al., 2013) and Iraq (Al-Samara et al., 2014). In addition, genomic best linear unbiased predictor has been applied to generate genomic breeding values for Lacaune dairy ewes from France (Duchemin et al., 2012), and Latxa, Manech and Basco-Bearnaise dairy ewes from Spain (Legarra et al., 2014).

BLUP breeding values have been estimated for the following traits; milk yield in the Laxta (Gabina et al., 1993; Ugarte et al., 1996), milk yield in the Awassi (Al-Samara et al., 2014), milk yield, fat content, somatic cell score (Duchemin et al., 2012) and udder traits in the Lacaune (Marie-Etancelin et al., 2005), milk yield (Sanna et al., 2002) and udder traits in the Sarda (Casu et al., 2006) and reproduction and live weight in the D’man (Boujenane et al., 2013).

2.3.2.2 Estimation of genomic breeding values

These mixed-model equations are also extended to predict genomic breeding values (GBV) based on genetic markers (Meuwissen et al., 2001). Genomic selection involves the use of statistical methods with genomic data to evaluate the genetic merit of individuals (Daetwyler et al., 2010). Genotyping technologies such as single-nucleotide polymorphism (SNP) markers, are methods of implementing genomic selection using predictive models based on whole-genome molecular markers. This method was proposed by Meuwissen et al. (2001) to predict estimated breeding values using the following equation;

$$yi = \mu + \Sigma j\ Xij\ bj + ei \tag{2.13}$$

where yi is the phenotype (or deviation from contemporary mean phenotype) of individual i, μ is the general mean, Σj is the sum of all genotyped SNPs, Xij is the number (0, 1, or 2) of copies of allele ‘1’ (versus allele ‘0’) that individual i carries at SNP j, bj is the allele substitution effect for SNP j, and ei is a random residual. More recent studies have allowed marker-assisted selection on a genome-wide scale, as well as the discovery of large numbers of single-nucleotide markers and development of cost-effective methods to genotype them (Meuwissen et al., 2013).

Genomic selection allows improved accuracy of predicting breeding values and genetic gain for quantitative traits (Tecle et al., 2014), by using information on the variation in DNA sequence between animals. This technique is also assumed to reduce the chance of inbreeding (Meuwissen et al., 2013). In addition, the accuracy of this procedure allows breeders more control of what DNA segments come from each animal, as well as the opportunity, if more variability is desired, to know where DNA segments originate (Boichard et al., 2015).

2.3.3 Selection schemes

A selection scheme is designed to maximise the potential rate of genetic gain (Rendel and Robertson, 1950). The main decisions influencing this rate of gain are which animals should be selected and how many (Harris et al., 1984). With this said, the reproductive rates of the animals as well as the uncertainty of their true genetic merit are two core factors which could limit the rate of genetic gain (Lopez-Villalobos and Garrick, 2005). Therefore, an appropriate method of calculating the potential rate of genetic gain includes the selection intensity, accuracy of prediction (correlation between breeding objective and selection index), generation interval and the genetic standard deviation, as follows;

$$\Delta g = \frac{i \cdot r \cdot \sigma_g}{L} \qquad (2.13)$$

where

Δg is the rate of genetic gain,

i is the selection intensity,

r is the accuracy of selection,

σ_g is the genetic standard deviation and

L is the generation interval.

The accuracies are ideally maximised by the selection index, while the generation interval is influenced by the specifications of the animal evaluation system (Harris et al., 1984). The time at which the selection animals reach puberty largely determines the proportion available for selection, as well as the number of relatives, which increases the accuracy of selection (Harris et al., 1984).

Genetic gain is maximised by greater selection intensity, higher accuracy and a shorter generation interval (Nicholas and Smith, 1983). Applying artificial breeding techniques in a selection scheme enables greater accuracy (Hazel, 1943). In addition, as the animal ages, accuracy also tends to increase, however, the generation interval will also increase (Hazel, 1943). Generation interval is also increased with the use of progeny testing (Dickerson and Hazel, 1944). In contrast, genomic selection enables increased accuracy while also decreasing the generation interval, thus, assuming unwanted traits are not included, providing access to rapid genetic improvement (Meuwissen et al., 2013).

This formula for selection schemes can be extended to four selection pathways to generate the maximum rate of genetic gain (Rendell and Robertson, 1950). In this particular case, these include rams to breed rams, rams to breed ewes, ewes to breed rams and ewes to breed ewes (Mirkena et al., 2012). These are also referred to as; progeny test, mass selection, pedigree selection and selection based on collateral relatives (Mavrogenis, 1995).

The more common, and seemingly more efficient selection scheme for animal breeding, is a pyramidal structure, with a closed nucleus at the top of the pyramid where genetic improvement is controlled by artificial insemination and natural mating (Carta et al., 2009). This scheme was applied in the French Lacaune, which rapidly improved the rate of genetic gain for milk production (Barillet et al., 2001a). A similar scheme was later implemented for the Corse, Manech and Basc-Bernaise in France, the Sarda in Italy and the Churra, Manchega and Latxa breeds in Spain (Carta et al., 2009).

In Cyprus, the Chios breed has two nucleus flocks and numerous private flocks under milk-recording schemes (Serradilla and Ugarte, 2006). Selection within flock is based on individual records, while sire selection in the nucleus is achieved by progeny testing (Mavrogenis, 1995).

In Greece, there are two published selection programs for dairy sheep, the Chios and the Karagouniko (Serradilla and Ugarte, 2006). The Karagouniko breed was established in central Greece by way of artificial breeding. Progeny testing enabled the selection of three superior rams, which were then used for planned mating in the control population (Georgoudis et al., 1995). Performance data of each ewe determined the selection of the best producers to enter the flock, and poor producers for culling.

The breeding program for dairy sheep in France utilises progeny testing and artificial breeding (Larroque et al., 2014). Blood from superior rams in the 1990s was stored and became available in 2009, to set up a reference population for the beginning of genomic selection (Astruc et al., 2012). A study comparing genomic selection to conventional selection in the Lacaune confirmed the superiority of genomic rams (0.52 standard deviation of total merit index) (Baloche et al., 2014). Consequently, the change to genomic selection in the Lacaune breed was official in 2015, however, the switch will occur in 2017 for the Pyrenean breed (Astruc et al., 2016).

In Spain, the selection schemes for Latxa, Manchega and Churra breeds are combined (Serradilla and Ugarte, 2006). In comparison to these common Spanish breeds, the selection scheme for the Assaf is more recently developed. The National Association of Breeders of Asaaf Sheep manages the recently developed herd book (Serradilla and Ugarte, 2006). In addition, the selection schemes for the French Lacaune breed implement artificial breeding and progeny testing within the two small-sized nuclei flocks and, with the ram-to-ram pathway, achieve a generation interval of four years (Larroque et al., 2014).

Despite the use of progeny testing and artificial breeding, selection schemes in some countries are often hindered by inadequate pedigree recording, small population size and lack of structured breeding plans (Mirkena et al., 2012). The New Zealand sheep dairy industry is currently in the same situation; with a small population of dairy sheep and limited pedigree recording, progeny testing is not applicable.

2.3.4 Dissemination system

Once superior animals have been identified, the challenge for the industry is the method of quickly disseminating the genes from superior animals into the population (Harris et al., 1984; Groen, 2000). The decision regarding which transfer strategy to use depends largely on the size of the population, as well as the cost and efficacy of the available technology (Lopez-Villalobos and Garrick, 2005). Possible methods include; artificial breeding, sexed-semen, multiple ovulation and embryo transfer (MOET), and progeny testing (Granleese et al., 2015). Artificial insemination is the main reproductive technique in dairy cattle, however, it is not as common in sheep (Carta et al., 2009) due to the complex structure of the ewe's cervix (Buckrell et al., 1994), and the tendency to administer hormones to obtain synchronised oestrus (Ugarte and Gabina, 2004).

If artificial insemination is practiced, it generally follows synchronisation of oestrus, and uses fresh semen (Carta et al., 2009). Despite popularity with the Churra breed in Spain (Ugarte and Gabina, 2004), use of frozen semen is limited, as this semen has to be deposited directly in uterus, a method which requires laparoscopic or surgical techniques (Carta et al., 2009). The use of frozen semen by laparoscopic intrauterine insemination is the method currently favoured in New Zealand, mainly due to the lack of fresh semen (Green et al., 2013).

Sexed semen would enable more progeny to be females, thus, enabling a greater selection differential for replacements (Rendell and Robertson, 1950). A similar outcome can be achieved by MOET, by the transportation of sexed embryos from superior ewes into host ewes (Rendell and Robertson, 1950). Despite the opportunity to increase the potential rate of genetic gain, both sexed-semen and MOET on a large scale, are generally more costly than the benefits, and thus, may not be commercially viable (Granleese et al., 2015). With this said, other factors such as location, value of the animals and demand for animals of high genetic merit will influence the feasibility of such procedures.

Progeny testing was described by Dickerson and Hazel (1944) as an accurate method of increasing the rate of genetic improvement, however, not the most appropriate (due to the increased generation interval). With this said, the option of using this method in conjunction with other technologies, such as artificial insemination, could lead to rapid genetic improvement (Rendell and Robertson, 1950).

Artificial insemination is practiced in Spanish dairy sheep breeds (Manchega, Churra and Latxa), however, this technique is restricted to breeding programmes aimed to progeny test young males (Ugarte and Gabina, 2004): instead, natural mating is the general reproductive medium of disseminating genetic improvement (Ugarte et al., 2002). Artificial insemination with cooled semen is widely used for Lacaune, Manech, Corse, Sarda, Manchego, Churra, Latxa and Assaf breeds (Ugarte et al., 2002). In 2014, dissemination programs for Manech and Lacaune breeds were progeny testing respectively, 150 and 440 young rams in France each year (Larroque et al., 2014). In contrast, sexed-semen, superovulation and MOET were not routinely used in selection schemes (Ugarte et al., 2002). Currently, in New Zealand, small dairy sheep operations use natural mating (King et al., 2014), however, fresh semen services are available, and on-going developments for progeny testing (McMillian et al., 2014b). In addition, 1,700 pure East Friesian embryos were purchased and implanted during April 2015, with hoggets ready to be milked in the 2016 season, some of which have been artificially inseminated.

2.3.5 Crossbreeding

Genetic gain has been achieved within the Lacaune and Awassi breeds (Ugarte et al., 2001; Gootwine, 2011). Lacaune are mainly farmed as purebreds, indoor and under intensive conditions, however, they can also be used for absorption crossbreeding (Ugarte et al., 2001). In Spain, the Lacaune was crossed with the Churra, resulting in the first generation of offspring producing 51% more milk than Churra purebreds (Arranz et al., 1993).

Within-breed genetic gain of the Awassi has led to the “Improved Awassi”- a dairy-type strain of the original Awassi breed, which is capable of producing over 500 L milk/ewe under intensive management (Pollott and Gootwine, 2001). With this said, crossbreeding can be exploited to achieve heterosis effects for specific traits. In Israel, the Awassi was crossed with East Friesian to develop the Assaf breed, which, in regards to prolificacy and breeding, is superior to the Improved Awassi (Gootwine, 2011). These traits, along with high milk production and lamb growth have resulted in the Assaf becoming an important dairy breed in Israel and Spain (Ugarte et al., 2001; Gutierrez et al., 2007).

Achieving genetic gain by crossbreeding requires reliable and in-depth information regarding additive and heterotic effects on the economically important traits (Dickerson, 1970). Also, when introducing foreign breeds for crossbreeding, consideration must be given to the adaptability of the animal to produce high yields under traditional local management and environmental conditions (Ugarte et al., 2001).

Introducing high-yielding foreign breeds was attempted in Spain, however, due to the lack of structure and support, did not achieve the expected increase in milk yield (Ugarte et al., 2001). The Sarda was introduced in Spain in 1961, with the objective of crossing with the local Churra breed to improve milk yield (Ugarte et al., 2001). However, numerous problems arose from this cross, such as; low growth rates, lateral teat placement and the udders were too large, causing adaptation problems under the grazing conditions in Spain (Ugarte et al., 2001).

Crossbreeding is common in most New Zealand dairy sheep operations (King et al., 2014; McMillan et al., 2014b; Peterson and Prichard, 2015), with the majority of milking ewes descending from an East Friesian crossed with a Coopworth, Border Leicester or Polled Dorset. As mentioned, East Friesian genes were introduced into New Zealand with the aim of improving milk production and ewe fertility (Allison, 1995). East Friesian cross ewes in New Zealand are managed differently to overseas counterparts (pasture-fed vs housed), but, still manage to produce high milk yields. Heterosis effects for milk yield have not been evaluated in New Zealand, but can be favourable, and may explain high milk yields.

2.3.6 Economic analysis of the breeding program

It is important to carry-out an economic analysis of the breeding program, to evaluate the effectiveness of the selection program (Lopez-Villalobos and Garrick, 2005). A variety of parameters can be used to evaluate the sustainability of the program such as, net present value, net average yield per head or hectare, the internal rate of return, net marginal returns, profitability per animal and the cost-benefit ratio (Toro-Mujica et al., 2015). Such an exercise is very complex and requires modelling of the entire farm system (Harris et al., 1984). Factors that should be considered include, the cost of the selection scheme, derivation of the economic values, as well as determining the overall profit and beneficiaries of the breeding program.

In Israel, an economic analysis was conducted on the introgression of the Booroola gene into Assaf and Awassi populations (Gootwine et al., 2001). This analysis used the net present value, which included the annual production of lambs and milk, cost of inseminating ewes with the semen of a ram with the homozygous Booroola genotype, and a range of prices for meat and milk. The analysis demonstrated that only when meat prices were high would this project be marginally profitable (Gootwine et al., 2001).

No such analysis has been conducted for the sheep dairy industry in New Zealand, however, this is a key step in the design of an animal breeding program and should be considered.

2.3.7 Estimation of genetic parameters

Estimation of breeding values requires the knowledge of genetic correlations (r_g) and heritability (h^2) of the traits included in the breeding objective and selection index (Safari et al., 2005).

Most genetic parameters for milk production traits are estimated by test-day records (Hamann et al., 2004; Pelmus et al., 2014; Makovicky et al., 2014; Oravcova, 2016). These include the collection of daily milk production on specific “test-days” throughout the lactation period (collected weekly (Al-Samarai et al., 2014) or monthly (Carriedo et al., 1995)). The records for each test-day are used in a statistical calculation to generate the average daily milk production through the entire lactation (Cappio-Borlino et al., 1997; Oravcova et al., 2015). Alternatively, if practicable, full lactation records can be obtained by the collection of data for each milking throughout the entire lactation period (Kominakis et al., 1998; El-Saied et al., 1999; Mavrogenis and Papachristoforou, 2000). There are numerous statistical methods used to analyze milk production records, however, the general linear model is common, as it includes the effect of various fixed factors on milk yield (Carriedo et al., 1995; Al-Samarai et al., 2014).

In animal breeding, there are various algorithms adopted to estimate the variance components within each individual animal model (Kruuk, 2004). The method used to estimate these variance components of each trait depends on the derivatives calculated, and is the crucial part of this process (Kominakis et al., 1998). Methods predominantly employed with dairy sheep include; restricted maximum likelihood estimation (REML) (Rupp and Boichard, 1999; Ligda et al., 2000; Snowder et al., 2001; Duguma et al., 2002; Ligda et al., 2003; Hamann et al., 2004; Al-Samarai et al., 2014), derivative-free restricted maximum likelihood estimation (DFREML) (Baro, 1994; Carriedo et al., 1995; Legarra and Ugarte, 2001; Portolano et al., 2001) and Henderson’s method I, II or III (Barillet and Boichard, 1987).

For this study, the traits of potential consideration for the breeding objective and selection index are; lactation length, total milk yield, total fat yield, total protein yield, total lactose yield, live weight, somatic cell count, first let-down time, first let-down yield and litter size. These traits were decided by personal preference of the farmers, Kat and Andy Gunson. The heritability of each trait considered in the selection index was obtained from a wide range of literature (Table 2.3). But, due to the lack of published data for dairy sheep, the phenotypic and genetic correlations for first let-down time and first let-down yield were from studies on dairy goats. In addition, there is a notably large range of estimated heritability values for lactation length, however, this is due to the type of data and methods used.

Table 2.3. Estimation of heritability values for traits considered in a breeding objective for dairy sheep in New Zealand, sourced from publications listed.

Trait	Heritability	Average
Lactation length	0.015[a], 0.048[b], 0.055[b], 0.07[c], 0.08[c], 0.09[c], 0.128[d], 0.147[e], 0.3[f], 0.37[g]	0.13
Milk yield	0.10[d,h], 0.12[i], 0.13[b], 0.15[j], 0.17[b], 0.20[k,l] , 0.21[m], 0.22[k], 0.23[n], 0.24[o], 0.27[a,c], 0.29[c], 0.30[p], 0.31[p], 0.32[j], 0.42[f], 0.45[q], 0.54[q]	0.25
Fat yield	0.12[h], 0.14[i], 0.16[l], 0.23[c], 0.24[p], 0.25[p,r], 0.26[c], 0.27[c]	0.21
Protein yield	0.09[h], 0.12[i], 0.18[l], 0.22[c], 0.24[c,r], 0.25[p], 0.27[p]	0.20
Lactose yield	0.23[s]	0.23
Live weight	0.76[t], 0.79[t]	0.78
Somatic cell score[1]	0.04[u], 0.08[v], 0.09[w,x], 0.12[h,o], 0.13[m], 0.14[i],	0.10
First let-down time	0.35[y], 0.47[y], 0.48[y]	0.43
First let-down yield	0.39[y]	0.39
Litter size	0.06[z], 0.07[z], 0.08[h], 0.16[n], 0.3[g]	0.13

[1] Somatic cell score SCS = Log2(somatic cell count).

[a] El-Saied et al., 1998a (Churra)

[b] Gutierrez et al., 2007 (Spanish Assaf)

[c] Barillet and Boichard, 1987 (Lacaune)

[d] Pollot and Gootwine, 2001 (Improved Awassi)

[e] Portolano et al., 2001 (Barbaresca Siciliana)

[f] Al-Samarai et al., 2014 (Awassi)

[g] Mavrogenis, 1996 (Awassi)

[n] Ligda et al., 2000 (Chios)

[o] El-Saied et al., 1998a (Churra)

[p] Sanna et al., 1997 (Sarda)

[q] Mavrogenis and Papachristoforou, 2000 (Chios)

[r] Pelmus, 2014 (Teleorman Black Head)

[s] Afolayan et al., 2009 (Crossbred)

[t] Mavrogenis et al., 1998 (Chios)

[h] De Vries et al., 2005 (East Friesian)

[i] Riggio et al., 2007 (Valle del Belice)

[j] Carriedo et al., 1995 (Spanish Churra)

[k] Ugarte et al., 1996 (Latxa)

[l] Legarra and Ugarte, 2001 (Latxa)

[m] Legarra et al., 2005 (Latxa)

[u] Baro et al., 1994 (Churra)

[v] Barillet et al., 2001 (Lacaune)

[w] Riggio et al., 2010 (Valle del Belice)

[x] Tolone et al., 2013 (Valle del Belice)

[y] Marie-Etancelin et al., 2002 (Lacaune)

[z] Kominakis et al., 1998 (Boutsico)

Table 2.4. Estimated phenotypic (above diagonal) and genetic correlations (below diagonal) between traits considered in the breeding objective for New Zealand dairy sheep, sources listed over page.

Trait	LL	MY	FY	PY	LY	LWT	SCS	FLDT	FLDY	LS
LL		0.57[a] 0.66[b]								
MY	0.55[a] 0.61[s] 0.67[b]		0.85[c] 0.93[d]	0.96[c] 0.97[d]	0.22[e] 0.48[f]	0.08[g] 0.1[h]	-0.39[i] -0.12[j]	0.08[k]	0.25[l]	0.06[m,n] 0.2[o]
FY		0.82[t] 0.86[t] 0.88[g] 0.89[d] 0.97[u]		0.76[f] 0.84[c] 0.88[j] 0.95[d]	-0.52[f]	0.06[h]	-0.05[j] 0.17[h]	0.06[p]		-0.03[m]
PY		0.92[t] 0.93[g] 0.94[d,t] 0.97[u]	0.88[c] 0.90[t] 0.93[d,t] 0.95[j,u]		-0.51[e]	0.0[h]	-0.03[q] -0.05[j] 0.14[e]			0.02[m]
LY		0.07[e]		-0.43[e]			-0.33[e]			-0.01[m]
LWT		0.08[g] 0.94[v]	0.99[v]	0.94[v]	0.94[v]		0.0[h]			0.01[r]
SCS		-0.3[w] -0.15[q] 0.04[i] 0.23[j]	0.31[j]	0.12[q] 0.15[e] 0.31[j]	-0.49[e]					
FLDT		0.10[k]	0.03[k]	0.01[k]					-0.52[l]	
FLDY		0.06[p]	-0.01[p]	0.07[p]			0.51[p]			
LS		0.03[x] 0.07[n] 0.44[m]	-0.14[m]	-0.03[m]	0.07[m]	-0.13[r] 0.12[v]				

[1]LL = lactation length, MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, LWT = live weight, SCS = somatic cell score = Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, LS = litter size.

[a] Pollot and Gootwine, 2001 (Improved Awassi)

[b] Portolano et al., 2001 (Barbaresca Siciliana)

[c] Legarra and Ugarte, 2001 (Latxa)

[d] Sanna et al., 1997 (Sarda)

[e] Cloete et al., 2011 (Merino)

[f] Fuertes et al., 1998 (Churra)

[g] Mavrogenis and Papachristoforou, 2000 (Chios)

[h] Perez-Cabal, 2013 (Spanish Assaf)

[i] Barillet et al., 2001 (Lacaune)

[j] Riggio et al., 2007 (Valle del Belice)

[k] Ilahi et al., 2000 (Alpine goats)

[l] Ilahi et al., 1999 (Alpine goats)

[m] Afolayan et al., 2009 (Crossbred)

[n] Mavrogenis, 1996 (Awassi)

[o] Gutierrez et al., 2007 (Spanish Assaf)

[p] Palhiere et al., 2014 (Alpine and Saanen goats)

[q] El-Saied et al., 1999 (Spanish Churra)

[r] Boujenane et al., 2013 (D’man)

[s] El-Saied et al., 1998b (Churra)

[t] Barillet and Boichard, 1987 (Lacaune)

[u] Pelmus, 2014 (Teleorman Black Head)

[v] Walkom et al., 2016 (Merino)

[w] Legarra et al., 2005 (Latxa)

[x] Ligda et al., 2000 (Chios)

2.3.8 Conclusion

The desired improvement of dairy sheep is formalised in the breeding objective which should represent economically important traits that will achieve the breeding goal. Defining a breeding goal and breeding objective for New Zealand dairy sheep should relate to the current and future aspects of the dairy sheep industry. Numerous authors have documented the implementation of genetic improvement programs for animal breeding which has provided a coherent and systematic approach that may be adopted for designing genetic improvement programs for dairy sheep. Economic weightings of each trait should be derived from an associated farm model (or industry model) and updated annually. By identifying the traits of economic importance, the breeding objective enables the interpretation of the role of genes in defining farm profitability and assists in the development of selection strategies.

The selection index to be implemented in the genetic improvement program requires measurable traits of relative economic importance to the breeding objective, to enable the identification of individuals with greatest genetic merit. Care must be taken when deciding on the most appropriate breeding scheme as the rate of genetic gain will be influenced by the selection intensity, the accuracy of selection and the interval between generations. Therefore, the New Zealand dairy sheep industry also needs to consider the type of dissemination system, to be used to transfer the genes from the genetically superior individuals already included in the breeding scheme, into the commercial population. Also, a compromise among breeding companies needs to be achieved in such a way that breeding companies will provide superior animals to the farmers that ensure that the farmers will be making genetic progress for each trait in the right direction, in the right proportion. Whole-system modelling is required to economically analyse the effectiveness of the intended breeding program to ensure the design of a sustainable and profitable breeding program for the New Zealand dairy sheep industry.

Chapter 3

Material and methods

3.1 Materials

The sheep farm used for this study is located in Waiwhare in the Hawkes Bay (-39.453684 latitude, 176.479725 longitude). This farm is commercially owned and operated by Kat and Andy Gunson, who have just started their third season milking sheep. The home farm consists of 20 ha for rotational grazing during the milking period.

The flock consisted of 123 crossbred ewes with a mixture of East Friesian, Highlander, Polled-Dorset and Poltex breeds. The flock was split into two groups (to provide a longer period of supply for the milk processor (Origin Earth)). Lambing for the first group was 1st July until 6th August. The lambs were left with ewes for six weeks and machine milking started on 9th September. The lambing date for the second group was in November and milking commenced six weeks later, and continued until drying off on 5th February. As milk composition varies greatly during late lactation, drying-off date was quite early to avoid any influence on product development (i.e., cheese and yoghurt). In an attempt to avoid these changes in their milk supply, milk yield and composition are monitored. When milk composition changed during late lactation of the first group, milking ewes from the second flock began. As a set standard, once a ewe starts producing as little as 1 litre/day then that ewe is dried off. Based on this criterion, half of the ewes from the first flock were able to maintain the lactation throughout the season (9th September through to 5th February), while others were dried off earlier.

During the milking season, ewes graze lucerne and plantain/clover pastures. In the milking shed ewes are given a small ration of maize then grazed on lucerne, before being moved to a new paddock of plantain/clover pastures for the night. Lucerne is given as a supplement during bad weather, when paddocks are badly pugged. Over the dry lactation period, ewes are fed maintenance levels of pasture with baleage, if required. Ewes are moved on to swedes after scanning (winter), then on to plantain (or, if not enough plantain, some are put on grass with maize supplement), two-weeks prior to lambing.

Average lamb birth weight was 5.3 kg for singles and 4.6 kg for twins. Lambs were weaned at six weeks and sold ‘store’ as soon as possible (due to a bad intestinal worm problem on the property). From the 123 ewes, there were approximately 100 ram lambs, of which the farmers kept 5-10 and sold the rest. A terminal sire was put over the “lower performing ewes” and ewe lambs were sold. Lambs that were not mated to a terminal sire were kept as replacements (25%).

The owners have implemented a database system to record productive and reproductive performance of individual animals, as well as live weight and health records. A pedigree file was compiled containing information for two generations. The breed composition of each ewe, ram and dam was estimated by phenotypic appraisal and using pedigree records.

3.2 Methods

3.2.1 Recording

A total of 479 monthly flock tests (2-4 tests on each ewe), for milk volume and percentages of fat, protein and lactose and somatic cell count (SCC) were obtained over the 2015/16 milking season. Waikato MKV milk meters (Waikato Milking Systems, New Zealand) were attached to each set of cups, enabling the measurement of individual yields, and collection of proportional samples for analysis. Milk yields were recorded in the morning milking, while milk yields and samples for analysis were taken from the afternoon milking. Fat, crude protein, true protein (actual protein content, not including non-protein nitrogen), casein, lactose, and SCC were determined using infrared spectroscopy using a MilkoScan FT120 (Foss, Hillerød, Denmark) calibrated for sheep (MilkTestNZ, Hamilton, New Zealand). Somatic cell score (SCS) at each flock test was calculated as SCS = Log2(SCC).

First let-down time (FLDT) and milk yield (FLDY) were measured during the test-day milkings. The milk meters collect milk samples for each ewe during milking while the time was manually recorded as the time from when cups go on each ewe, to when they finish their first let-down. The same people carried out the same measurements at each flock test to reduce variation among operators. The ewe's first let-down was considered to end once the milk flow slowed to a complete stop in the milk meters.

The live weight of each ewe was recorded 2-4 times on the 11 May 2015, 8 Sept 2015, 26 Oct 2015 and 13 Nov 2015. This produced a great range of weights and enabled an average weight for each ewe during the lactation to be obtained.

The ewes were managed as two different flocks for lambing. The lambing date for ewes ranged from 6 July to 16 December 2015 with median lambing date of 31 July. In order to adjust for lambing date, a deviation of lambing date from the median lambing data of the flock was calculated for each ewe. Litter size at birth was recorded for each ewe.

3.2.2 Lactation curves and prediction of total yields

Lactation curves for each ewe were derived using a random regression procedure with the MIXED procedure of SAS (SAS, 2004). The polynomial equation presented, included the fixed regression coefficient for the population and random regression coefficients as deviations from the fixed population for each ewe. Milk yield (y) for animal "*i*" at "*t*" days in milk, can be represented as follows:

$$Y_{ti} = (\beta_0 P_0 + \beta_1 P_1 + \beta_2 P_2 + \cdots \beta_n P_n) + \alpha_{0_i} P_{0_i} + \alpha_{1_i} P_{1_i} + \alpha_{2_i} P_{2_i} + \cdots \alpha_{n_i} P_{n_i} + e_{ti}$$

Where β is the fixed regression coefficient of the population, α is the random regression coefficients for each combination ewe, and e_{ti} is the random error associated with each observation of day *t* and ewe *i*.

As outlined by Kirkpatrick et al. (1990), the Legendre polynomial's functions of P_j were calculated as:

$$P_0(t)=1, P_1(t)=x,\ P_2(t)=\frac{1}{2}(3x^2-1),\ P_3(t)=\frac{1}{2}(5x^3-3x) \text{ and } P_4(t)=\frac{1}{8}(35x^4-30x^2+3)$$

where, according to the method of Schaeffer (2004),

$$x=-1+2\cdot\frac{(t-t_{\min})}{(t_{\max}-t_{\min})},\ \text{with } t_{\min} = 1 \text{ and } t_{\max} = 210.$$

The order of the polynomial that best fitted the data was selected based on the Akaike information criterion (AIC). An orthogonal polynomial of 3rd order was the best model fitting the lactation curves for fat and lactose daily yields, whereas an orthogonal polynomial of 4th order was the best fit for the lactation curves of milk and protein daily yields.

Total lactation yields for milk production traits were estimated for each individual's lactation using the polynomial equation. These yields were estimated as the sum from day 1 to 60, 90, 150 and 210 days in milk. SCS values were calculated as the mean of SCS during the lactation.

3.2.3 Estimation of breeding values

Breeding values for lactation length, 150-day yields of milk, fat, protein and lactose, live weight, SCS, FLDT, FLDY and litter size at birth were obtained using the ASReml 3.0 software package (Gilmour et al., 2009) using a multiple-trait animal model.

The model was written according to Mrode (2014) as;

$$\begin{bmatrix}\mathbf{y_1}\\ \vdots \\ \mathbf{y_{10}}\end{bmatrix} = \begin{bmatrix}\mathbf{X_1} & \cdots & \mathbf{0}\\ \vdots & \ddots & \vdots \\ \mathbf{0} & \cdots & \mathbf{X_{10}}\end{bmatrix}\begin{bmatrix}\mathbf{b_1}\\ \vdots \\ \mathbf{b_{10}}\end{bmatrix} + \begin{bmatrix}\mathbf{Z_1} & \cdots & \mathbf{0}\\ \vdots & \ddots & \vdots \\ \mathbf{0} & \cdots & \mathbf{Z_{10}}\end{bmatrix}\begin{bmatrix}\mathbf{a_1}\\ \vdots \\ \mathbf{a_{10}}\end{bmatrix} + \begin{bmatrix}\mathbf{e_1}\\ \vdots \\ \mathbf{e_{10}}\end{bmatrix}$$

where $\mathbf{y_i}$= vector of observation for trait i, $\mathbf{b_i}$= vector of fixed effects for trait i, $\mathbf{a_i}$= vector of additive genetic effects for trait i, $\mathbf{e_i}$= vector of random residual effects for trait i; and $\mathbf{X_i}$ and $\mathbf{Z_i}$ are incidence matrices relating records of trait i to fixed and random animal effects, respectively. Fixed effects included in $\mathbf{b}_\mathrm{i}$ were parity number and deviation from median lambing date. The following assumption were considered: $\mathrm{E}(\mathbf{y_i}) = \mathbf{X_i b_i}$, $\mathrm{E}(\mathbf{a_i}) = \mathbf{0}$ and $\mathrm{E}(\mathbf{e_i}) = \mathbf{0}$. The random effects were assumed to be normally distributed with zero mean and the co(variance) structure was assumed as;

$$\mathrm{var}\begin{bmatrix}\mathbf{a_1}\\ \vdots \\ \mathbf{a_{10}}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma^2_{\mathrm{a_1}} & \cdots & \mathbf{A}\sigma_{\mathrm{a_{1,10}}}\\ \vdots & \ddots & \vdots \\ \mathbf{A}\sigma_{\mathrm{a_{1,10}}} & \cdots & \mathbf{A}\sigma^2_{\mathrm{a_{10}}}\end{bmatrix}$$

and

$$\mathrm{var}\begin{bmatrix}\mathbf{e_1}\\ \vdots \\ \mathbf{e_{10}}\end{bmatrix} = \begin{bmatrix}\mathbf{I}\sigma^2_{\mathrm{e_1}} & \cdots & \mathbf{I}\sigma_{\mathrm{e_{1,10}}}\\ \vdots & \ddots & \vdots \\ \mathbf{I}\sigma_{\mathrm{e_{1,10}}} & \cdots & \mathbf{I}\sigma^2_{\mathrm{e_{10}}}\end{bmatrix}$$

where **A**= is the numerator relationship matrix among animals, $\sigma^2_{\mathrm{a_i}}$= additive genetic variance for trait i and $\sigma_{\mathrm{a_{ij}}}$= additive genetic covariance between trait i and trait j, $\mathbf{I}$ = is an identity matrix which corresponds to the number of ewes with records, $\sigma^2_{\mathrm{e_i}}$= residual variance for trait i and $\sigma_{\mathrm{e_{ij}}}$= residual covariance between trait i and trait j.

Genetic and residual variances and covariances derived from genetic parameters are presented in Table 3.1. Heritability and genetic correlations are averages of values published in the literature and phenotypic standard deviations were obtained from the data set using the linear model that included the fixed effect of lactation number and deviation from median lambing date of the flock. When estimates of genotypic and phenotypic correlations were not found in literature, the genetic correlations were assumed to be equal to phenotypic correlations obtained from the data set.

Reliabilities (rel) of estimated breeding values were obtained using the following expression:

$$\text{rel} = \left[1 - \frac{\text{PEV}}{\sigma_a^2}\right] \times 100$$

where PEV is the prediction error variance obtained as a by-product from ASReml calculated as the square of the standard error of the solution for each animal effect.

Table 3.1. Genetic parameters for traits[1] considered in the genetic evaluation of the Gunson's dairy sheep flock. Phenotypic (above diagonal) and genetic correlations (below diagonal).

Trait	h^2	σ_p	LL	MY	FY	PY	LY	LWT	SCS	FLDT	FLDY	LS
LL	0.13	239.85		0.61	0.84	0.88	0.61	0.00	0.00	0.00	0.00	0.00
MY	0.27	593.20	0.61		0.89	0.97	0.89	0.12	-0.25	0.08	0.25	0.11
FY	0.21	2.33	0.84	0.88		0.86	0.80	0.12	0.06	0.06	0.20	-0.03
PY	0.24	1.81	0.88	0.94	0.92		0.18	0.11	0.02	0.06	0.20	0.00
LY	0.27	1.92	0.61	0.70	0.60	0.60		0.12	-0.22	0.06	0.20	0.11
LWT	0.65	33.72	0.00	0.47	0.66	0.65	0.47		0.00	0.00	0.00	0.01
SCS	0.09	0.26	0.00	-0.13	0.31	0.19	-0.49	0.00		0.44	0.51	0.00
FLDT	0.42	176.39	0.00	0.10	0.03	0.01	0.10	0.00	0.44		-0.52	0.00
FLDY	0.38	0.01	0.00	0.06	-0.01	0.07	0.06	0.00	0.51	-0.52		0.00
LS	0.11	0.05	0.00	0.21	-0.14	-0.03	0.07	-0.01	0.00	0.00	0.00	

[1] σ_p = phenotypic standard deviation, LL = lactation length, MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, LWT = live weight, SCS = somatic cell score = Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, LS = litter size.

3.2.4 Economic values and relative economic weights

The economic value (EV) of each trait was not calculated using a profit equation; instead the economic values considered as a part of a selection index were derived from desired relative economic weights (REW) following the methods of VanRaden (2002) and Komlósi et al. (2010).

The REW equals the EV multiplied by the genetic standard deviation σ_g divided by the sum of the absolute values of these products, then multiplied by 100. In an algebraic expression the REW for trait i was calculated as:

$$\mathrm{REW_i} = \frac{|\mathrm{EV}_i \times \sigma_{\mathrm{gi}}|}{\sum_{i=1} |\mathrm{EV}_i \times \sigma_{\mathrm{gi}}|}$$

The genetic standard deviation for each trait was derived from the genetic parameters presented in Table 3.1. The sum of REW is 100% and this creates the opportunity for the farmer to decide the contribution of a trait in a selection index. The relative economic weightings decided by the farmers on a 100% basis, are presented in Table 3.2 as well as the corresponding EVs, which were derived using the solver algorithm as implemented in Excel (Microsoft Office, 2010). During the calculations of EV and REWs, all values were treated as absolute values.

Table 3.2. Relative economic weights (REW) and economic values of traits included in the selection index for the Gunson's dairy sheep flock.

Trait	Genetic SD	REW	EV ($)
Lactation length	15.2	5	0.516
Milk yield	23.6	30	2.000
Fat yield	0.70	3	6.732
Protein yield	0.56	3	8.374
Lactose yield	0.62	0	0
Live weight	5.85	3	-0.805
Somatic cell score[1]	0.50	15	-46.765
First let-down time	13.3	15	-1.767
First let-down yield	0.10	20	332.312
Litter size	0.21	6	44.003

[1] Somatic cell score SCS = Log2(somatic cell count).

3.2.5 Selection index

The economic values were used in conjunction with the estimated breeding values of each trait, to derive the selection index. The index is the sum of the economic value of each trait, multiplied by the estimated breeding value of each trait, for each individual animal. The index was called "dairy sheep economic breeding index" (dsEBI) and expressed with the following equation:

$$\mathrm{dsEBI} = (0.516\times\mathrm{EBV_{LL}}) + (2.000\times\mathrm{EBV_{MY}}) + (6.732\times\mathrm{EBV_{FY}}) + (8.374\times\mathrm{EBV_{PY}}) - (0.805\times\mathrm{EBV_{LWT}}) + (-46.765\times\mathrm{EBV_{SCS}}) + (-1.787\times\mathrm{EBV_{FLDT}}) + (332.312\times\mathrm{EBV_{FLDY}}) + (44.003\times\mathrm{EBV_{LS}})$$

Because lactose yield was given a relative economic weight of zero, this trait was not included in the breeding objective or index, but could be included in the evaluation due to correlations with traits in the objective. High values for some traits are considered undesirable (live weight, somatic cell score and first let-down time), so they were allocated negative economic values.

3.2.6 Genetic gain

A selection scheme was simulated and genetic gain for the breeding objective was calculated using the selection index theory (Hazel, 1942). Superior ewe lambs for ewe replacement and superior ram lambs to replace old rams used for natural mating, were selected based on the dsEBI. For this simulation, it was assumed that the main source of information to build the dsEBI, was one record per trait, of the dams of the lambs available for selection. It was assumed that, from 117 ewe lambs, the top 24 were selected. The farmer has a team of 10 rams, which are used for two years. In order to achieve the desired team of rams required the selection of the top five from the 117 ram lambs available. The standard deviation of the index was calculated using the selection index theory (Cameron 1997) assuming the genetic parameters from Table 3.1 and economic values from Table 3.2.

Chapter 4

Results

4.1 Descriptive statistics

Descriptive statistics for the animal traits considered in the breeding objective and selection index for the 2015/16 season are presented in Table 4.1. Average lactation length was 126 days and averages of accumulated yields were 234 litres milk, 16.5 kg fat, 13.0 kg protein and 12.6 kg lactose. Average let-down time and yield were 79 seconds and 0.5 litres, respectively. Averages were 17.5 for somatic cell score, 75.9 kg for live weight and two lambs born per ewe. The coefficients of variation were between 42 and 47% for yields and 38% for lactation length, indicating a large variation among animals. The ewe with the highest yield had a lactation length of 197 days and accumulated 438 litres milk, 24.8 kg fat, 19.4 kg protein and 22.9 kg lactose in 150 days after lambing.

Table 4.1. Descriptive statistics of variables considered in the genetic evaluation of the Gunson's dairy sheep flock for the 2015/16 season.

Trait	N	Mean	SD[1]	Minimum	Maximum	CV[2]
Lactation length (days)	122	126	47.7	44	208	38
Lactation yield (kg)						
Milk	122	234	101	47.5	526	43
Fat	122	16.5	7.2	2.7	38.7	43
Protein	122	13.0	6.1	2.8	28.9	47
Lactose	122	12.6	5.3	2.5	27.1	42
Somatic cell score[3]	121	17.5	1.7	15.1	22.4	10
First let-down time (s)	121	78.8	22.2	45.0	157.6	28
First let-down yield (L)	121	0.5	0.2	0.2	0.9	33
Live weight (kg)	92	75.9	8.4	52.0	99.3	11
Litter size	115	2.0	0.7	1	5	34

[1] SD = standard deviation.

[2] CV = coefficient of variation.

[3] Somatic cell score SCS = Log2(somatic cell count).

4.2 Lactation curves

Figure 4.1. shows the lactation curves for daily yields of milk, fat, protein and lactose with the average representation of the population as well as a high-yielding ewe and a low-yielding ewe. Based on the Akaike information criterion, an orthogonomial polynomial of 3rd order was the best model for fitting the lactation curves for daily yields of fat and lactose, while an orthogonal polynomial of 4th order was the best fit for daily yields of milk and protein.

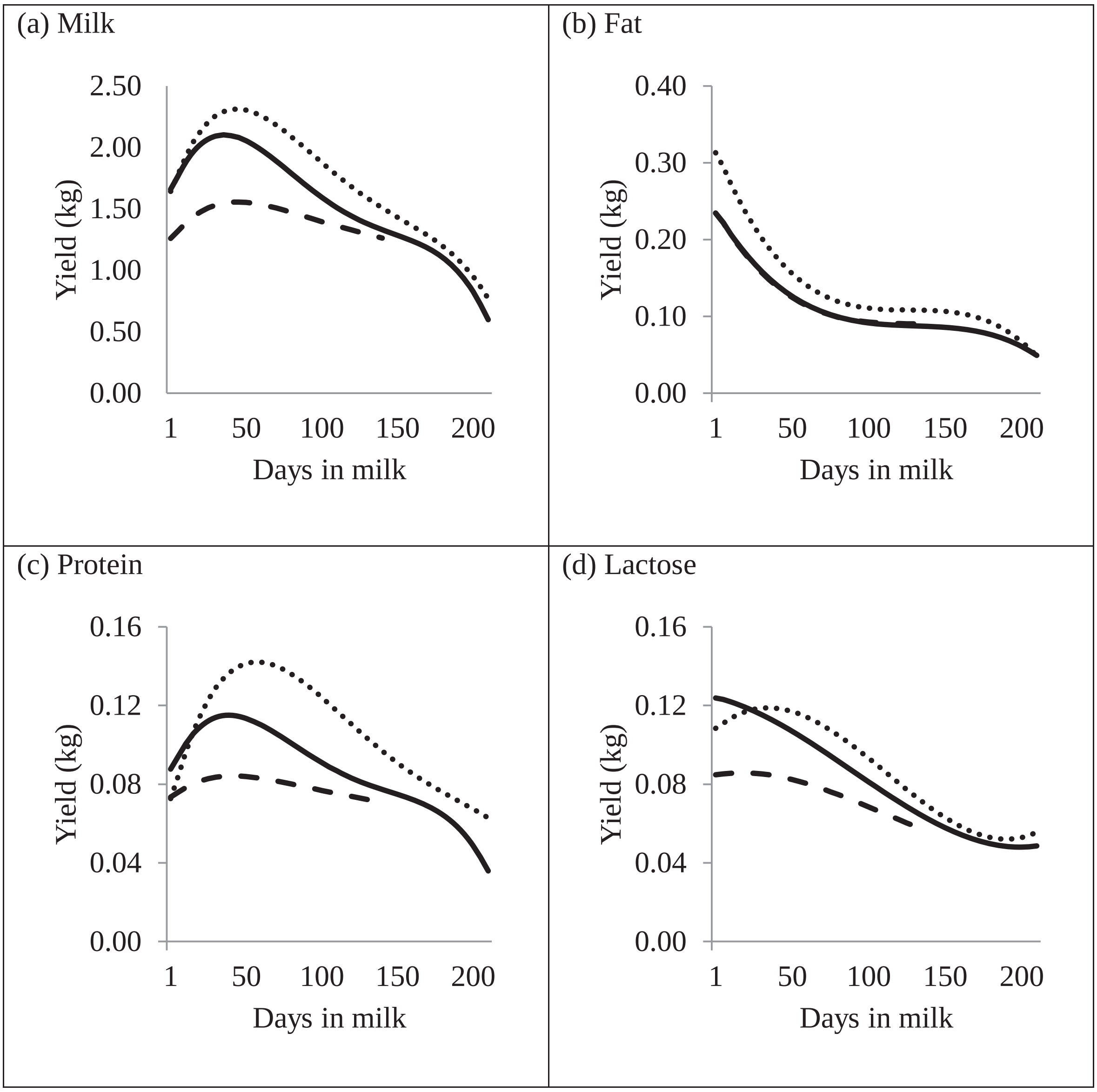


Figure 4.1. Lactation curves for daily yields of milk (a), fat (b), protein (c) and lactose (d) for the Gunson's dairy sheep flock, mean (solid) and a high- (dotted) and a low-yielding ewe (dashed).

4.3 Effect of lactation number

The least squares means of lactation length, accumulated yields of milk, fat, protein and lactose, live weight, first let-down time and yield, and litter size for different lactation numbers are shown in Table 4.2. Means for lactation length, FLDT, FLDY and live weight in first-lactation ewes were significantly ($P<0.05$) lower than in older ewes. Lactation yields for fat, protein, and lactose all increased with increasing lactation number up to the fourth lactation and then reduced in fifth-lactation animals.

Table 4.2. Lactation length, predicted yields at 150 days in milk, milking characteristics, live weight and litter size of the Gunson's dairy ewes of different lactation number. Data are means and standard errors (SE).

Lactation number	n	LL	SE	MY	SE	FY	SE	PY	SE	LY	SE	SCS	SE	FLDT	SE	FLDY	SE	LWT	SE	LS	SE
1	22	92.2^{b}	9.7	208^{c}	10	12.9^{d}	0.7	10.9^{c}	0.62	10.7^{c}	0.58	16.7^{c}	0.36	63.1^{b}	4.4	0.36^{b}	0.03	63.0^{c}	3.0	1.5^{b}	0.16
2	48	125.9^{a}	6.5	266^{b}	7	18.8^{c}	0.49	14.9^{b}	0.42	14.2^{b}	0.39	17.4^{bc}	0.24	78.3^{a}	3.0	0.48^{a}	0.02	73.8^{b}	1.2	2.0^{a}	0.09
3	24	138.5^{a}	9.2	265^{b}	10	18.9^{bc}	0.69	15.6^{ab}	0.59	14.6^{b}	0.55	18.0^{ab}	0.36	78.7^{a}	4.3	0.48^{a}	0.03	81.4^{a}	1.6	2.0^{a}	0.13
4	6	140.8^{a}	18.5	324^{a}	20	22.2^{a}	1.38	18.0^{a}	1.19	17.4^{a}	1.10	17.7^{abc}	0.69	93.0^{a}	8.4	0.59^{a}	0.06	75.0^{ab}	3.2	2.3^{a}	0.26
5	22	142.8^{a}	9.7	288^{ab}	10	20.6^{ab}	0.72	16.0^{ab}	0.62	15.2^{ab}	0.58	18.2^{a}	0.36	91.9^{a}	4.4	0.54^{a}	0.03	78.2^{a}	1.6	2.1^{a}	0.14

LL = lactation length, MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, SCS = somatic cell score = Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, LWT = live weight, LS = litter size.

^{a,b,c,d} Means with different superscripts are significantly different ($P < 0.05$).

4.4 Estimated breeding values

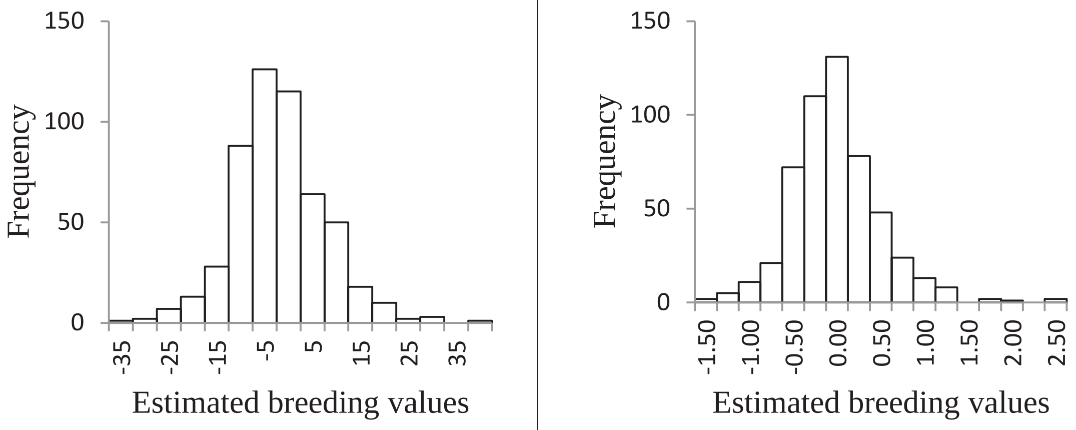
Distributions of EBVs for the traits considered in the selection index are presented in Figures 4.2 and 4.3. All breeding values follow a normal distribution. Range of milk yield EBVs was -35 to +35 kg per lactation. Estimated breeding values for fat yield showed a range of 4 kg (-1.5 to +2.5 kg). The range of EBVs for lactose was bigger than the range of the EBVs for fat and protein. Distribution for live weight EBVs showed some skewness to the left. Somatic cell score EBVs were normally distributed with one outlier with a desirable negative breeding value of -1.25. Milk flow EBVs ranged from -16 to +20 seconds for first let-down time and -0.125 to +0.1 kg for first let-down yields. Estimated breeding values for lactation length ranged from -25 to +30 days while litter-size EBVs were between -0.15 and +0.30 lambs.

The means for breeding values for each trait considered in the selection index for the different birth years are shown in Table 4.3. Estimated breeding values for lactation length, milk and lactose yield, FLDY and litter size all increased with the different birth year. Estimated breeding values for live weight were the highest among animals born in the year 2012, and showed a gradual decrease for animals born in 2013 and 2014.

Table 4.4 shows the productive performance and breeding values of the top 20 ewes selected based on the dsEBI, compared to the rest of the population. The top average dsEBI was superior to the population dsEBI. This is reflected in better for EBVs of milk (+16.41 vs. -10.78 kg) and lactation length (+8.45 vs. -6.57 days). These agree with the actual phenotypic values for each trait where the top ewes produce an average of 323.3 litres/milk vs 250.4 litres/milk for the rest of the population and an average lactation length of 147.6 vs. 121.6 days in milk, respectively.

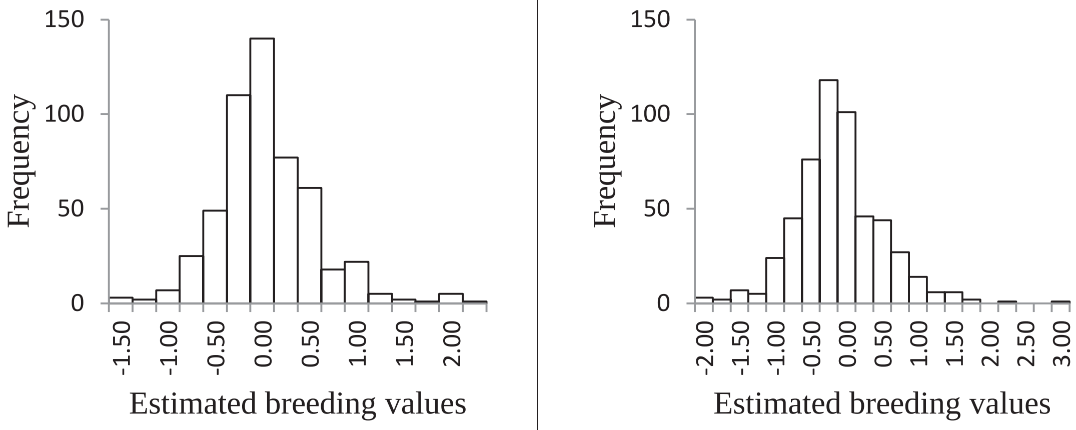
4.5 Genetic gain

Figure 4.4 shows the genetic gain after 20 years of selection, based on the selection of the top 24 ewe lambs and 5 ram lambs, from 117 available lambs for each sex. Average rate of genetic gain was \$16.20 per year. The standard deviation of the breeding objective was \$103.40, the selection intensity in ewe lambs was 1.39 and the selection intensity in ram lambs was 2.13. The accuracy of selection, the correlation between the breeding objective and the index (rTI), was 0.31.



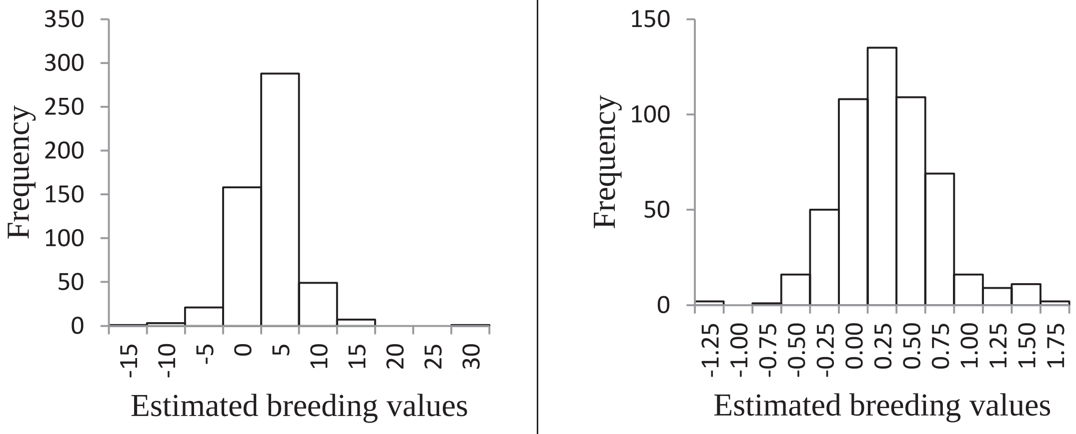
(a) Milk yield

(b) Fat yield



(c) Protein yield

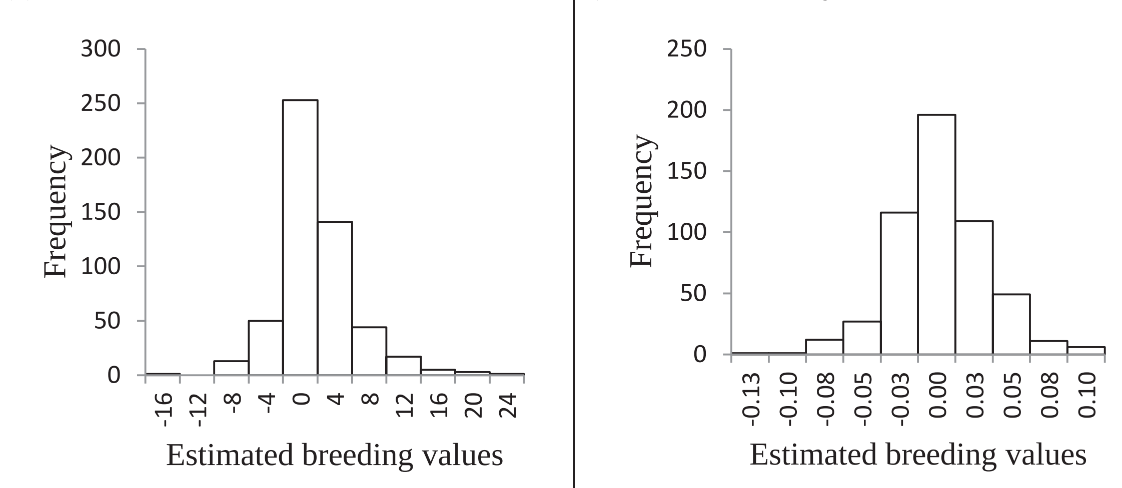
(d) Lactose yield



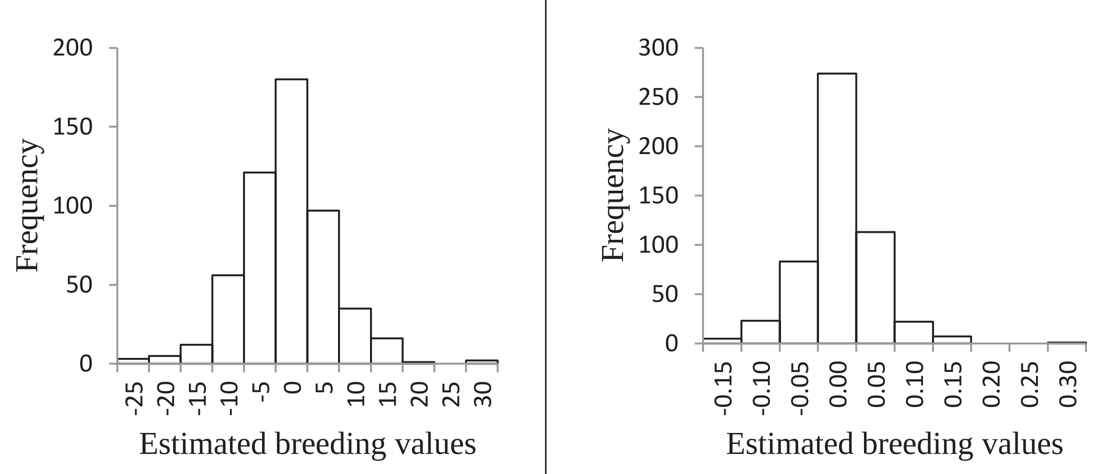
(e) Live weight

(f) Somatic cell scores

Figure 4.2. Distribution of estimated breeding values for 150-day yields for milk (a), fat (b), protein (c) and lactose (d), and live weight (e) and somatic cell scores (f) of Gunson's dairy sheep flock.


(a) First let-down time

(b) First let-down yield


(c) Lactation length

(d) Litter size

Figure 4.3. Distribution of estimated breeding values for First let-down time (a), First let-down yield (b), lactation length (c) and litter size (d) of Gunson's dairy sheep flock.

Table 4.3. Estimated breeding values for lactation length, 150-day accumulated yields of milk, fat, protein and lactose, milking characteristics, live weight, litter size and the economic breeding index (dsEBI) of the Gunson's dairy ewes for different birth years. Data are means and standard errors (SE).

Birth year	n	LL	SE	MY	SE	FY	SE	PY	SE	LY	SE	SCS	SE	FLDT	SE	FLDY	SE	LWT	SE	LS	SE	dsEBI	SE
2012	28	-7.96^{c}	1.14	-12.33^{b}	1.54	-0.10^{a}	0.08	-0.04^{a}	0.08	-0.63^{b}	0.10	0.62^{a}	0.07	0.53^{a}	0.72	-0.03^{b}	0.01	3.75^{a}	0.64	-0.04^{b}	0.01	-74.59^{b}	7.00
2013	32	-5.33^{bc}	1.06	-6.27^{a}	1.44	-0.25^{a}	0.08	-0.08^{a}	0.08	-0.33^{a}	0.09	0.27^{b}	0.06	-0.43^{a}	0.67	-0.01^{a}	0.00	1.08^{b}	0.59	-0.03^{ab}	0.01	-34.49^{a}	6.56
2014	106	-3.3^{ab}	0.58	-4.27^{a}	0.79	-0.20^{a}	0.04	-0.11^{a}	0.04	-0.25^{a}	0.05	0.18^{bc}	0.03	-0.01^{a}	0.37	-0.01^{a}	0.00	1.06^{b}	0.33	-0.03^{ab}	0.00	-26.21^{a}	3.60
2015	259	-2.65^{a}	0.37	-3.87^{a}	0.51	-0.13^{a}	0.03	-0.09^{a}	0.03	-0.21^{a}	0.03	0.13^{c}	0.02	-0.54^{a}	0.24	-0.01^{a}	0.00	0.85^{b}	0.21	-0.02^{a}	0.00	-20.93^{a}	2.30

LL = lactation length, MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, SCS = somatic cell score = Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, LWT = live weight, LS = litter size.

^{a,b,c,d} Means within columns with different superscripts are significantly different ($P < 0.05$).

Table 4.4. Lactation length, predicted yields at 150 days in milk, milking characteristics, live weight and litter size and estimated breeding values and the economic breeding index (dsEBI) of the top 20 dairy ewes of the Gunson's dairy sheep flock (TOP) and the rest of the population (POP). Data are means and standard errors (SE).

	n	LL	SE	MY	SE	FY	SE	PY	SE	LY	SE	SCS	SE	FLDT	SE	FLDY	SE	LWT	SE	LS	SE	dsEBI	SE
Phenotypic values																							
TOP	20	147.6^a	4.6	323.3^a	10.6	22.5^a	0.86	17.5^a	0.32	17.3^a	0.63	16.67^b	0.38	86.6^a	4.92	0.67^a	0.03	81.8^a	2.16	2.1^a	0.15		
POP	102	121.6^b	10.5	250.4^b	4.7	17.4^b	0.38	14.1^b	0.71	13.3^b	0.28	17.71^a	0.17	77.3^a	2.19	0.44^b	0.01	74.9^b	0.92	1.9^a	0.07		
Estimated breeding values																							
TOP	20	8.45^a	2.1	16.41^a	2.3	0.82^a	0.14	0.74^a	0.15	1.11^a	0.14	-0.36^b	0.13	-1.42^a	1.50	0.03^a	0.01	3.70^a	1.3	0.00^a	0.02	75.8^a	9.9
POP	102	-6.57^b	0.9	-10.78^b	1.0	-0.35^b	0.06	-0.24^b	0.07	-0.60^b	0.06	0.41^a	0.06	0.49^a	0.66	-0.02^b	0.00	0.96^a	0.6	-0.03^a	0.01	-59.4^b	4.4

LL = lactation length, MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, SCS = somatic cell score = Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, LWT = live weight, LS = litter size.

^{a,b,c,d} Means with different superscripts are significantly different ($P < 0.05$).

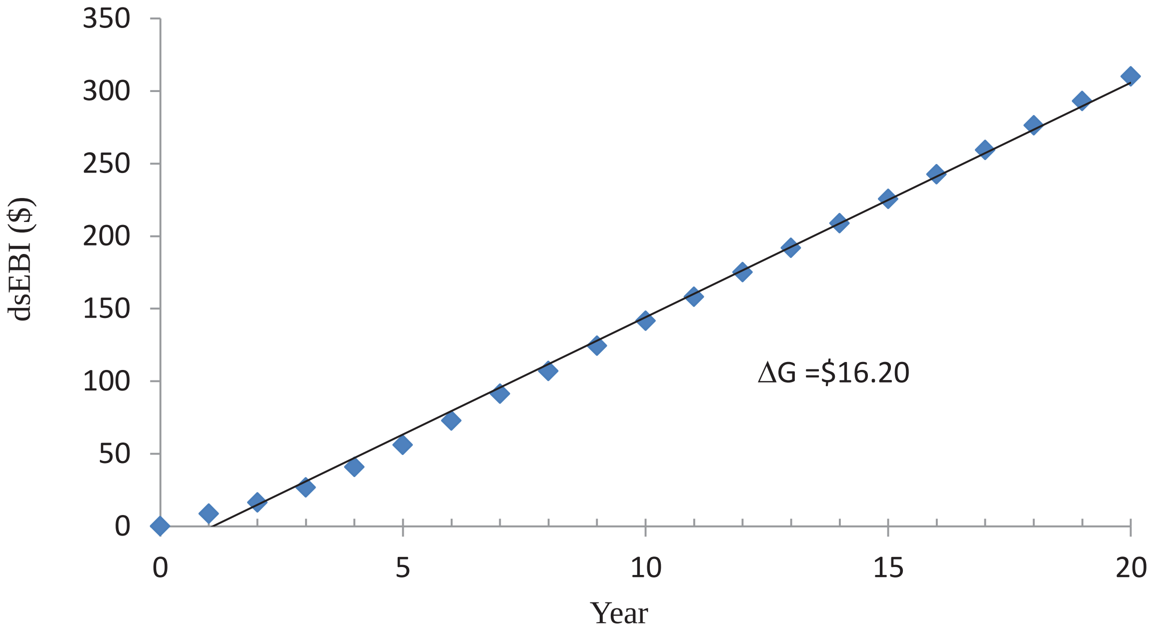


Figure 4.4. Estimated genetic gain for the dairy sheep economic breeding index (dsEBI) in Gunson’s dairy sheep flock after 20 years of selection, based on the dsEBI.

Chapter 5

Discussion

The purpose of this thesis was to estimate breeding values for milk traits, live weight, somatic cell score and litter size at birth and development of a selection index in dairy sheep.
This was achieved by defining the most important traits to be considered in the breeding objective, determining economic values for these traits, using these values as weighting factors to enable the estimation of breeding values for each animal, thus, enabling the construction of a selection index and ranking the animals for profit.

The breeding objective of a genetic improvement program requires the identification of the most important traits that will affect overall farm profit (Newman, 1992; Charfeddine, 2000). Discussions with the farmers resulted in a clear desired direction for improvement, aiming to improve milk yield, milk quality, milking speed and ewe efficiency. This resulted in the traits chosen to be considered in the breeding objective: total yields of milk, fat and protein, first let-down time and yield, live weight, somatic cell score, lactation length and litter size.

Economic values for the traits considered in the breeding objective were generated from the genetic standard deviation and relative economic weight of each trait. The relative economic weights enabled the farmer to decide the contribution of each trait in the selection index. As the size/volume of some traits in the breeding objective are undesirable (live weight, somatic cell score and first let-down time), these were denoted negative values.

The selection index was created by combining information about several desirable traits into a single estimate of estimated genetic merit. The selection index comprises of genetic and phenotypic information on traits which are known to be included, or genetically correlated with, the traits identified in the breeding objective. However, instead of using genotypes and phenotypes, this index was derived with the economic values and estimated breeding values. Henderson (1950) developed mixed-model equations to derive best linear unbiased predictions of breeding values. These mixed linear models are used in the majority of animal breeding programs, with best linear unbiased estimates used for estimating the linear functions of the fixed effects (parity number and deviation from median lambing date), and the best linear unbiased predictor for estimating the random elements of the model (animal effect).

The economic weights and estimated breeding values of the traits of each animal were used to create a single value or ‘selection index’. This selection index was then used to rank the animals for selection.

5.1 Performance of the flock

The level of production of the sheep in the present study was higher than the values reported with Romney, Dorset and Romney-Dorset crosses (Geenty, 1979), Dorset (Gosling et al., 1997), Polled Dorset-East Frisian crosses (Newman and Stieffel, 1999), but lower than that of other dairy sheep flocks with East Friesian crosses in New Zealand reported by McMillan et al. (2014a) (see Table 2.2).

Compared to production levels of sheep from other countries, the sheep from this commercial flock achieved similar production to the East Friesian ewes in the United States (McKusick et al., 2001) and the Lacaune ewes in France (Barillet, 2007), but higher production levels than the East Friesian ewes in Australia (Morgan et al., 2006) and Machega ewes (Ramon et al., 2010) and Latxa ewes in Spain (Legarra and Ugarte, 2001) (see Table 2.2).

Comparison of SCS with other studies is difficult because SCS are calculated using different logarithmic scales, such as Log2, Log10 and natural logarithm.

Mean litter size in the present study was two lambs per ewe, which is greater than the Awassi (1.1-1.45) (Gootwine and Pollot, 2000; Alkass and Juma, 2005; Kassem, 2005), however slightly less than D’man and other East Friesian ewes (2.3-4.43) (McKusick et al., 2001; Hamann et al., 2004; De Vries et al., 2005; Boujenane et al., 2013).

In regards to live weight, ewes in the present study weighed an average of 75.9 kg, which is similar to other reported values for East Friesian ewes in New Zealand (62.7-78.4 kg) (Peterson et al., 2005) and the Spanish Assaf and Romney (75.74 and 80 kg, respectively) (Wolfova et al., 2011; Perez-Cabal et al., 2013), however, heavier than the Latxa, D’man and Valle del Belice dairy ewes (44.8-70 kg) (Tolone et al., 2011; Boujenane et al., 2013; Mandaluniz, 2015).

The contribution of heterosis for each trait was not estimated in this study due to a large number of crossbred groups and a small number of animals in each group.

5.2 Lactation curves

The common lactation curve pattern seen in dairy cattle is an increase in milk yield during early lactation, attaining a peak and then slowly decreasing until the end of lactation (Chang et al., 2001). This pattern, however, cannot be assumed to be uniform among other species. In fact, Cappio-Borlino et al. (1997) found significant effects of flock and feed supply combinations on lactation curves for dairy sheep. In addition to the effect of flock and feed supply, other factors which have significant effects on the pattern of the lactation curve include; lambing season (Peterson et al., 1990; Carta et al., 1995), lambing number (parity) (Portolano et al., 1997), breed (Hassan, 1995) and the length of time ewes have lambs at feet (suckling period) (Geenty, 1980).

There are two types of curves found in dairy sheep to explain the effect of stage of lactation on milk traits (Komprej et al., 2012). The first is common to intensive production systems and shows the daily milk yield increasing until a peak at three to five weeks of lactation. From the peak there is a gradual decline until the end of lactation. This persistency varies depending on factors such as the breed, environmental conditions and the individual.

The second type of lactation curve is considered atypical and is expressed in dairy ewes from extensive production systems. This type of curve indicates milk yield declining from the beginning of lactation right through to the end with no peak. A study by Oravcova et al. (2006) observed ewes of first-parity expressing a lower and earlier peak in the lactation curve, with a general better persistency than that of later parities. In addition, a study on the lactation curve of Valle del Belice dairy sheep in Slovakia showed significant effects of flock and feed supply combinations on test-day models of the lactation curve (Cappio-Borlino et al., 1997). With this said, both studies by Oravcova and Cappio-Borlino started milking at days 15 and 30 postpartum, which, according to the results from Peterson et al. (1994; 2005; 2006) was after the time of peak milk yield. Results from ewes milked daily for the first 12 days of lactation showed increasing milk yields (Peterson et al., 1994). Further studies by Peterson et al. (2005; 2006) cemented these findings, showing milk yields increasing from day one to seven. These results resemble the findings of McMillian et al. (2014a), where peak milk yield of dairy ewes grazing pasture was observed at the end of the first week postpartum. Conclusions from these studies indicate that milk yield peaks around day 10 or

12 and therefore, agree with the results of Oravcova and Cappio-Borlino, who presented declining milk yields from days 15 and 30.

Among the numerous factors previously mentioned, are additional environmental and genetic effects which strongly influence the shape of the lactation curve (Bauer et al., 2012). Environmental factors have been extensively documented in cattle, and more recently, in Slovakian sheep (Krupova et al., 2009). In order to distinguish between the genetic and environmental factors which influence daily milk yield, quantification of genetic and environmental variance parameters is required. These parameters, specific to each animal, can be treated as unobservable variables when undergoing genetic evaluation. When defining the breeding objective in an animal-breeding program, such parameters can be selected. Linear and non-linear mixed effect models obtain estimates of breeding values for modifying the shape of the lactation curve pattern by way of selection. Depending on the pattern of the curve, animals which show potential low performance can be culled.

The use of random regression methodology in this flock enabled the modelling of the lactation curve for each individual ewe with different lactation lengths. For example, the lactation curves for milk, fat and protein were obtained for a ewe which has 150 days in milk, as well as lactation curves for a ewe which has 210 days in milk (Figure 4.1). Random regression models are part of the routine genetic evaluation of most evaluation systems. This random methodology has several advantages (Jamrozik et al. 1997); a) permits the removal of environmental variation in phenotypic data on milk yield, since test-day milk yield considers the specific environmental effects for each herd-test record, b) grants a more accurate evaluation of animal with records, due to the use of a larger number of records per animal, and d) it facilitates the genetic evaluation of lactation persistency.

In the past, animal breeding strategies have been focused on maximising milk yield. However, this approach does not represent the best economic choice. A more economical choice seems to be improving farm profitability by extending the milking period, or, to change the components of milk. A way of doing this is to increase the lactation length or improve persistency of lactation. Lactation length and lactation persistency are both suitable ways of increasing total milk yield, however, a major drawback for implementing lactation persistency into a breeding goal is the difficulty of identifying an objective measure of such a trait (Cannas et al., 2002). There have been several attempts to measure persistency of lactation (Swalve, 1995; Galal et al., 2008), which include a combination of measuring parameters and calculations to fit into lactation curves. Although these methods were suggested, none have been implemented as the standard model. A more recent, multivariate factor analysis has been used to estimate an index of lactation persistency in dairy cattle (Macciotta et al., 2002). Independent of the index used, heritability of lactation persistency is low to moderate (0.10 – 0.30) (Chang et al., 2001). Care must be taken when including lactation persistency in a breeding goal as its relationship with milk yield is variable. Some studies indicate that a lactation curve with a flatter pattern expresses a lower total milk yield, while others had the same production level (Macciotta et al., 2002).

Sheep milk has twice the amount of fat (7.62 vs. 3.67%) and protein (6.21 vs. 3.23%) than cow's milk (Jandal, 1996), and is mainly used for making cheese and yoghurt. As a result, breeding programs should consider milk constituents rather than selecting solely on milk yield (Fuertes et al., 1998). Studies of lactation curves in dairy sheep demonstrate a relationship between milk yield and the levels of milk components (Carta et al., 1995; Oravcova et al., 2007). Selection for high milk yield is consequently accompanied by a decrease in milk fat and protein concentrations, while selection for high fat and protein content is known to result in lower milk yields (Oravcova et al., 2015). This relationship must be carefully examined when deciding on the most appropriate breeding objective as milk price in New Zealand may become dependent on milk yield and milk composition.

The mechanism for recording milk production data is known as a test-day approach. This model is characterised by the stage of lactation and days-in-milk. This test-day approach is achieved by a mathematical equation model. A fixed regression model is commonly used in milk-yield analysis (Hamann et al., 2004) as it is known to more accurately reflect the effect of days-in-milk on milk yield than that of a random regression model (Bauer et al., 2012). Most dairy sheep farms allow lambs to suckle during the early stage of lactation. This can lead to difficulties in accurately fitting complete lactation trajectories. Because of this, the lactation curve should only include milk yields and composition values from the milking period, and not include values for the entire lactation period.

5.3 Economic values

The negative EV for SCS indicates that an increase in the value of this trait is economically unfavourable (Komlósi et al., 2010). Live weight of the animals has a negative EV because increasing weight of an animal leads to increased maintenance feed costs without increasing revenue (Lôbo et al., 2011). Also, the negative value for FLDT is because the longer the animal takes to let down her milk the longer the time for milking and thus, increasing labour costs.

The most economically important trait was milk yield, which contributed 30% to the sum of absolute values of the relative economic weights of all traits. The second most important trait, first let-down milk yield, accounted for 20%. First let-down time and SCS had the same contribution of 15% each. Lactation length and litter size had similar values of 5-6% respectively. The relative importance of fat and protein yield and live weight were all 3%. The lowest economic impact was for lactose yield of 0%, because lactose is not of high priority in the dairy sheep milking industry at the moment.

For example, the EV of milk is $2.00 and $44.00 for litter size. In hindsight, it looks as though there is a large economic value for litter size compared to milk. However, the BV for milk ranges between -50 and +50, whereas the range for litter size is between -0.2 to +0.4. Therefore, the large BV with the small EV of $2.00 produces a large EBV (+$100) for milk, while the large EV of $44.00 for litter size, and the small BV results in a small EBV (+$17.6) for litter size. Thus, indicating that, although the EV for litter size is much greater than that of milk, the range of breeding values results in milk production being more economically important than litter size.

The relationship between litter size and plasma placental lactogen concentrations contributes to the superior lactational performance of multiple bearing ewes (Butler et al., 1981). In addition, as previously mentioned, the East Friesian breed was introduced into New Zealand with the aim of improving milk production and fertility. Therefore, a positive correlation between milk yield and litter size would be beneficial for sheep dairy farmers, as an increased litter size would lead to increased milk yields. With this said, it would be even more beneficial, if dairy ewes had a single lamb, while still producing high milk yields, thus, reaping the benefits of greater milk production without the cost of rearing extra lambs. However, despite the projected benefits, the genetic correlation between milk yield and litter size was low (0.03-0.44), suggesting that selection for litter size is likely to have little impact on milk yield of ewes.

5.4 Estimated breeding values and selection index

The ranges of EBVs were 70 kg for milk, 4.0 kg for fat and protein and 5 kg for lactose, which represented 30, 24, 31 and 40% of the mean. The variation coefficients agree well with the higher estimates of heritability for lactose compared to the estimates of heritability for the other traits.

In this study, one ewe had an EBV for milk yield close to +35 kg, which indicates that she can produce 35 kg more milk compared to her contemporaries of the flock. This is similar to the ewes from Blue River Dairy, where their mean EBV for milk yield was +23 kg, however, much less than their top ewes which are almost achieving +200 kg of milk (McMillan et al., 2014b). But, this is at 180 days in milk compared to the standardised 150 days for this study. Progeny of such ewes are expected to inherit half of their genetic potential (as well as half from the sires). Hence, estimated breeding values are a helpful tool for aiding selection of replacements.

EBVs for live weight were left-skewed, with one animal having an EBV of +25 kg. This suggests the flock is on the lighter side, with one animal which is much heavier. As heavy animals are non-desirable, positive breeding values for live weight indicate that the animal is heavier than her contemporaries of the flock.

The range for somatic cell score EBVs was 3 units (from -0.75 to +1.75), with one outlying EBV less than -1.25. As a high somatic cell score indicates increased incidence of subclinical mastitis, animals with negative SCS EBVs are desirable.

The range of EBVs for first let-down time was 36 seconds (from -16 to +20 seconds) while first let-down yield EBVs were between -0.125 and +0.1 kg. Animals which have long first let-down times result in longer milking times and higher labour costs. Therefore, animals which have short first let-down times are desirable. A ewe with an EBV of -16 indicates the potential to release the first let-down 16 seconds faster than her contemporaries of the flock.

In comparison, a ewe with an EBV of +20 has the potential to let-down her milk 20 seconds slower than her contemporaries of the flock. Breeding values for first let-down yield represent the potential yield for the ewe to produce in its first let-down. For example, a ewe with an estimated breeding value of +0.02 indicates the genetic potential of that ewe to produce 0.02 L milk more than her contemporaries of the flock, in the first let-down. In contrast, an estimated breeding value of –0.03 indicates the potential for the animal to produce, in their first let-down, 0.03 L milk less than her contemporaries of the flock.

The range of EBVs for lactation length was 55 days with the lowest EBV of -25 days and the highest of +30 days. The smallest range of EBVs for all traits considered in the selection index was for litter size of 0.45 lambs. Both lactation length and litter size had potential outliers creating a slight left-skewness in distribution indicating potential animals to be selected or culled.

The trends for breeding values for lactation length, 150-day accumulated yields of milk and lactose, FLDY and litter size increased with the different birth years, while the estimated breeding values for ewe live weight and SCS decreased with the different birth years. This type of trend is desirable and what the farmer will aim to maintain with the aid of the dsEBI.

This genetic evaluation showed large ranges of estimated breeding values for the different traits that may be the result of the diverse breed composition of the flock. This creates an opportunity to use the economic index to identify superior animals to be parents for the following generation and achieve genetic gain.

5.5 Genetic gain

The economic genetic response to 20 years of selection, based on the dsEBI, for the Gunson’s dairy flock was $16.2. This value demonstrates highly promising genetic progress in the flock. This calculation assumes a very simple scheme using natural mating, but high selection intensity (i=1.39 for ewe lambs and i=2.13 for ram lambs) because the flock had a high prolificacy (2 lambs per ewe at birth). This genetic gain expressed in genetic standard deviations of the breeding index is equivalent to $0.15\sigma_T$. This genetic gain is comparable to the simulated gains in the Red Faced Manech ($0.15\sigma_T$) and Alpine ($0.12\sigma_T$) breeds under a traditional progeny test of France (Shumbusho et al., 2013).

5.6 Practical implications and conclusions

A prototype model for genetic evaluation of dairy sheep in New Zealand was developed in this thesis. A breeding objective was defined as the improvement of profit per ewe and the most important animal traits included in the breeding objective were lactation length, lactation yields of milk, fat and protein, first let-down time and yield, average somatic cell score, live weight, and litter size at birth. Economic values for these traits were derived using the relative weights decided by the farmer in combination with the genetic standard deviations of the traits. A selection index was developed using estimated breeding values for the traits considered in the breeding objective and the economic values.

Although genetic improvement is not immediate, it is recommended that the Gunsons use this index to rank ewes and rams to be selected as parents of the next generation. Not only will this produce genetic gain for each of the traits in the right direction, but will also result in progeny with improved milk yield, milk quality, milking speed and overall efficiency. This prototype model can be extended to other dairy sheep farmers, to create selection schemes at industry level and start a systematic breeding program for the emerging dairy sheep industry.

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