

Copyright is owned by the Author of the thesis. Permission is given for a copy to be downloaded by an individual for the purpose of research and private study only. The thesis may not be reproduced elsewhere without the permission of the Author.

**The effects of genes/QTL for muscle and fat on the  
weights of saleable carcass components in sheep**

**A thesis presented in partial fulfilment of  
the requirements for the degree of  
Masterate of Science in Animal Breeding  
and Genetics  
at Massey University, Palmerston North,  
New Zealand.**

**Olivia Mary Gibson**

**2005**

## ***Abstract***

Sheep farmers in New Zealand have the opportunity to increase income through selection based on genetic markers linked to Quantitative Trait Loci (QTL) and/or genes for a variety of traits. A small number of muscle-related QTL/genes have been discovered in sheep and include the Callipyge gene, myostatin gene and the LoinMAX™ QTL. All of these QTL/genes result in an increase in the proportion of lean meat that is produced by the lamb; the size of the increase is different between the QTL/genes. The LoinMAX™ QTL has the smallest effect on carcass composition and results in an increase in the weight and area of the eye muscle. The Callipyge gene shows a larger change in carcass composition than the LoinMAX™ QTL, resulting in a visible increase in the muscles in the hind quarter of the sheep. The myostatin gene has a more general effect on the carcass of a sheep and results in an increase in the weight of all the muscles of the carcass and a decrease in the fat content of the carcass. Both the Callipyge and the myostatin gene also result in an increase in the dressing out percentage of the animal. There is limited information on the economic effects of introducing such QTL/genes into sheep populations.

This study involved using a modelling approach to examine the impact of muscle and dressing out percentage QTL in a sheep flock. A model was established to simulate the growth of 1000 lambs from weaning to slaughter. Further models were used to simulate the processing of carcasses into cuts, with the value of the carcass estimated for both processors and farmers, based on the weight of the individual cuts. A base scenario established the size of cuts and carcass value for lambs, without the presence of known QTL/genes. Four experimental scenarios were examined based on the Callipyge gene, the myostatin gene, the LoinMAX™ QTL, and the effects of the Callipyge and myostatin gene on dressing out percentage. Within each scenario, the QTL effect was estimated at four different magnitudes. The model output for each of the QTL effects was compared to the base model to estimate the additional income of the meat processor when purchasing lambs from farmers who had used the QTL/gene and also the additional income to the farmers.

This study found that the use of muscle QTL/genes in a New Zealand flock has variable effects on the income generated for the processor and the farmer. All the QTL/genes in the study, which were loosely based on muscle QTL/genes currently identified in sheep, resulted in an increase in income for both farmers and processors. The scenario that was based on the LoinMAX™ QTL generated an additional \$0.80 to \$1.80 per lamb for the processor and an additional \$0.56 to \$1.26 per lamb for the farmer. The effect of the Callipyge gene resulted in an increase in the income generated for the processor of between \$12.59 and \$14.97 per lamb, and between \$8.81 and \$10.48 per lamb for the farmer. The last of the muscle QTL/genes analysed was the myostatin gene, the use of this gene in a commercial flock resulted in between \$4.19 and \$7.99 per lamb additional income for the processor and between \$2.93 and \$5.59 per lamb for the processor. When the effect of a dressing out percentage QTL was run through the model the additional income generated for the processor, when the QTL effect was between 5% and 10%, was within \$3.56 and \$8.11 and the additional income for farmers was between \$2.49 and \$5.68.

It can be concluded from this study that the size of the QTL/gene effect and the muscles that are affected by the QTL/gene will influence the additional income that can be generated for the farmer and the processor. In general additional income can be achieved; however, whether or not this outweighs any additional costs that may be associated with using such QTL/genes needs further investigation.

<b>1</b>	<b>INTRODUCTION</b>	<b>1</b>
<b>2</b>	<b>REVIEW OF LITERATURE</b>	<b>2</b>
2.1	INTRODUCTION	2
2.2	SELECTION OF ANIMALS IN LIVESTOCK PRODUCTION SYSTEMS	3
2.2.1	CURRENT METHODS OF SELECTING LIVESTOCK	3
2.2.2	QUANTITATIVE-TRAIT LOCI DISCOVERED IN LIVESTOCK SPECIES	5
2.2.3	DNA MARKERS USED TO SELECT FOR QTL	7
2.2.3.1	Linkage Equilibrium Between Markers and QTL	8
2.2.3.2	Linkage Disequilibrium Between Markers and QTL	8
2.2.4	USE OF MARKERS TO SELECT FOR BREEDING ANIMALS	8
2.2.4.1	Current Industry Examples of QTL	10
2.2.5	EFFECT OF USING MARKERS THAT HAVE BEEN INCORRECTLY IDENTIFIED TO SELECT ANIMALS	11
2.3	THE EFFECT OF THE QTL ON THE PHENOTYPE OF THE ANIMAL	12
2.3.1	LOINMAX™ QTL	12
2.3.2	CALLIPYGE GENE	13
2.3.3	MYOSTATIN GENE	16
2.4	SHEEP FARMING IN NEW ZEALAND	19
2.4.1	IMPORTANCE OF SHEEP FARMING TO THE ECONOMY OF NEW ZEALAND:	19
2.4.2	ASPECTS BEHIND PRODUCTION OF LAMBS ON NEW ZEALAND FARMS	20
2.4.3	LAMB PRODUCTION SYSTEMS ON NEW ZEALAND FARMS	21
2.4.4	ASPECTS BEHIND PROCESSING OF LAMBS SENT TO SLAUGHTER	23
2.5	PAYMENT METHODS FOR NEW ZEALAND LAMB	25
2.5.1	PAST PAYMENT METHOD	25
2.5.2	CURRENT PAYMENT METHOD	25
2.5.3	FUTURE PAYMENT METHODS	26
2.5.3.1	Payment based on the weight of individual cuts	27
2.5.3.2	Payment based on image scanning methods	27
2.6	ANATOMY OF THE SHEEP AND CARCASS CUTS	29
2.7	DEVELOPMENT OF COMPUTER MODELS	32
2.8	LITERATURE REVIEW SUMMARY	33
<b>3</b>	<b>MATERIALS AND METHODS</b>	<b>35</b>
3.1	COMMERCIAL SECTOR	35
3.2	PROCESSOR	37
3.3	DATABASE GENERATION	40
3.4	SCENARIOS TO BE EXAMINED	44
3.4.1	LOIN MAX™ QTL	45
3.4.2	CALLIPYGE GENE	46
3.4.3	MYOSTATIN GENE	46
3.4.4	DRESSING OUT PERCENTAGE QTL	47
3.5	COMPARISON OF BASE MODEL TO QTL/GENE EFFECTS	48
<b>4</b>	<b>RESULTS</b>	<b>49</b>
4.1	BASE MODEL	49
4.1.1	MODEL VALIDATION	49
4.1.2	PAYMENT TO FARMERS BASED ON CARCASS WEIGHT AND GR	49

<b>4.2 LOIN MAX™ QTL</b>	<b>52</b>
4.2.1 LOIN MAX™ QTL WITH A 5% EFFECT	52
4.2.2 LOIN MAX™ QTL WITH A 10% EFFECT	53
4.2.3 LOIN MAX™ QTL WITH A 15% EFFECT	54
4.2.4 LOIN MAX™ QTL WITH A 20% EFFECT	55
<b>4.3 CALLIPYGE GENE</b>	<b>57</b>
4.3.1 CALLIPYGE GENE WITH A 15% EFFECT	57
4.3.2 CALLIPYGE GENE WITH A 20% EFFECT	58
4.3.3 CALLIPYGE GENE WITH A 25% EFFECT	59
4.3.4 CALLIPYGE GENE WITH A 30% EFFECT	60
<b>4.4 MYOSTATIN GENE</b>	<b>62</b>
4.4.1 MYOSTATIN GENE WITH A 5% EFFECT	62
4.4.2 MYOSTATIN GENE WITH A 10% EFFECT	63
4.4.3 MYOSTATIN GENE WITH A 15% EFFECT	64
4.4.4 MYOSTATIN GENE WITH A 20% EFFECT	65
<b>4.5 DRESSING OUT PERCENTAGE QTL</b>	<b>67</b>
4.5.1 DRESSING OUT PERCENTAGE QTL WITH A 5% EFFECT	67
4.5.2 DRESSING OUT PERCENTAGE QTL WITH A 10% EFFECT	68
4.5.3 DRESSING OUT PERCENTAGE QTL WITH A 15% EFFECT	69
4.5.4 DRESSING OUT PERCENTAGE QTL WITH A 20% EFFECT	70
<b><u>5 DISCUSSION</u></b>	<b><u>72</u></b>
<b>5.1 LOIN MAX™ QTL</b>	<b>72</b>
5.1.1 PROCESSOR	72
5.1.2 FARMER	73
<b>5.2 CALLIPYGE GENE</b>	<b>75</b>
5.2.1 PROCESSOR	75
5.2.2 FARMERS	76
<b>5.3 MYOSTATIN GENE</b>	<b>77</b>
5.3.1 PROCESSOR	77
5.3.2 FARMER	78
<b>5.4 DRESSING OUT PERCENTAGE QTL</b>	<b>79</b>
5.4.1 PROCESSOR	79
5.4.2 FARMER	80
<b>5.5 GENERAL DISCUSSION</b>	<b>81</b>
<b>5.6 LIMITATIONS OF THE STUDY</b>	<b>86</b>
<b><u>6 CONCLUSION</u></b>	<b><u>87</u></b>
<b><u>7 REFERENCE LIST</u></b>	<b><u>88</u></b>
<b><u>8 APPENDIX ONE: CALCULATIONS TO DETERMINE YIELD PROPORTIONS FOR EACH OF THE SCENARIOS INVESTIGATED.</u></b>	<b><u>98</u></b>

## List of Tables

Table 2.1: Value of New Zealand Exports*(Modified from Meat and Wool New Zealand 2003-04 Annual Report).....	19
Table 2.2: The adjustments that are made to dressing percentages for time off feed before final weight is made (Flynn, ).....	24
Table 2.3: Composition of the cuts generated by Richmonds Ltd and used in this study.....	31
Table 3.1: Lamb and Mutton Prices for P Grade Carcasses: Commencing 02/02/03 Richmonds Schedule No. 19.....	38
Table 3.2: Description of carcass parts used in the model, values of the cuts(\$/kg), and raw means and standard deviations(kg)(Johnson <i>et al.</i> , 2002).....	39
Table 3.3: Generation of yield proportions using cuts weights and standard deviations from a Romney population.....	41
Table 3.4: Worked example of generating cut weights for a 17kg carcass. ....	42
Table 3.5: Yield proportions for the base model, Loin Max™ 5%, Loin Max™ 10%, Loin Max™ 15%, and Loin Max™ 20%. There is a 5%, 10%, 15%, and 20%, increase in the frenched rack and strip loin for Scenario One to Four respectively. ....	45
Table 3.6: Yield proportions for the base model, Callipyge 15%, Callipyge 20%, Callipyge 25%, and Callipyge 30%. There is a 15%, 20%, 25%, and 30%, increase in the boneless leg, frenched rack, strip loin, and fillet for Scenario Five to Eight respectively. ....	46
Table 3.7: Yield proportions for the base model, Myostatin 10%, Myostatin 15%, Myostatin 20%, Myostatin 25%. There is a 10%, 15%, 20%, and 25%, increase in the frenched rack and strip loin. ....	47
Table 4.1: Comparison of the five runs of the base model to validate the model.....	49
Table 4.2: Base model: comparison of the income generated for farmers when paid on carcass weight and the income generated for processors paid on cut size.....	50
Table 4.3: The average value received by a processor per lamb and for individual cuts for ram lambs. Lambs were drafted at 40 kg liveweight and cut down into individual cuts. ....	50
Table 4.4: The average value received by a processor per lamb and for individual cuts for ewe lambs. Lambs were drafted at 35 kg liveweight and cut down into individual cuts. ....	51
Table 4.5: The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 5% effect.....	52
Table 4.6: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 5% effect and the difference (D) in per-lamb value and cut values between the two scenarios.....	53
Table 4.7: The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 10% effect.....	53
Table 4.8: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 10% effect and the difference (D) in per-lamb value and cut values between the two scenarios.....	54
Table 4.9: The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 15% effect.....	54
Table 4.10: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 15% effect and the difference (D) in per-lamb value and cut values between the two systems. ....	55
Table 4.11 : The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 20% effect.....	55
Table 4.12: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 20% effect and the difference (D) in per-lamb value and cut values between the two scenarios.....	56
Table 4.13: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 15% effect. ....	57

Table 4.14: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 15% effect and the difference (D) between the per-lamb value and cut values between the two scenarios.....	58
Table 4.15: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 20% effect. ....	58
Table 4.16: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 20% effect, and the difference (D) between the per-lamb value and cut values between the two scenarios. ....	59
Table 4.17: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 25% effect. ....	59
Table 4.18: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 25% effect and the difference (D) between in the per-lamb value and cut values between the two systems.....	60
Table 4.19: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 30% effect. ....	60
Table 4.20: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 30% effect and the difference (D) between the per-lamb value and cut values between the two systems.....	61
Table 4.21: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the myostatin gene has a 5% effect.....	62
Table 4.22: The average value received by the processor per lamb, and for individual cuts in the base model and when the myostatin gene has a 5% effect and the difference (D) between the per-lamb value and cut values between the two scenarios. ....	63
Table 4.23: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the myostatin gene has a 10% effect.....	63
Table 4.24: The average value received by the processor per lamb, and for individual cuts in the base model and when the Myostatin gene has a 10% effect and the difference (D) between the per-lamb value and cut values between the two systems.....	64
Table 4.25: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the myostatin gene has a 15% effect.....	64
Table 4.26: The average value received by the processor per lamb, and for individual cuts in the base model and when the myostatin gene has a 15% effect and the difference (D) between in the per-lamb value and cut values between the two systems.....	65
Table 4.27: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Myostatin gene has a 20% effect. ....	65
Table 4.28: The average value received by the processor per lamb, and for individual cuts in the base model and when the myostatin gene has a 20% effect and the difference (D) between the per-lamb value and cut values between the two systems.....	66
Table 4.29: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 5% effect.....	67
Table 4.30: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 5% effect and the difference (D) between the per-lamb value and cut values between the two systems. ....	68
Table 4.31: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 10% effect.....	68
Table 4.32: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 10% effect and the difference (D) between the per-lamb value and cut values between the two systems. ....	69
Table 4.33: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 15% effect.....	69

Table 4.34: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 15% effect and the difference (D) between the per-lamb value and cut values between the two systems. ....	70
Table 4.35: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 20% effect.....	70
Table 4.36: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 20% effect and the difference (D) between the per-lamb value and cut values between the two systems. ....	71
Table 5.1: Comparison of the base model with Loin Max™ 5%, 10%, 15% and 20%.....	72
Table 5.2: Price paid to the farmer and the difference (D) compared to the base model when they are paid at 65, 70 and 75% of the value received by the processor.....	73
Table 5.3: Comparison of the base model with Callipyge 15%, 20%, 25% and 30% .....	75
Table 5.4: Price paid to the farmer when they are paid at 65, 70 and 75% of the value received by the processor .....	76
Table 5.5: Comparison of the base model with Myostatin 5%, 10%, 15%, and 20% .....	77
Table 5.6: Price paid to the farmer when they are paid at 65, 70 and 75% of the value received by the processor .....	78
Table 5.7: Comparison of the base model with a dressing out percentage QTL of 5%, 10%, 15% and 20%.....	79
Table 5.8: Price paid to the farmer when they are paid at 65, 70 and 75% of the value received by the processor .....	80

**List of Figures**

Figure 2.1: The effect of selection on domestic sheep(Anonymous, 1998)	3
Figure 2.2: Comparison of sheep and beef prices paid to farmers in from the 1992-93 season to the 2003-04 season.	20
Figure 2.3: Prices paid to the farmer per kilogram of carcass weight over the past ten years	26
Figure 2.4: The divisions of the lamb carcass that would be generated when the lambs are processed (Lirette <i>et al.</i> , 1984).	30
Figure 3.1: Flow diagram of the commercial sector that shows the progression of the lambs from weaning until they are sent to the processor	36
Figure 3.2: Flow diagram showing the income generated for the processor when the lambs are sent to slaughter.	39
Figure 3.3: Flow diagram showing the development of the carcass weight and cut database for ewe lambs	40
Figure 3.4: Flow diagram showing the development of the carcass weight and cut database for ram lambs	41

## ***1 Introduction***

Currently, genetic progress is being made in sheep flocks through the use of breeding values. Although this is effective, it is time consuming and costly for farmers to implement.

Recent research has focussed on finding quantitative trait loci or genes that are present in livestock species, which can increase the value of animals and allow producers to generate more income. Several QTL/genes affecting economically important traits have been documented for livestock species. Specifically the LoinMAX™ QTL, myostatin gene and Callipyge gene in sheep have been reported to have an effect on carcass composition.

There is however, limited information on the exact economic effects of the introduction of these QTL/genes into sheep flocks.

Sheep farming makes a large contribution to the economy of New Zealand and the ability to increase farmer profit from lambs will benefit not only the industry, but the nation.

This thesis will review the literature on livestock selection, QTL in livestock species, sheep farming in New Zealand, payment methods to farmers for lambs and the anatomy of the sheep. Models of lamb growth and carcass composition will be generated to show the effects of the use of the LoinMAX™ QTL, Callipyge gene, and the myostatin gene on the value of various cuts and hence carcass value. The aim of this thesis is to estimate the additional income that can be generated for the farmer and the processor when QTL/genes are introduced into New Zealand sheep flocks.

## ***2 Review of Literature***

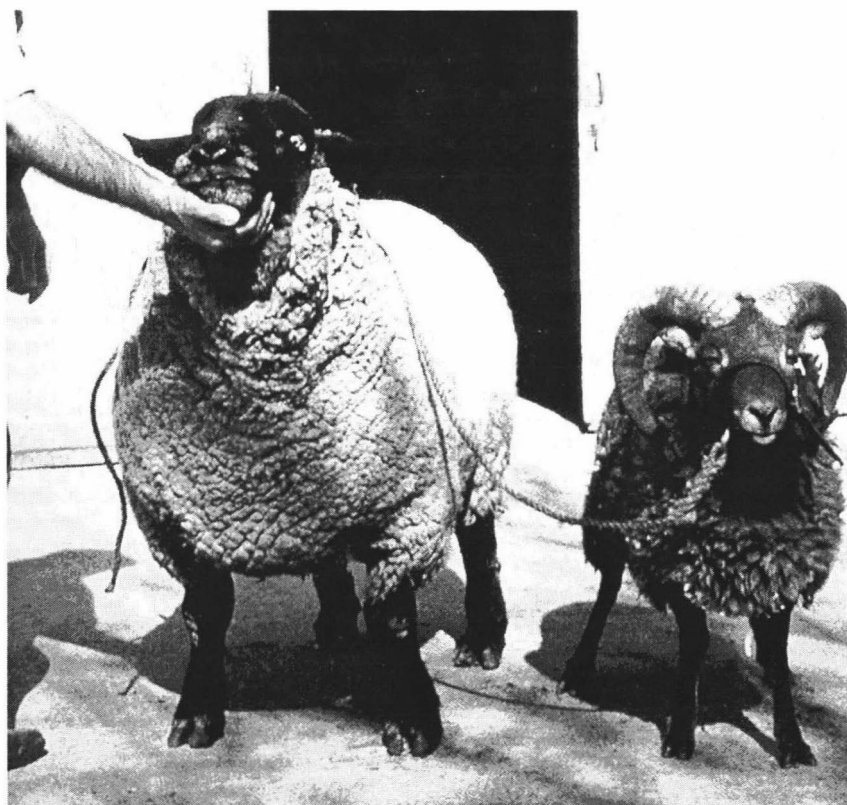
### ***2.1 Introduction***

Current selection methods in livestock production involve selecting animals based on their estimated genotypes based in their phenotype or the phenotype of their relatives. In the past two decades much research has focussed on molecular markers in livestock species. Many performance QTL/genes have been found for livestock species and plants, which could improve the performance of the species. Lamb production in New Zealand is a pasture based system which has the potential to improve through the use of molecular information. Lambs are sold to processing plants and farmers are currently paid on the carcass weight and GR of the lamb. Some processing plants in New Zealand are moving towards different payment methods using individual cut weights and image scanning. The discovery of muscle QTL/genes in sheep, in addition to the changes in payment methods currently being undertaken in New Zealand have generated an opportunity for New Zealand farmers to introduce molecular information into their farm systems. This literature review will cover the above topics and discuss them in more detail.

## ***2.2 Selection of Animals in Livestock Production Systems***

### ***2.2.1 Current Methods of Selecting Livestock***

Selection of animals to increase productivity dates back to the domestication of the first livestock species, which occurred over 10,000 years ago (Elson, 2003). An example of the effect selection has had on domesticated animals can be seen in Figure 2.1. Figure 2.1 shows a comparison between a Suffolk ram, on the left, a breed that has undergone a large amount of selection for growth and meat traits, and a Soay ram, a breed that has had very little artificial selection placed on it (Simm, 1998). The Soay ram is very similar to its predecessors and the difference between the two rams clearly indicates the effect selection can have on a species or breed (Simm, 1998). Since the 1940s more refined methods of selection have evolved with farmers selecting animals for specific properties such as increased lean meat in pigs and increased milk production in cows (Haley, 1995).



**Figure 2.1: The effect of selection on domestic sheep (Simm, 1998)**

The primary aim of most breeding programs is to improve the production characteristics of the breed through genetic gain. Genetic gain is controlled by the selection intensity, the accuracy of selection, the phenotypic standard deviation and the generation interval (Georges, 1999). Genetic gain can be increased by increasing the selection intensity, the heritability and the phenotypic standard deviation or decreasing the generation interval. However, care must be taken when increasing or decreasing these factors as they interact.

Currently selection of breeding stock in production animals involves the use of phenotypic measurements on performance traits from the animal and its relatives to predict breeding values (BVs) (Arendonk *et al.*, 1994; Dentine, 1990). The BV of an animal was defined by (Falconer and Mackay, 1996) (cited in (Dekkers, 1999)) as “the expected performance of the progeny under random mating” and the EBV is the estimate of the breeding value. Estimated breeding values are used to rank sires against each other and are a measure of their genetic value, based on adjustment of their phenotypic performance. The phenotype of an animal includes the observable features, such as coat colour or weaning weight that are coded for by the genotype.

Both genetics and the environment play a part in the formation of the phenotype of the animal (Hayes and Goddard, 2001). Caution must be taken when selecting on phenotypes because if the environment plays a large part in the phenotype then selection on the phenotype will not result in a fast rate of genetic gain. The most important phenotypic traits to measure in an economic sense are those traits that contribute to income and expenses, which are production traits. There are limitations associated with the current method of selection as some traits are hard to measure, appear later in life, have a low heritability, and have a negative correlation with other traits of economic importance (Schwerin, 2001)

For traits that cannot be measured on the animal, such as milk production on a bull or slaughter traits, progeny tests are performed. Progeny testing is a very useful technique as it allows the estimated breeding value (EBV) of an animal to be generated for traits that cannot be measured directly, as EBVs are derived from the phenotypic records from an animal and its relatives (Dekkers, 1999). A progeny test involves mating the sire to a number of females and taking measurements on the offspring. For example, to get

EBVs for meat traits for rams, the rams are mated to ewes and the offspring are tested. Testing involves slaughtering the lambs and taking measurements on the cuts. From these measurements an EBV is developed for the ram, the accuracy of the EBV is dependent on the number of offspring that are tested, with the accuracy increasing as the number of progeny tested increases. The advantages of progeny testing are that sires can be tested for sex limited traits and the use of progeny tests increases the accuracy of selection, as many records are used to generate EBVs. There are disadvantages to progeny testing as they are expensive and time consuming (Elson, 2003). Often by the time a sire has been proven to have a high genetic merit he has been surpassed, genetically, by younger males.

As progeny tests are expensive and time consuming, research has been performed on animal genotypes to allow animals to be selected directly on their genes. As opposed to selecting animal on their EBVs, which are based on their phenotype, and the phenotype of their relatives, which includes both genetic and environmental effects. Research in the last two decades has identified a large number of polymorphic marker loci and some candidate genes that can be used in animal breeding systems (Fernando, 1998). The use of a combination of both genetic and phenotypic records will allow animals to be selected more effectively than using phenotypic measurements alone (Meuwissen and Arendonk, 1992; Spelman and Garrick, 1997). Additionally, the use of marker information only gives extra gain when it is used in situations where current selection methods are ineffective (Smith, 1967 cited in Haley and Visscher, 1999).

### ***2.2.2 Quantitative-Trait Loci Discovered in Livestock Species***

Production or economic traits are also known as Quantitative Traits as the phenotype seen is controlled by many genes (Lin *et al.*, 1997). It is the action of all the genes working together that give the phenotype. Generally there are many genes that have a small effect and a few genes that have a large effect on the trait. The most important genes, known as major genes, are those that have a large effect on the phenotype. Major genes can account for as much as 10% or more of the phenotypic variation seen for the trait (Moore and Hansen, 2003). Major genes that have been identified in livestock species are the dwarf gene in poultry, the Booroola, Inverdale, and Callipyge

gene in sheep (Piper and Bindon, 1982 cited in Kinghorn *et al.*, 1994)(Cockett *et al.*, 1994; Davis *et al.*, 1991), the myostatin gene in cattle (Hanset and Michaux, 1985a; Hanset and Michaux, 1985b) both cited in (Kinghorn *et al.*, 1994), and the halothane gene for stress and performance traits in pigs (Kinghorn *et al.*, 1994).

The positions of major genes within the genetic code are known as Quantitative Trait Loci (QTL), if the gene itself is unknown (Kim and Park, 2001). These QTL can cover relatively large areas of the chromosome and the exact location of the genes involved can be hard to find. The process of finding QTL requires the use of one of two techniques; interval mapping or the candidate gene approach (Kim and Park, 2001). A good review of these methods can be found in Kim and Park (2001).

QTL can be used to select animals for breeding as certain forms of the QTL can be associated with desired phenotypes. Examples of these genes/QTL that result in favourable phenotypes are the Carwell gene (Jopson *et al.*, 2001) and the Callipyge gene (Cockett *et al.*, 1994) in sheep, both of which result in increased muscle production in certain areas of the carcass. Additionally, in other species QTL that have been discovered include the DGAT1 gene (Spelman *et al.*, 2002), and other unnamed milk production QTL in dairy cattle (Spelman *et al.*, 2001), and meat quality QTL in beef cattle (Van Eenennaam, 2004). These phenotypes are often the result of a mutation or nucleotide polymorphism that changes the genetic code in such a way that the protein is either not produced, is not functional, or is over produced (Schwerin, 2001).

There are two methods of identifying animals with a desirable QTL. If the mutation in the gene underlying the QTL is known then animals can be tested directly for gene (gene assisted selection, GAS). If the gene is unknown, markers are used to identify animals carrying the QTL (marker assisted selection, MAS). When testing animals using markers the linkage phase of the markers and QTL is important. The marker-QTL interaction can either be in linkage equilibrium or linkage disequilibrium (Dekkers, 2004).

### **2.2.3 DNA Markers used to Select for QTL**

The regions of the genome that contain functional genes make up less than 5% of the genome; the remaining areas are non-coding sequences (Cunningham, 1999). The purpose of these non-functional areas is as yet unknown, however, scattered within the non coding areas, between the functional genes, are microsatellites. Microsatellites are tandem nucleotide repeats that are highly variable, within a population, in the number of repeats and are inherited in a Mendelian fashion (Marle-Koster and Nel, 2003; Moore and Hansen, 2003). Microsatellites are unlikely to directly affect the quantitative trait of interest; however, they can be used as markers to identify the gene that does affect the trait (Cunningham, 1999; Spelman and Garrick, 1997). Microsatellites can be used as markers to identify genes if they are linked, such as, if the microsatellite and the gene are inherited together. Microsatellites are the most common form of markers used however other segments of the genome can be used to identify QTL. These other segments include restricted fragment length polymorphisms (PCR-FRLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), minisatellites, and single nucleotide polymorphisms (SNP) (Marle-Koster and Nel, 2003). A review of all markers can be found in Marle-Koster and Nel (2003).

Microsatellites that are used as markers for the gene of interest will be positioned some distance from the gene. QTL are defined by either a single marker, which will be positioned to one side of the gene, or two markers, which will flank the QTL (Moore and Hansen, 2003). The use of two markers is more beneficial than the use of one marker because if any changes in the inheritance pattern occur they are more likely to be seen when two markers are used. The distance between the marker and the gene will have an effect on the usefulness of the marker to select for the QTL. This dependence on the marker-QTL distance is because the smaller the distance between the marker and the QTL the greater the likelihood that the marker and the QTL will be inherited together (Ruane and Colleau, 1996). This occurs because the likelihood of recombination occurring is a function of the distance between the marker and QTL (Davis and DeNise, 1998).

Direct testing for the QTL is also more effective than using markers because the validity of marker-QTL interaction is limited to within the family in which they were mapped (

Schwerin, 2001; Elson, 2003). Therefore within every population the QTL-marker association must be tested before a marker can be used. The marker-gene association can be different between families; for example in one family one form of the marker may be associated with the favourable form of the gene, in another family it may be associated with unfavourable form of the gene, and in a third family the marker may show no obvious association with the trait at all (Haley, 1995).

### ***2.2.3.1 Linkage Equilibrium Between Markers and QTL***

When a marker and QTL are in linkage equilibrium the likelihood of the marker and the QTL being inherited together is the same as them not being inherited together. This means that the use of markers that are in linkage equilibrium with the QTL is not satisfactory as there is no way to know whether the QTL has been inherited along with the marker.

### ***2.2.3.2 Linkage Disequilibrium Between Markers and QTL***

Linkage disequilibrium is generated by three factors: hybridisation, random genetic drift, and epistatic selection (Lande and Thompson, 1990). Linkage disequilibrium occurs within families because alleles of a QTL and microsatellites that are located on the same chromosome tend to be inherited together (Ruane and Colleau, 1996). For this reason when a marker and QTL are in linkage disequilibrium the marker is effective in identifying animals with the favourable form of the genes. Linkage disequilibrium is often disrupted by recombination (Lande and Thompson, 1990); and therefore populations must be tested relatively regularly to determine the linkage phase of the QTL and the marker.

## ***2.2.4 Use of Markers to Select for Breeding Animals***

Markers are used to improve the genetics of a breed, either through marker-assisted introgression (MAI) or marker-assisted selection (MAS). Marker-assisted introgression involves introducing a gene from a donor breed into a recipient breed by crossing the two breeds and testing for the gene marker to follow the introgression of the gene (Groen and Smith, 1995; Waaij and Arendonk, 1999; Weller, 2001). After the original

cross the resulting offspring are then mated back to the recipient breed to give an almost pure recipient breed but with the addition of the favourable gene from the donor breed. The favourable gene must be tested and selected for in each successive generation of the recipient breed until the marker is fixed within the population (Dekkers, 2004). Alternatively, MAS involves the selection on markers associated with a gene or genes within the breed. Similar to MAS, is GAS (gene assisted selection), which involves the selection of individuals on the gene as opposed to the marker associated with the gene.

Marker information can be implemented into a breeding program in one of three ways. Either, the marker information is used in conjunction with phenotypic information to generate EBVs, marker information is used to preselect animals and selection occurs again at a later time using an updated EBV, or the third use of marker information is to select on marker information then select again using phenotypic information (Lande and Thompson, 1990). Marker-assisted selection is best used as a tool to enhance current selection methods rather than replacing them (Van Eenennaam, 2004).

The use of MAS is most beneficial when the trait has a low heritability and is difficult to select for using normal selection methods. It has been stated by Meuwissen and Goddard, (1996) that the extra gain generated by the use of MAS or GAS is inversely proportional to the ability to increase genetic gain using conventional selection methods. For meat production traits in sheep, the use of MAS would increase the genetic gain seen in nucleus flocks as rams could be tested on their genotype early in their reproductive life, and before they are slaughtered. This would increase genetic gain as a progeny test would not have to be performed and the generation interval would be decreased. However, a disadvantage of using MAS is that the marker-gene interaction needs to be retested regularly until the favourable allele is fixed in the population.

#### 2.2.4.1 Current Industry Examples of QTL

QTL that are currently being utilised in populations are the DGAT1 gene in dairy cattle, and the LoinMAX™ QTL and Inverdale gene in sheep. MAS is used by Livestock Improvement Corporation (NZ) (LIC) to test bulls to breed sons and their daughters, these animals are genotyped for 25 markers that characterise six QTL (Spelman, 2002). Of the six QTL currently being used by LIC, two have not been published as they are commercially sensitive (Spelman *et al.*, 2001). The four remaining QTL include one QTL for protein percent that has been located on chromosome six and has an inconsistent effect on fat, protein, and milk yield (Spelman *et al.*, 1996), and a QTL on chromosome 16 that has an effect on fat percentage (Spelman, 2002). Additionally, chromosome 20 has been identified as having a QTL that affects protein percentage and milk yield (Arranz *et al.*, 1998), and chromosome 14 contains the DGAT1 gene (Coppeters *et al.*, 1998), which increases fat yield and decreases protein and milk yield with each additional Q allele (Spelman, 2002).

The Inverdale gene is currently being incorporated into some New Zealand sheep flocks, with an estimated economic advantage of \$45,000 per annum in additional income in a 2500 ewe flock (Gray, 2004). Landcorp Farming Ltd (NZ) currently has flocks that carry the LoinMAX™ QTL and animals are selected for the expression of an increased eye muscle area through the use of CT scanning and DNA marker genotyping (Landcorp Farming Ltd, 2005). Some markers that are commercially available and are associated with carcass quality traits in beef cattle are GeneSTAR® Marbling, which is associated with increased marbling, Igenity™-L, also associated with marbling and appetite, TenderGENE™, two markers associated with increased tenderness, and GeneSTAR® Tenderness, another marker reported to increase tenderness (Van Eenennaam, 2004). In plant populations molecular markers are being used to facilitate the introgression of cotton fibre quality traits from one cotton cultivar, *Gossypium hirsutum*, to another, *G. barbadense* (Lacape *et al.*, 2005).

### ***2.2.5 Effect of using Markers that have been Incorrectly Identified to Select Animals***

When animals are selected using markers and QTL there is a risk that the marker information used is not correct. When this occurs and selection is based on incorrect marker information there is generally a decrease in the genetic gain and a genetic loss may even occur (Spelman and Arendonk, 1997). Genetic gain decreases in this situation because when an animal is selected using the marker, the animal will carry an unfavourable gene, which will result in genetic loss. The genetic loss is related to the size of the QTL and the incorrect estimation of a QTL that explains 10% of the variation seen in the trait will result in a 7% loss in genetic response, and a 5% QTL will result in 3% loss in the first generation (Spelman and Arendonk, 1997). Comparatively, Meuwissen and Goddard (1996) found that incorrect estimation of a 9% QTL resulted in a 14% loss in genetic response in the first generation. The difference seen between these results is believed to be due to Meuwissen and Goddard (1996) selecting their animals before records were available meaning that the marker information was more influential in that study than the study performed by Spelman and Arendonk (1997)

### ***2.3 The Effect of the QTL on the Phenotype of the Animal***

The effect of a QTL depends on many factors including the mode of inheritance and the size of the QTL effect. If the mode of inheritance is recessive, then animals will require two copies of the QTL/gene to show the phenotype. Conversely, if the mode of inheritance is dominant then only one copy of the QTL/gene is required for the animal to show the phenotype. Implementing a QTL/gene that has a dominant mode of inheritance will show results faster than when the QTL/gene is recessive. Another aspect that needs to be considered is if the QTL/gene has an additive gene action, in which an animal with two copies of the QTL/gene will show twice the additional gain than when only one copy of the gene is present. Some genes have relatively rare modes of inheritance, for example two copies of the Inverdale gene results in infertile ewes and therefore only the heterozygote animals are desirable (Davis *et al.*, 1992). Additionally, the Callipyge gene only causes an increase in muscling if the individual inherited a Callipyge gene from its sire and a normal gene from its dam; all other genotypes give a normal phenotype (Cockett *et al.*, 1996).

A number of QTL/genotypes have been documented for production traits in livestock species. However, this literature review will be limited to discussion of the myostatin gene, Callipyge gene and the LoinMAX™ QTL in sheep. Only these QTL/genotypes will be discussed as they fit specifically with the objectives of this thesis.

#### ***2.3.1 LoinMAX™ QTL***

The Loin Max™ QTL was first discovered at the Carwell stud in Australia (Jopson *et al.*, 2001) and semen was imported into New Zealand where animals with the Carwell QTL were produced. The QTL was originally named the Carwell QTL, but was later renamed the rib-eye muscle (REM) locus by Jopson *et al.* (2001), with the Carwell allele being the favourable form of the QTL. Recently in a marketing plan Ovisa produced a marker test for the REM locus and named it LoinMAX™.

The position of the LoinMAX™ gene has been mapped to chromosome 18 in a similar position to the Callipyge gene (Nicoll *et al.*, 1998). It was suggested that the Loin

Max<sup>TM</sup> QTL, is allelic to the Callipyge gene (Jopson *et al.*, 2001), however, (McLaren *et al.*, 2003) reported that the LoinMAX<sup>TM</sup> QTL does not overlap with the Callipyge gene and concluded that LoinMAX<sup>TM</sup> is a discrete locus from Callipyge.

The effects of Loin Max<sup>TM</sup> are minimal compared to those of the Callipyge gene as Loin Max<sup>TM</sup> lambs do not look physically different; however, they do have an increased eye muscle area, which can only be detected ultrasonically (Jopson *et al.*, 2001). The increase in the rib eye muscle (*Longissimus dorsi*) area has been reported by Jopson *et al.* (2001) to be 10%. There is an increase in the weight of the muscle of approximately 8% (Nicoll *et al.*, 1998). It has not been reported that animals with the Loin Max<sup>TM</sup> QTL have a decreased fat level as is seen in lambs with the Callipyge and Myostatin gene. It is believed that the tenderness and taste of Loin Max<sup>TM</sup> lamb is not as greatly reduced as is seen with the Callipyge gene (Jopson *et al.*, 2001)

### 2.3.2 Callipyge Gene

The Callipyge gene was first observed in a ram named Solid Gold in 1983 in Oklahoma by a sheep producer who noticed that the ram exhibited increased muscling in the leg and loin region (Cockett *et al.*, 1994; Cockett *et al.*, 1999; Freking *et al.*, 1998a). Mating of Solid Gold to ewes showed that the change in phenotype was the result of a heritable mutation that could be passed on to his offspring (Cockett *et al.*, 1994). The effect seen in the offspring was the result of a single autosomal gene located on ovine chromosome 18 (Cockett *et al.*, 1994). Due to the larger back end of sheep with a copy of the gene it was named Callipyge, which is Latin for beautiful buttocks (Cockett *et al.*, 1994).

The Callipyge gene effects the growth of muscles, but unlike the myostatin gene the expression of the trait is limited to the hindquarters of the animal (Cockett *et al.*, 1999). The Callipyge gene has been shown to affect the activity of calpastatin, which inhibits calpain, a protease that degrades protein (Koohmaraie *et al.*, 1995). The activity of calpastatin is increased differentially in the muscles of Callipyge lambs with the greatest increase being seen in the muscles that have the largest increase in growth (Koohmaraie *et al.*, 1995). The increase in calpastatin results in an increase in the muscle as it

inhibits calpain which degrades the muscle. If the activity of calpain is reduced in Callipyge lambs the muscle has a greater capacity for growth than in a normal lamb.

The increase in muscling seen in Callipyge lambs due to the increased level of calpastatin occurs between three and six weeks of age (Cockett, 1999; Jackson *et al.*, 1997a; Jackson *et al.*, 1997c; Koohmaraie *et al.*, 1995) or 7 to 20 kg liveweight (Duckett *et al.*, 2000). The effect is not seen until this time because the Callipyge gene causes muscle hypertrophy of the fast twitch muscle fibres (Koohmaraie *et al.*, 1995), which is an increase in the size of constituent cells of an organ, as apposed to hyperplasia, which is an increase in the number of constituent cells of an organ. As the fast twitch fibres are hypertrophied, the proportion of them and their diameter is increased in the muscles of Callipyge lambs (Charlier *et al.*, 2001). Therefore, Callipyge lambs have the same number of myoblasts, and therefore similar weights, as normal lambs at birth. However, between three and six weeks of age the myoblasts of Callipyge lambs grow at an increased rate compared to that of non Callipyge lambs. This is an advantage as there is not an increased risk of dystocia in lambs expressing the Callipyge gene as is seen with the myostatin gene ( Jackson *et al.*, 1997a; Koohmaraie *et al.*, 1995). Studies have shown that Callipyge ewes have no difficulty in delivering lambs naturally (Jackson *et al.*, 1997a).

The Callipyge gene results in a redistribution of the muscles and fat as opposed to an increase in the liveweight of the animals. Callipyge lambs do not have significantly different birth weights, weaning weights, or growth rates compared to normal lambs (Cockett *et al.*, 1994; Cockett *et al.*, 1996). Data from Jackson *et al.* (1997a) suggests that in a 54.5kg Callipyge ram lamb the proportion of leg and loin muscle in the carcass will be greater than a non Callipyge lamb. In support of this theory, Freking *et al.* (1998b) found that the percentage of carcass protein deposited in the anterior, middle, and posterior sections of a Callipyge lamb were 33.3, 28.3, and 38.4% respectively, compared with 34.8, 28.0, and 37.2% respectively for a normal lamb. This shows that Callipyge lambs deposit more carcass protein to the middle and posterior regions than normal lambs.

Different muscles are increased in affected lambs with many values being given for the increases in the different muscles. The muscle groups that show the most effect from

the Callipyge gene are the semitendinosus, semimembranosus, gluteus medius (Carpenter *et al.*, 1996), bicep femoris (leg muscles), (Koochmaraie *et al.*, 1995) the longissimus dorsi (loin muscle) (Jackson *et al.*, 1997a). Reports for the increase in the muscles include an increase of 46% for the semimembranosus (Cockett *et al.*, 1999) and an increase of 14% for the semitendinosus (Carpenter *et al.*, 1996). Figures for the size of the effect on the longissimus dorsi include a 31% (Carpenter *et al.*, 1996), a 30% (Cockett *et al.*, 1999) and a 47% increase in the area of the muscle (Cockett *et al.*, 1996). The bicep femoris is also affected by the Callipyge gene and is said to increase by 42.1% (Koochmaraie *et al.*, 1995). Estimates of the total increase in the weight of muscles in Callipyge lambs have been reported to be between 27.6% and 42% (Cockett *et al.*, 1994; Jackson *et al.*, 1997c; Koochmaraie *et al.*, 1995). When the yield of trimmed leg, loin, rack and shoulder is calculated as a proportion of liveweight, Callipyge lambs have an 11% to 16% increase in yield compared to normal lambs (Cockett *et al.*, 1996).

In addition to the increased muscle in the hind quarters, Callipyge lambs have an increased dressing out percentage (Jackson *et al.*, 1997b), decreased fat (Carpenter *et al.*, 1996), and decreased bone (Jackson *et al.*, 1997b). The increase in the dressing out percentage of Callipyge lambs is significant with two studies giving figures of an approximately 4% increase in the dressing out percentage, which results in Callipyge lambs having a higher carcass weight for a given liveweight (Cockett *et al.*, 1996; Freking *et al.*, 1998b). The increase in the dressing out percentage of Callipyge lambs is due to the decrease in the weight of the pelt, liver, kidney, and pelvic fat. The decrease in the level of fat is generally seen in the pelvic and torso region of the lamb and a figure of 7.8% has been given for the decrease in fat seen in Callipyge lambs (Cockett *et al.*, 1994). Callipyge lambs also have an increased feed efficiency as they gain more weight per unit of feed eaten and less food is consumed (Jackson *et al.*, 1997a).

The Callipyge gene has an unusual mode of inheritance as only animals that have inherited a copy of the Callipyge gene from their father and a normal gene from their mother have increased muscling (Cockett, 1999; Freking *et al.*, 2002). This mode of inheritance is known as paternal polar overdominance {Cockett, Jackson, et al. 1996 #2190}, and any copy of the Callipyge gene inherited from the mother is converted

back to the normal form of the gene (Freking *et al.*, 1998a). Additionally, a homozygous Callipyge animal will not show an increase in muscle due to the inheritance of a *CLPG* allele from its maternal side (Cockett *et al.*, 1999). It is believed that the female gene is reactivated when it travels through the male germ line (Cockett, 1999). The reactivation of the Callipyge gene when it travels through the male germ line is not absolute (Cockett, 1999).

One of the major downfalls of Callipyge lambs is the decrease in tenderness of the muscles that show hypertrophy (Duckett *et al.*, 2000). It appears that the same mechanism that increases the size of the muscle also results in the decreased tenderness. Calpastatin has a major effect on muscle toughness as it decreases the activity of calpain (Shackelford *et al.*, 1997). It has been shown that calpain mediated degradation of muscle proteins has a large effect of the tenderisation of meat post-mortem (Koochmaraie, 1988 cited in Koochmaraie *et al.*, 1995). Therefore, if calpastatin decreases the activity of calpain then the amount of post-mortem degradation of muscle will be reduced and the meat will therefore be less tender.

### 2.3.3 *Myostatin gene*

Myostatin is a naturally occurring protein that has been shown to negatively regulate muscle growth in most animals (Mateescu and Thonney, 2002; McMahon *et al.*, 2003; Reisz-Porszasz *et al.*, 2003; Rios *et al.*, 2002). This protein is a member of the transforming growth factor (TGF) -  $\beta$  superfamily (Kambadur *et al.*, 1997; Marchitelli *et al.*, 2003; Mateescu and Thonney, 2002; Rios *et al.*, 2002). Proteins within the TGF -  $\beta$  superfamily are known to inhibit the proliferation of many cell types (Tortora and Grabowski, 2000). Myostatin in particular inhibits the proliferation of myoblasts (Mateescu and Thonney, 2002; Rios *et al.*, 2002), which are primitive muscle cells that have the potential to develop into a muscle fibre (Tortora and Grabowski, 2000). If myoblasts are regulated by myostatin then it can be assumed that myostatin will also negatively regulate the number of muscle fibres and hence the size of the muscles.

Myostatin has been shown to inhibit myoblast proliferation by preventing myoblasts completing the cell cycle (Mateescu and Thonney, 2002; Rios *et al.*, 2002). Rios *et al.*(2002) commented that recombinant myostatin has the ability to inhibit the

proliferation of mouse myoblasts by causing cells to arrest in the G1 and G2/M stages of the cell cycle. Similarly, Mateescu and Thonney (2002) suggest that myostatin regulates myoblast proliferation by arresting cells in the G1 stage of the cell cycle. As the myoblast cells are arrested in the G1 or G2/M stage of the cell cycle, the cells will not divide and, therefore, the number of muscle fibres will be reduced.

Myostatin is involved in the development of skeletal muscles of prenatal animals and will therefore determine the number of muscle fibres that the animal has at birth (Kambadur *et al.*, 1997). An animal that has two copies of the mutated gene (e.g. a double muscling Belgian Blue calf) will have approximately twice the number of muscle fibres of a normal animal at birth (Kambadur *et al.*, 1997). Mateescu & Thonney (2002), and McMahon *et al.* (2003) both documented that myostatin null mice weighed approximately two to three times more than mice with the functional gene. Additionally, adult Belgian Blue cattle that have two copies of the non-functional gene will have, on average, 20% more muscle than animals with the normal gene (Shahin and Berg, 1985) cited in Kambadur *et al.*, 1997). This suggests that an animal's potential to grow muscle is predetermined at birth by the number of muscle fibres present.

In addition to increased muscle mass in animals homozygous for the double muscling gene, there is also a decrease in the weight of fat, bone, and the digestive tract (Shahin and Berg, 1985 cited in Kambadur *et al.*, 1997; Aurther, 1995). This decrease in other body components will result in these animals having a higher dressing out percentage and therefore heavier carcasses for a given liveweight. Double muscled individuals have leaner carcasses due to the increase in muscle mass and decrease in fat (Casas *et al.*, 1998). The production of leaner, larger beef carcasses is very favourable for both farmers and processors as consumers require leaner cuts of meat (Jones *et al.*, 2003). However, as farmers are paid on the size and fatness of the carcasses (Anon, 1996) they will not be paid more for double-muscled carcasses as the proportion of muscle on the carcass increases rather than the carcass increasing. This makes double-muscled carcasses more beneficial for the processor than the farmer.

The myostatin gene is considered to be "partially recessive" as an animal having only one copy of the gene will show mild increases in muscle mass (Kambadur *et al.*, 1997). The double muscling phenotype in Belgian Blue cattle is due to the inactivation of the

myostatin gene, which is located on the end of bovine chromosome 2 (Casas *et al.*, 1998). This loss of function of the myostatin gene in three cattle breeds, Belgian Blue, Piedmontese, and Asturiana de los Valles, is due to a nucleotide deletion, a translation, or a transversion within the coding region of the gene in the three breeds respectively (Mateescu and Thonney, 2002). In Belgian Blue cattle the mutation is an 11 base pair deletion within the coding region of the gene (Kambadur *et al.*, 1997). Conversely, in the Piedmontese breed there is a translation of one type of base to another, resulting in the production of a tyrosine instead of a cysteine at that position (Berry *et al.*, 2002). Both of these mutations result in a non functional protein that does not regulate myoblast proliferation.

Recently work has been performed in the Texel sheep, which is known for its superior muscling, to determine if the myostatin gene is involved in the increased muscling phenotype. The muscle hypertrophy in some Texel sheep in Belgium is so extreme that they have been classified as having double muscling, similar to that seen in certain breeds of cattle (Marcq *et al.*, 2002). Early work has suggested that a QTL affecting carcass traits is present in the region of the myostatin gene in sheep. Reports from Johnson *et al.* (2005) and Marcq *et al.* (2002) suggest that the position of the QTL affecting muscling in Texel sheep is in the region of the myostatin gene. However Marcq *et al.* (2002) found that no single polymorphism in the myostatin gene sequence could explain a loss of function in the myostatin gene. This result from Marcq *et al.* (2002) suggests that either the mutation occurs in one of the flanking regions of the myostatin gene, which regulate its function, or it is in fact another gene that causes the phenotype (Johnson *et al.*, 2005). The effect of this QTL in Texel sheep has been shown to result in a 5 to 8% increase in the carcass muscles and a 10 to 14% decrease in the fat of the carcass (Johnson, 2003).

## 2.4 Sheep Farming in New Zealand

### 2.4.1 Importance of sheep farming to the economy of New Zealand:

In 2003 agriculture in New Zealand generated 17% of the country's Gross Domestic Product (GDP), this is a growth of 80% since 1990-91 (Meat New Zealand, 2003). Sheep farming makes up a significant proportion of the agricultural sector, with lamb meat making up 42.7% of the total revenue generated from meat exports in 2004 (Table 2.1). Between 1985 and 2000 sheep numbers in New Zealand dropped by 32% from 67.85 million sheep to 45.82 million sheep (Davidson, 2000). It would be expected that this decrease in the number of sheep in New Zealand would also cause a decrease in the production (lambs, meat, and wool) of the sheep industry. However, this is not the case and a 10% increase in production has occurred during this time (Meat New Zealand, 2003). This increase in production is due to an increase in lambing percentage, from 100% to 124%, and an increase in average lamb carcass weight, from 14.4kg to 17kg (Meat New Zealand, 2003). Better management practises performed by the farmer, better feeding of animals, pregnancy scanning, hogget mating, and the use of non traditional sheep breeds (Davidson, 2000) will have also contributed to the increased productivity of sheep in New Zealand.

**Table 2.1: Value of New Zealand Exports\*(Modified from Meat and Wool New Zealand 2003-04 Annual Report)**

\$ million FOB (1)			
Year Ended 30 September		2004	% of Total Meats
Meat -	Lamb	1,970.0	42.7
	Mutton	244.4	5.3
	Beef and Veal	1,921.7	41.7
	Edible Offals	198.7	4.3
	Other Meats	277.8	6.0
Total Meats		4,612.6	

\*excludes re-exports 1 FOB: free on board

### 2.4.2 Aspects behind production of lambs on New Zealand farms

Sheep farming in New Zealand is generally a pasture-based system, with little use of supplements to feed animals. New Zealand farmers are able to produce lambs on pasture alone as New Zealand has a relatively temperate climate with a good annual rainfall. This means that year round lambs and ewes live out doors and generally have sufficient feed for lambs to grow well. Supplements may be used in times of extreme environmental conditions such as drought or a wet and cold winter. The limited use of supplements in New Zealand reduces the costs associated with sheep production.

An additional method for decreasing costs when producing lambs is to run both sheep and beef cattle on the farm. Prices for wool, lamb and beef fluctuate year by year so the production of both sheep and cattle minimises the economic risk of farming (Figure 2.2). Sheep and beef cattle are complementary when it comes to pasture utilisation, for this reason running both sheep and cattle on a property can make the most of the pastures grown. Beef cattle are generally run on the tougher areas of the farm with the pregnant ewes and the fattening lambs being given the better pasture. Additionally, running sheep and cattle on a farm reduces the problems associated with parasites because when two species follow each other on a grazing rotation the parasites of each species are reduced by consumption by the alternate species, which remain unaffected.

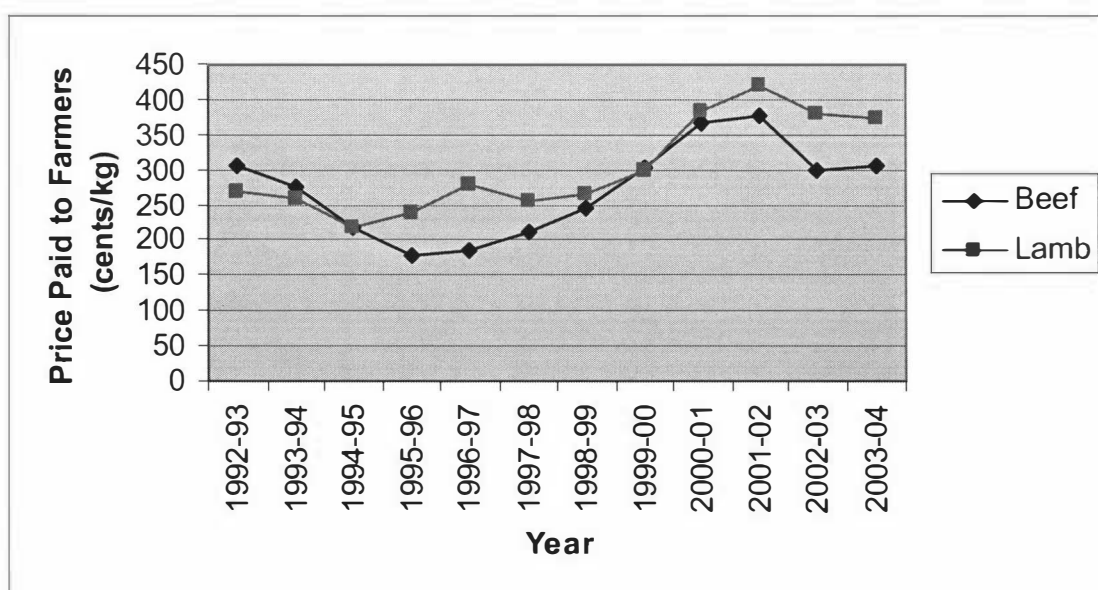


Figure 2.2: Comparison of sheep and beef prices paid to farmers in from the 1992-93 season to the 2003-04 season.

### ***2.4.3 Lamb production systems on New Zealand farms***

There are two main systems for producing lambs for slaughter, either, lambs are born on the farm and grown through to slaughter or the lambs are sold store and brought by a finisher who grows them through to slaughter. The system a farmer will use will depend on the farm's objectives, the location of the property, the price of lamb at the time, and environmental factors. Some properties due to their topography and altitude sell the majority of their lamb's store, however, for most lowland properties if the lamb prices are good more lambs will be taken through to slaughter than sold store. If adverse weather has been experienced and there is a grass shortage, farmers are more likely to sell lambs store earlier. The system of most interest to this study is lambs that have been born on the farm and are grown through to slaughter on the same property.

There is a lot of planning behind the production of lambs; firstly ewes must be mated to rams in the autumn. The choice of ram will be dependent on the goals of the production system. In a commercial self-replacing flock both rams of the same breed (to generate replacement ewes) and terminal sire rams (to generate lambs for slaughter) will likely be used. In a nucleus flock a ram of the same breed as the ewes will always be used, as the aim of a nucleus flock is to breed ewes as replacements and rams to sell. In order to sell rams successfully, the nucleus farmer must seek to improve the genetic merit of the breed (see section 2.2.1).

Rams will be run with ewes at ratios which are dependent on the physical features of the farm. If sheep are run in large, hilly paddocks more rams are required per mob of ewes. Conversely, if the ewes are grazed in smaller paddocks the mating ratio can be higher as it is easier for the ram to mate with a larger number of ewes in a smaller area.

On some farms pregnant ewes will be scanned to determine the number of lambs they are carrying. Scanning is performed so ewes can be separated according to whether they are carrying singles or multiples and can be fed accordingly. Additionally, pregnancy scanning allows dry ewes to be culled from the flock earlier. Ewes carrying multiple lambs require greater energy intake in the final stages of pregnancy. Separating ewes of different birth rank gives the lambs an improved likelihood of survival as the ewes carrying multiples will be on better pasture at lambing.

Lambing date is also an important part of the system. The lambing date will be predetermined to ensure that the best pasture is available for ewes and lambs at lambing. The date of lambing depends on the location of the farm, as warmer areas are able to lamb earlier than colder regions, as their spring flush is earlier. For this reason lambing dates are early in the north and are later on farms further south and in high altitude areas. Lambing dates are set to maximise lamb survival and growth.

Lamb survival after birth is dependent on many factors including birth weight, birth rank, weather conditions, and infections. Birth rank and birth weight are correlated as single lambs are generally the largest lambs followed by twins and then triplets. Birth weights have been documented to be 5.8kg, 4.7kg, and 3.9kg for singles twins and triplets respectively under the same conditions (Muir, 2004). Small lambs take longer than larger lambs to adapt to the environment outside the womb. There is a positive correlation between birth weight of lambs and their ability to digest food (Greenwood *et al.*, 1998), therefore smaller lambs are less able to digest food and obtain nutrients that are needed to survive and grow. Smaller lambs are also more susceptible to adverse environmental conditions, especially if the weather is bad soon after their birth. However, if weather conditions are extreme all lambs will be adversely affected.

Lambs will remain with their mother until weaning, which generally occurs between three and four months of age. The date of weaning will be dependant on the farms lambing date. Lambs are docked prior to weaning, at between three to ten weeks of age, and some farmers will weigh lambs at docking. Some more progressive nucleus farms will DNA test lambs at weaning to ascertain the pedigree of the lambs. Lambs weigh on average 25kg at weaning with sex differences seen between rams and ewe lambs (Garrick *et al.*, 1986). Rams generally weigh 3kg more than ewes at weaning with ram lamb weaning weights averaging 26.5kg and ewe lamb weaning weights averaging 23.5kg (Garrick *et al.*, 1986)

If lambs have reached the drafting criteria at weaning they will be sent to slaughter at that time. Lambs that are not sent to slaughter will be primarily grown on pasture, with limited supplements offered. Average reported growth rates after weaning for lambs in Ireland on grass are 293, 253, and 224g/day  $\pm$ 20g/day for ram, wether, and ewe lambs

respectively (Wylie *et al.*, 1997). Comparatively, (Flanagan and O'Riordan, 1993) documented a growth rate of 200g per day for New Zealand lambs

#### ***2.4.4 Aspects behind processing of lambs sent to slaughter***

Lambs are sent to slaughter either when they reach a certain age, weight, or condition (fat) level. Once the lambs have been transported to the processing plant they will be penned overnight to ensure that their gut fill is minimised. Lambs are also put through a wash prior to slaughter to remove dirt from the animals that may cause contamination of the meat.

The day after the lambs have been delivered to the processing plant they will be slaughtered. Animals are first stunned and then their jugulars are cut to kill them. Every animal is cut down to a carcass by the removal of the head, pelt, internal organs and legs (below the knee and hock joints). At this stage the weight of the carcass is known as the hot carcass weight. The carcass weight is linked to the liveweight by the dressing out percentage, which is the carcass weight as a percentage of the liveweight.

The dressing out percentage is not constant between animals and is dependent on sex and age of the lamb, size of the internal organs, gut fill, and fat around the gut and internal organs. Dressing out percentage increases as lambs get heavier with the dressing out percentage of a wether lamb increasing by three units between 20 and 30kg of liveweight, 1.5 units between 30 and 40kg and only 1 unit between 40 and 50kg (Kirton *et al.*, 1984). Ewe lambs have the highest dressing out percentage, followed by wether and ram lambs. With 30kg ewe, wether, and ram lambs having dressing out percentages of 41.3, 40.9 and 40.5% respectively (Kirton *et al.*, 1984). Gut fill has a large effect on liveweight and therefore dressing out percentage, with the effects of time off grass, prior to liveweight being measured, on dressing out percentage shown in Table 2.2.

**Table 2.2: The adjustments that are made to dressing percentages for time off feed before final weight is made (Flynn, 2005)**

Time off feed prior to weighing	Add % to dressing percentage
0-3 hrs	0
4-5 hrs	+0.5
6-8 hrs	+1
9-12 hrs	+2 to 3
13-24 hrs	+3.5 to 4.5

Carcasses are hung and chilled over night giving the cold carcass weight, which is approximately 4.5% less than the hot carcass weight (Kirton *et al.*, 1984). Once the carcass is chilled it is processed down to individual cuts; the cuts processed will be dependent on the processing plant and the market they are supplying (see section 2.6). In January 2003 Richmonds processing plants were processing carcasses destined for the European markets (among other destinations) into eleven “cuts” or piles (Johnson *et al.*, 2002). These were the neck fillet, flaps, frenched rack, boneless leg, boneless shoulder, fillet, strip loin muscle trim, fat trim, leg bone and other bone (Johnson *et al.*, 2002). Payment is made to the processor on the individual cuts, but currently the processor pays the farmer on carcass weight and GR measurements (refer section 2.5.2).

## ***2.5 Payment Methods for New Zealand Lamb***

### ***2.5.1 Past payment method***

Prior to the 1980's payment for lamb carcasses within New Zealand was based on carcass weight alone. This would have meant that farmer's main objectives would have been to produce the heaviest possible lambs irrespective of their fatness or the distribution of cut weights within the carcass. The main reason this method was used was because fat levels in lambs were not considered important. However, feed back from the United Kingdom, the main export destination at the time, suggested that New Zealand lamb was too fat (pers. comm. Patricia Johnson). This encouraged research into the area of fatness in lambs and the concept of using GR, "total tissue thickness between the surface of a lamb carcass and the rib at the point 11cm from the midline in the region of the 12<sup>th</sup> rib" (Kirton, 1989), as a measurement of carcass fatness.

### ***2.5.2 Current payment method***

From 1983 a new export lamb carcass grading system was used to grade carcasses; this system was based on the weight and GR of the carcass (Kirton *et al.*, 1985). With this grading system it <sup>was</sup> optimal for farmers to produce heavy lean lambs as apposed to heavy fat lambs, which would have been acceptable prior to 1983. The price paid to farmers per kilogram of carcass weight changes between years as can be seen in Figure 2.3. The per-kilogram price is determined every month by the processing plant and is dependent on many factors including market demands and processing costs (Bray, 1984).

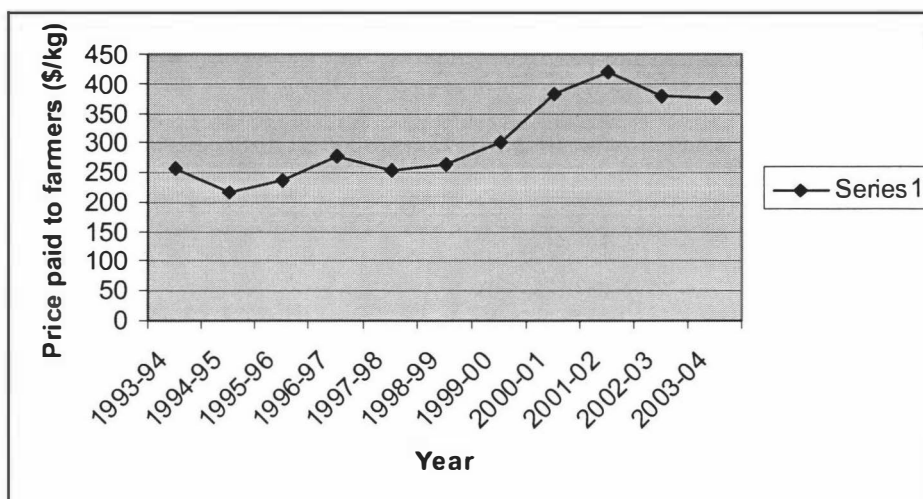


Figure 2.3: Prices paid to the farmer per kilogram of carcass weight over the past ten years

There is an averaging effect seen through the use of this payment option. Within a carcass grade, such as PM where GR ranges from 7mm up to and including 12mm and carcass weights range from 13 to 16kg, there will be thousands of carcasses within these limits. Of these carcasses the ones that are at the upper end of the scale will produce more money for the processor than the ones at the lower end. However, farmers will not be rewarded for generating more profitable lambs as they will be paid on the average of all the lambs within the grade. On the other hand farmers producing animals at the lower end of the grade will be paid more than the carcass is worth. So in essence the farmers producing the better lambs are compensating for the farmers producing the smaller lambs.

The proportion of the variation seen in the composition (total muscle, fat, and bone) of lamb carcasses that is accounted for by GR and HCW (hot carcass weight) is low, with values of over 50% to 70% for fat and bone, and 26% to 47% for muscle (Kirton *et al.*, 1985). For this reason more accurate methods of predicting carcass composition are required to ensure that farmers are accurately rewarded for the lambs they produce, to encourage the production of lambs that meet the requirements of overseas markets.

### 2.5.3 Future payment methods

It has been suggested that lamb payment options are to be changed in the future. Two likely scenarios are the use of image scanning to determine carcass composition and payment on the weight of individual cuts.

### **2.5.3.1 Payment based on the weight of individual cuts**

With this payment method farmers are paid on the weights of the individual cuts as opposed to the carcass weight and GR measurements. Each cut will be priced differentially with some cuts, such as the frenched rack, having a higher value than other cuts. The value of the cuts will reflect the market values and will therefore change accordingly. This approach will allow the processor to send market signals to the farmer so they can produce lambs that fit the specifications required. If higher prices are paid for certain cuts then farmers will strive to produce animals that have increased weights in those cuts, which will result in the farmer receiving more income, and processors obtaining carcasses that are more desirable. Progressive Meats Ltd is currently updating their processing plant to enable farmers to be paid on the weights of individual cuts (pers. comm. Craig Hickson).

### **2.5.3.2 Payment based on image scanning methods**

Image scanning is used to determine the muscle, fat and bone content of the carcass. Two methods of image scanning have been developed, the use of DXA/DEXA (dual-energy x-ray absorptiometry) and VIAscan<sup>®</sup>.

The principle behind the DXA scanning system is that measurements of fat and lean are determined by the greater attenuation of X-rays by lean (water and protein) than by fat (Mitchell *et al.*, 1997). These measurements are taken at different sites of the carcass that do not overlie bone (as the X-ray is greatly attenuated by bone) (Clarke *et al.*, 1999; Mitchell *et al.*, 1997).

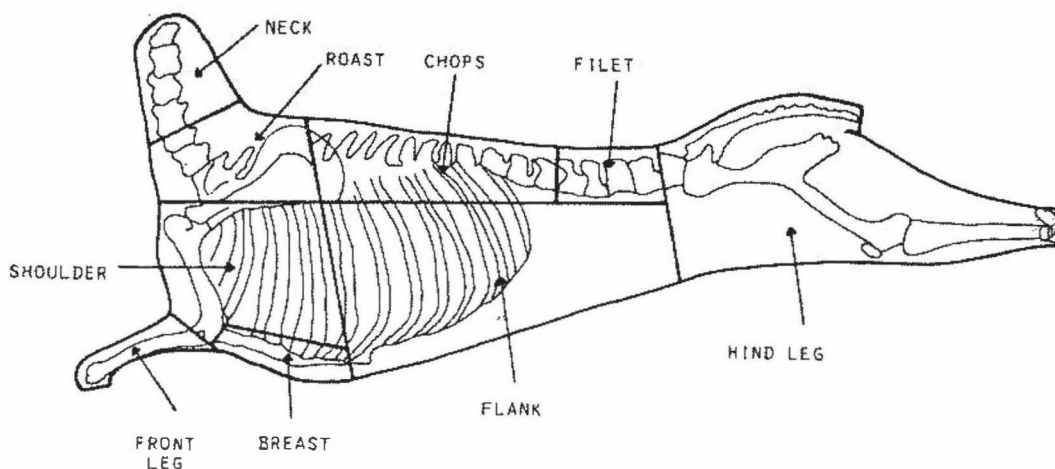
The VIAscan<sup>®</sup> system uses a colour video camera, and a computer that analyses the images obtained from the camera (Ross, 2005). A photograph of the carcass is taken as it passes the camera on the chain, from this photograph the computer derives the expected yield (of lean meat) from the colour and shape of the carcass (Chalmers, 2003). This system gives objective measurements on the final cut conformation, and boned out meat yield, in addition to measuring carcass weight and GR (Anon, 2003). The VIAscan<sup>®</sup> has an accuracy of 94-96% for predicting expected yield from the photograph (Chalmers, 2003). The VIAscan<sup>®</sup> system is currently being implemented into Alliance meat company processing plants (Chalmers, 2003).

The basis of both the image scanning and the weight of cuts payment method is for farmers to produce carcasses with improved cut distribution that contain a large amount of muscle and little fat. This requirement for leaner carcasses has come from a change in consumer perceptions whereby leaner cuts are more acceptable than fatter cuts (Johnson *et al.*, 2002).

## 2.6 *Anatomy of the sheep and carcass cuts*

The anatomy of the sheep carcass is important with respect to the muscles that are increased through the use of muscle QTL/genes. The muscles of the shoulder include the *pectoralis*, the *latissimus dorsi*, *triceps brachii*, and the *trapezius* (Swatland, 2005). All of these muscles will be part of the shoulder cut when the carcass is processed. The main muscles in the loin region consist of the *longissimus dorsi*, which is also known as the *longissimus thoracis and lumborum*, the *psoas major* and the *gluteus medius* (McCracken, Kainer, and Spurgeon, 1999; Swatland, 2005). The *longissimus dorsi* is the main muscle in the frenched rack and strip loin cuts, and it is cut approximately in half to generate the two cuts. The *psoas major* is the main muscle in the fillet and is processed as pure muscle. The leg of the lamb contains many muscles some of which are the *biceps femoris*, *semitendinosus*, *semimembranosus* and the *gluteus medius* (McCracken, Kainer, and Spurgeon, 1999; Swatland, 2005).

The carcass of the sheep is cut into three main sections. These sections will be processed into “cuts” depending on the market that is being targeted. A general overview of the sections can be seen in Figure 2.4. Details of carcass cuts can be found in (Anon, 2001). The leg of the lamb, when it is chump on, can be processed as the boneless leg, the long leg, which consists of the part boned long leg, femur bone leg, and hind shank. When the lamb is processed so the chump is part of the middle section of lamb then the leg is processed into the part boned short leg, when this occurs the chump is processed into the chump and boneless chump.



**Figure 2.4: The divisions of the lamb carcass that would be generated when the lambs are processed (Lirette *et al.*, 1984).**

The middle section of the carcass, chops, flanks, and fillet in Figure 2.4, is processed in many ways depending on the market that the lamb is destined for. One way the middle of the carcass is marketed is the saddle, processed into reformed saddle cutlets. The saddle can also be processed as the chump on long loin, or the long loin chump off. Additionally, the 1 rib short loin, 7 rib rack, and boneless chump can be generated from the saddle. One of the most common ways to process the saddle is to generate the boneless loin, tenderloin (fillet), frenched rack cap on, or frenched rack cap off from the saddle. The flaps are always a separate cut generated from the middle section of the carcass.

The forequarters of the carcass are processed into either the shank, square cut shoulder and neck slices, the boneless shoulder, the 5 rib fore or the oyster shoulder. The processing of one cut will affect other cuts for example if the leg is processed into the boneless leg then the chump on long loin cannot be generated. Similarly, within a section of the carcass certain cuts have to be processed together because if the 5 rib fore is processed then neck slices cannot be produced. More detail on carcass cuts and the way the carcass is processed can be seen in (Anon, 2001).

A common method of cutting carcasses is into eleven “cuts”, which include the boneless leg, boneless shoulder, frenched rack, strip loin, fillet, flaps, neck fillet, muscle trim, fat

trim, leg bone and other bone. All of these cuts vary as to their muscle, fat and bone content, which can be seen in Table 2.3.

**Table 2.3: Composition of the cuts generated by Richmonds Ltd and used in this study**

Cut	Muscle	Bone	S. Fat <sup>1</sup>	I. Fat <sup>1</sup>
Boneless leg	✓	×	✓	✓
Boneless shoulder	✓	×	×	✓
Frenched rack	✓	×	×	×
Strip loin	✓	×	×	×
Fillet	✓	×	×	×
Flaps	✓	✓	✓	✓
Neck Fillet	✓	×	✓	✓
Muscle Trim	✓	×	✓	✓
Fat Trim	✓	×	✓	✓
Leg Bone <sup>2</sup>	✓	✓	×	×
Other Bone <sup>2</sup>	✓	✓	×	×

<sup>1</sup>subcutaneous fat and intermuscular fat

<sup>2</sup>cutting of the carcass is not perfect and some muscle will be left on the bones

## ***2.7 Development of Computer Models***

Simulation models are used to mimic a real situation as closely as possible, and allow changes to be made to the situation without having to perform the experiment. (Spedding, 1998) (cited in (Dooley, 2002)) defines models as “representations of the real thing, simplified for some purpose: they include those features that are essential for the purpose and leave out those that are inessential”. Models can be used in situations where the costs of performing the experiment are too high or the time that would be required to perform the experiment would not be practical. Additionally, if the situation that is being analysed does not exist then models can be used to determine the effect of the situation.

There are many types of models that can be use to simulate a situation and can include; static or dynamic models, or deterministic or stochastic models (Sorenson, 1998). Static models, as the name implies, are constant over time, whereas dynamic models have time as a variable and will therefore change over time (Dooley, 2002). When a stochastic model is being used, variables are represented by probability distribution, while when using a deterministic model the variables are represented by a single value, such as a mean (Dooley, 2002). As the variables in a deterministic model are represented by a single value, the outputs from the model will always be the same. Conversely, using a probability distribution to represent the variables in a stochastic model allows chance to play a part and the outputs will be different. As chance plays a part in a stochastic model, this model would most accurately represent an agricultural system.

## ***2.8 Literature Review Summary***

Since animals were first domesticated, selection has been applied to improve traits, which are important for human needs. Selection methods have evolved and currently sires are selected using estimated breeding values, which are calculated using performance measurements obtained from the animal itself and its close relatives. While progeny testing provides accurate estimates of breeding values, it is expensive to perform and also time consuming, therefore, recent research has focused on finding QTL for performance traits to enable animals to be selected on their genotypes versus their phenotype and the phenotypes of their relatives.

Markers are often used to observe the presence of a QTL if the position of the gene is unknown. If the position of the gene is known, variants of the gene (alleles) will be selected for. Care must be taken when using markers to select for genes, to ensure that the marker information is correct, as genetic loss can occur when markers selected for are not associated with the QTL of interest.

Three QTL/genes of interest to this study are the LoinMAX™ QTL, the Callipyge gene, and the myostatin gene. The presence of the aforementioned QTL/genes in a sheep genome results in an increase in the muscle content of the sheep carcass. The Callipyge gene results in an increase in the muscles of the hind quarter of the animal. Animals carrying the LoinMAX™ QTL exhibit increases in the weight of the eye muscle. The effects of the myostatin gene are more general and result in an increase in the weight of all the muscles in the carcass. The Callipyge and myostatin genes also result in a decrease in the fat content of the carcass.

Farming in New Zealand is an important part of the economy, as it accounts for 17% of the gross domestic profit for the country. The number of sheep in New Zealand has decreased in the past decade but the production has increased through the use of better management practices, including better feeding, pregnancy testing, hogget mating, and non-traditional sheep breeds. In New Zealand lambs are either bred on-farm, or brought onto the farm, and grown through to slaughter. Farmers are currently paid on the basis of carcass weight and fat depth (GR). However, GR is not a good indicator of total

saleable yield; therefore, a more accurate way of rewarding farmers for more desirable carcasses is required. Future payment methods include image scanning to determine carcass composition and paying farmers on individual cuts as they are processed.

Models are used to simulate real-life situations when they cannot be subject to direct experimentation, due to cost, time to implement, or maybe the situation being examined does not exist. Models can be static or dynamic, or deterministic or stochastic. A stochastic model most accurately mimics an agricultural system as change can play a part in the results obtained from the model.

There is a gap in knowledge with respect to the production and financial benefits of introducing QTL/genes, specifically muscle QTL/genes, into sheep production systems. This thesis seeks to address these deficiencies using stochastic modelling.

### 3 *Materials and Methods*

#### 3.1 *Commercial Sector*

The model for the commercial sector was developed to follow the growth of a mob of lambs from weaning through to slaughter (Figure 3.1). One thousand lambs were generated and a ram to ewe lamb ratio of 50:50 was assumed. No wether lambs were incorporated into the model. The weaning weights of the lambs were generated using the random number generated add-in option in Excel using data obtained from Garrick *et al.* (1986). Ram lambs were weaned at an average weight of 26.5kg with a standard deviation of 3kg, whereas ewe lambs were weaned at an average weight of 23.6kg with a standard deviation of 3kg. These values were derived from an average lamb weaning weight of 25kg ( $\pm 3$ kg) with sex effects of +1.5kg for ram lambs and -1.5kg for ewe lambs.

The weaning date was set at December the 1<sup>st</sup> and lambs were weighed every two weeks after weaning. The growth rates for the period between weaning and the first draft (12<sup>th</sup> January) were generated using the random number generator in Excel. The growth rates between weaning and the first draft averaged 293g/day and 224g/day for rams and ewes respectively, based on the work of (Wylie *et al.*, 1997), a standard deviation of 20g/day was applied to these growth rates (Garrick *et al.*, 1986). The growth rates for the following periods between drafting were generated using the growth rate for each animal for the previous period and adding a randomly generated number between 20 and -20g/day. The number between 20 and -20g/day gives variation in the growth rates between kills but keeps some consistency between the growth rates for an individual lamb.

At each draft lambs were weighed and ram lambs that were greater than 40kg and ewes that were greater than 35kg at drafting were slaughtered, condition (fat) level was not used as a drafting criterion. When a lamb reached the slaughter criteria the Excel cell for that lamb at the next draft will have a zero for live weight so that animals do not continue to “grow” past slaughter. To ensure that a reasonable number of lambs are slaughtered at each draft, the first slaughter date was 12<sup>th</sup> January and the final slaughter

date was 23<sup>rd</sup> February. To ensure that all lambs are slaughtered by the 23<sup>rd</sup> of February, on this date all remaining lambs were sent to slaughter regardless of their weight.

To generate different populations, the weaning weights and growth rates in the commercial model were recalculated every time the model was run.

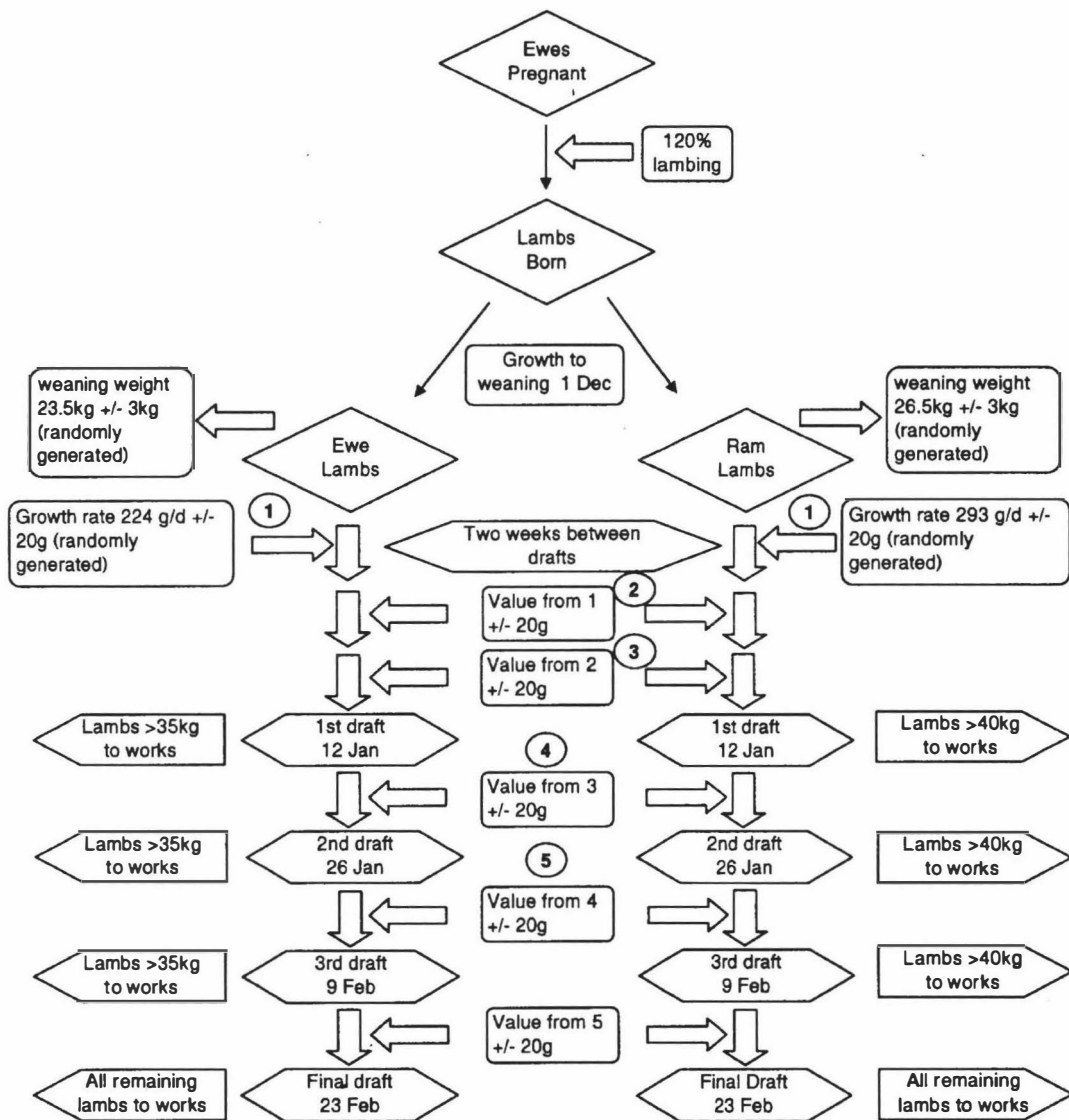


Figure 3.1: Flow diagram of the commercial sector that shows the progression of the lambs from weaning until they are sent to the processor

### 3.2 Processor

At each slaughter date, when a lamb reaches the liveweight selection criteria (40kg, rams and 35kg, ewes) the liveweight of the lamb is transferred to a new Excel workbook. Each drafting date has a separate Excel workbook where the live weights of the lambs that have been killed on that date are listed. The liveweights of the lambs are converted to carcass weights allowing for rams and ewes to have different dressing out percentages. The difference between dressing out percentages of ram and ewe lambs is due to differences in carcass composition between the sexes (Zgur *et al.*, 2003). The formula used to generate carcass weights for ram lambs was (Garrick *et al.*, 1986):

$$\text{CWT} = -2.04 + 0.473 \times \text{LWT}$$

The formula used to generate carcass weights for ewe lambs was:

$$\text{CWT} = -1.80 + 0.473 \times \text{LWT}$$

The value of 0.473 (47.3%) used to generate carcass weight is relatively high compared to New Zealand averages which have been estimated to be 40.5% and 41.3% for 30kg ewe and ram lambs respectively (Kirton *et al.*, 1984). The higher value used by Garrick *et al.* (1986) could be due to animals in the study being weighted at the processing plant where they would have had reduced gut fill (Dorian Garrick, pers. comm). After carcass weights were calculated a residual standard deviation of  $\pm 0.67$  kg (Garrick *et al.*, 1986) was added to the carcass weight so that two animals of the same liveweight did not have the same carcass weight.

Currently farmers are paid for their lambs on the basis of carcass weight and fat depth over the 12<sup>th</sup> rib. All carcasses were assumed to be P grade for carcass fat, which stipulates a medium fat cover, which is a fat depth of between 6mm and 12mm over the 12<sup>th</sup> rib (Anon, 1995). The prices used to generate the values paid to the farmer under the current payment scheme were taken from a February 2003 Richmond schedule. The table of prices used are shown in Table 3.1.

**Table 3.1: Lamb and Mutton Prices for P Grade Carcasses: Commencing 02/02/03 Richmonds Schedule No. 19**

Carcass Grade (Kg)	Price c/kg
PL1 9.1/12.0	357
PL2 12.1/13.2	364
PM1 13.3/14.8	377
PM2 14.9/17.0	377
PX1 17.1/19.0	377
PX2 19.1/22.0	377
PH1 22.1/25.0	304
PH2 25.1/over	287

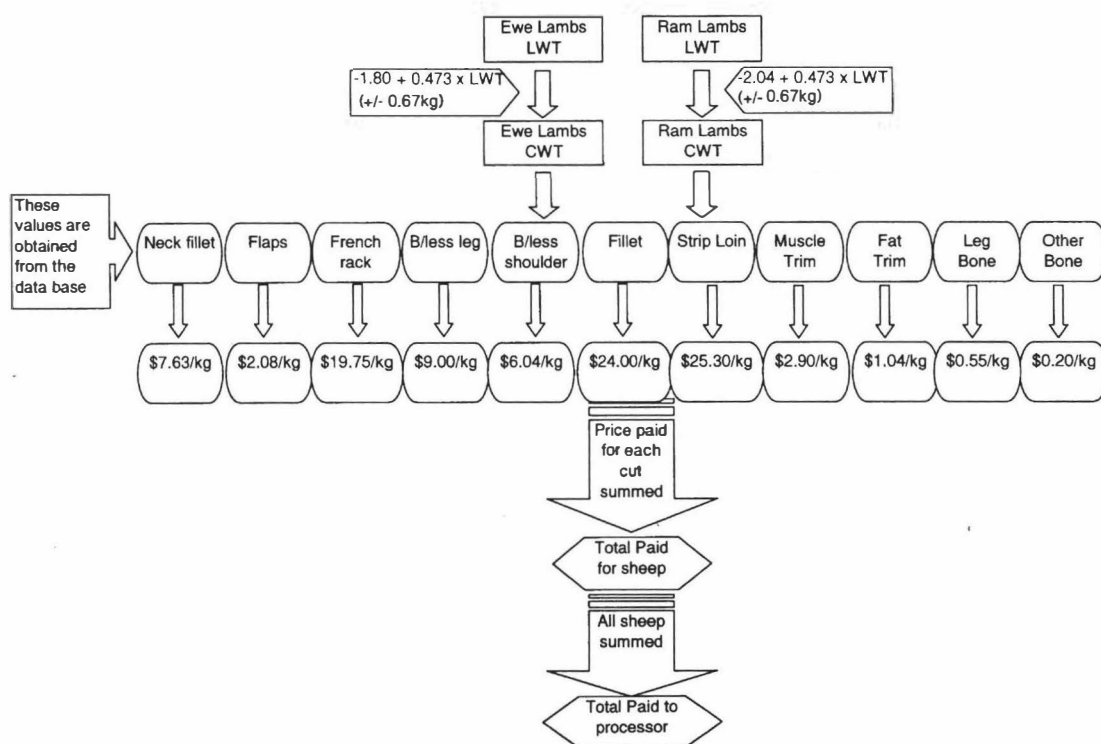
Carcasses were processed in the model from whole carcasses into individual cuts. The cuts used were based on those used by Johnson *et al.* (2002) and included, neck fillet, flap, frenched rack, boneless leg, boneless shoulder, fillet, strip loin, muscle trim, fat trim, leg bone, and all other bone. The cut weights for each animal are obtained from a database (refer to section 1.1) and are dependent on the carcass weight of the animal. The carcass weight of the animal is matched with a carcass weight in the database and the cuts from the database for that carcass weight are used in the model. This step is performed by a Vlookup function in Excel.

The per kilogram values of the cuts to the processor were obtained from a Richmonds processing plant and are shown in Table 3.2, the value given by Johnson *et al.* (2002) for carcass weight is lower than the national average and was only used to work out the relative size of each cut. To create the income generated for the processor, the cut weights for each lamb are multiplied by the value for the cut (Table 3.2) and then summed to give a per lamb value (Figure 3.2). The model was run five times to ensure that consistent values were being obtained each time the model was run (base model). The consistency of the model was evaluated by visually comparing the outputs from each run of the model. For the different QTL scenarios (refer to Sections 3.4.1 to 3.4.4) the model was run once, because the outputs from the base model were consistent, for each scenario and the results from the model for each scenario were compared to the average of the five runs for the base model.

**Table 3.2: Description of carcass parts used in the model, values of the cuts(\$/kg), and raw means and standard deviations(kg)(Johnson *et al.*, 2002)**

Carcass Part	Description	Value (\$/kg)	Mean $\pm$ sd (kg)
Carcass Weight (CW)	Hot carcass weight taken on slaughter floor		14.94 $\pm$ 1.90
Neck Fillet (NF)	Both sides weighed together	7.63 <sup>1</sup>	0.28 $\pm$ 0.05
Flap (F)	Weight of flap from rack and loins bone in	2.08 <sup>1</sup>	1.66 $\pm$ 0.28
Frenched rack (FR)	Weight of 8-rib frenched rack	19.75 <sup>1</sup>	0.79 $\pm$ 0.12
Boneless leg (BL)	Weight of boneless chump-on legs	9.00 <sup>1</sup>	3.21 $\pm$ 0.40
Boneless Shoulder (BS)	Weight of boneless five-rib shoulder	6.04 <sup>1</sup>	2.17 $\pm$ 0.30
Fillet (F)	Weight of boneless fat-free fillet (tenderloins)	24.00 <sup>1</sup>	0.09 $\pm$ 0.02
Striploins (ST)	Weight of boneless fat-free loin-eye striploins	25.30 <sup>1</sup>	0.34 $\pm$ 0.06
Muscle Trim (MT)	Weight of muscle trim (>65% chemical lean)	2.90 <sup>1</sup>	0.79 $\pm$ 0.23
Fat trim (FT)	Weight of fat trim (15-20% chemical lean)	1.04 <sup>1</sup>	1.10 $\pm$ 0.34
Leg Bone (LB)	Weight of hind leg bone (femur, tibia and patella)	0.55 <sup>1</sup>	0.97 $\pm$ 0.12
Other Bone (BN)	Weight of all other bone from both sides	0.20 <sup>1</sup>	3.56 $\pm$ 0.51

<sup>1</sup>Personal communication Richmonds Ltd



**Figure 3.2: Flow diagram showing the income generated for the processor when the lambs are sent to slaughter.**

### 3.3 Database Generation

Databases were required for the cut data for both ram and ewe lambs as they have different average carcass weights and will therefore have a different range of cut sizes (Figure 3.3 & Figure 3.4). Ten thousand carcass weights were randomly generated for both ewe and ram lambs. The carcasses were randomly generated using an average carcass weight of 15.26kg and a standard deviation of 0.82kg for the ewes and an average weight of 17.83kg and a standard deviation of 0.86 for the rams. The standard deviations were generated by running the commercial model ten times, creating carcass weights from liveweight multiplied by the dressing out percentage, and finding the average carcass weights and standard deviations for ewe and ram lambs.

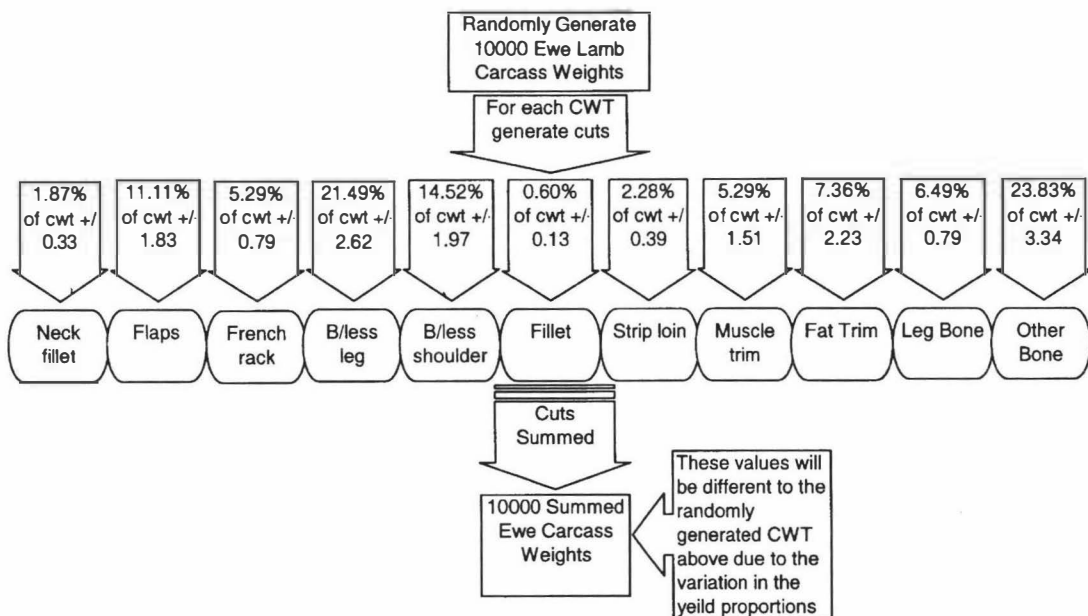
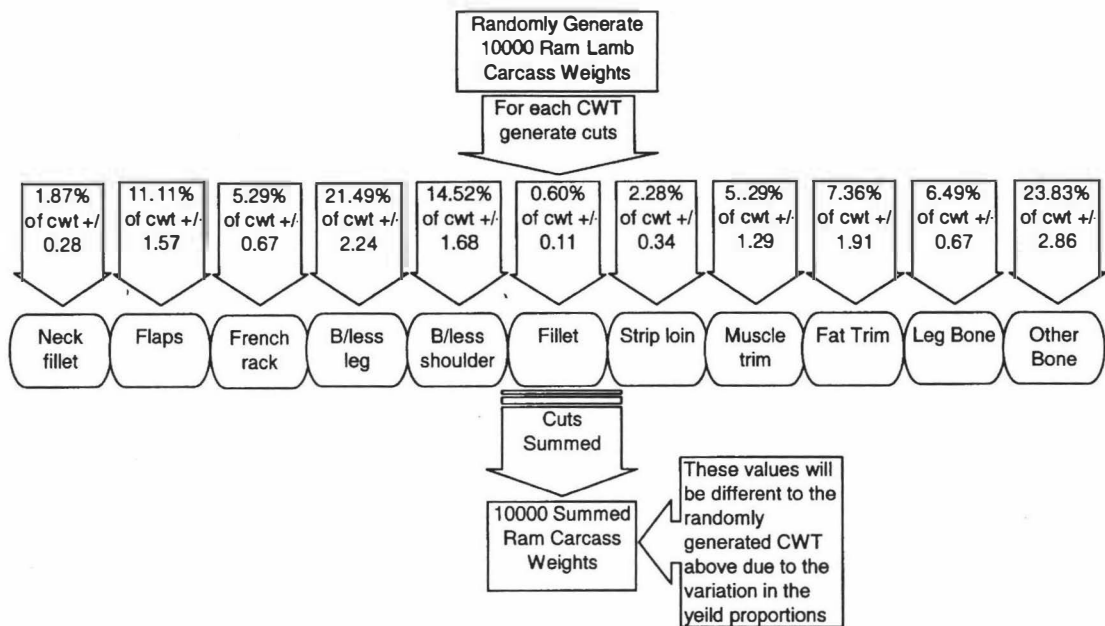


Figure 3.3: Flow diagram showing the development of the carcass weight and cut database for ewe lambs



**Figure 3.4:** Flow diagram showing the development of the carcass weight and cut database for ram lambs

The average yield proportion for each cut was generated by dividing the average weight of the cut (Romney) by the average carcass weight (Romney) and multiplying this by 100 to give a percentage (column three, Table 3.3). Standard deviations were generated in a similar way however, the Romney standard deviation was divided by the average carcass weight of the rams and ewes (generated by running the model five times), as opposed to the overall average, to generate different values for ewe and ram lambs (columns four and five, Table 3.3). Ten thousand values were randomly generated for each cut using the averages and standard deviations in Table 3.3.

**Table 3.3:** Generation of yield proportions using cuts weights and standard deviations from a Romney population

	Weight <sup>1</sup> (kg)	Romney Standard dev <sup>1</sup>	% of CWT	Lambs for the model Ewes %Standard dev	Rams %Standard dev
Carcass Weight (CWT)	14.94				
Neck Fillet (NF)	0.28	0.05	1.87	0.33	0.28
Flap (F)	1.66	0.28	11.11	1.83	1.57
Frenched Rack (FR)	0.79	0.12	5.29	0.79	0.67
Boneless Leg (BL)	3.21	0.40	21.49	2.62	2.24
Boneless Shoulder (BS)	2.17	0.30	14.52	1.97	1.68
Fillet (F)	0.09	0.02	0.60	0.13	0.11
Striploins (ST)	0.34	0.06	2.28	0.39	0.34
Muscle Trim (MT)	0.79	0.23	5.29	1.51	1.29
Fat trim (FT)	1.10	0.34	7.36	2.23	1.91
Leg Bone (LB)	0.97	0.12	6.49	0.79	0.67
Other Bone (BN)	3.56	0.51	23.83	3.34	2.86

<sup>1</sup> values from Johnson *et al.* (2002)

To generate the cut weight for a given carcass weight, the yield proportion (generated randomly) is multiplied by the carcass weight and divided by 100, see Table 3.4 for three examples. This generates a weight for the cut relative to the carcass weight. This is performed for all the cuts and then the cut weights are summed to give a new carcass weight. In Table 3.4 three 17.0kg carcasses are used to show how the application of standard deviations of the yield proportions results in different cut weights for the same carcass size. Values in columns B7 to L7 have been randomly generated. Column M contains the total of the percentages and shows that they do not add to 100, and can be higher and lower than 100, due to the standard deviations.

**Table 3.4: Worked example of generating cut weights for a 17kg carcass.**

CWT (kg)	NF	F	FR	BL	BS	F	ST	MT	FT	LB	BN	Total
A	B(%)	C(%)	D(%)	E(%)	F(%)	G(%)	H(%)	I(%)	J(%)	K(%)	L(%)	M(%)
17.0	1.79	12.08	5.74	22.10	17.99	0.72	2.66	5.49	9.82	6.50	22.30	107.19
17.0	1.51	8.74	4.80	20.09	14.85	0.69	2.47	6.15	5.84	5.96	26.36	97.46
17.0	1.57	10.93	4.28	23.30	11.22	0.46	2.51	3.39	8.35	6.14	23.13	95.27
	NF	F	FR	BL	BS	F	ST	MT	FT	LB	BN	CWT (kg)
	B*A	C*A	D*A	E*A	F*A	G*A	H*A	I*A	J*A	K*A	L*A	Sum(NF-BN)
	0.30	2.05	0.98	3.76	3.06	0.12	0.45	0.93	1.67	1.11	3.79	18.22255
	0.26	1.48	0.82	3.42	2.53	0.12	0.42	1.04	0.99	1.01	4.48	16.56754
	0.27	1.86	0.73	3.96	1.91	0.08	0.43	0.58	1.42	1.04	3.93	16.19569

The standard deviations used to generate the 10,000 carcasses were smaller than a random selection for a population because they were generated for the population of lambs after they had been killed at a specific liveweight, so all the carcasses were of a similar size for the rams and the ewes. This does not have any affect on the model as the database was only used to generate a distribution of cuts for a given carcass weight. Generating 10,000 carcasses, even with the small standard deviation, gave enough variation within the carcasses so that it was unlikely that the carcass weight cuts information would be reused, while identifying cut weights for 500 carcass weights per database (rams and ewes) per run. Additionally, as the carcass weights were generated to five decimal places the reuse of the same cut information for a carcass weight was unlikely.

There were differences seen in the standard deviations for the cuts for rams and ewes (Table 3.3). This occurred because the average ewe carcass weight was smaller than the average ram carcass. This generated larger cut standard deviations for the ewes because the Romney standard deviation was divided by a smaller number (giving a larger

number) than the rams. This would result in there being more variation among the cuts for the ewes than the rams. However this is unlikely to affect the results because the difference in the standard deviations between the rams and ewes was small.

### 3.4 Scenarios to be examined

Three muscle QTL or genes are currently known in sheep, these include the Loin Max™ QTL, the Callipyge gene, and the Myostatin gene. The genes are known for Callipyge and Myostatin whereas the causative gene is as yet unknown for the effect of the Loin Max™ QTL. A fourth QTL scenario is based on a dressing out percentage QTL in which the dressing out percentage of the lamb is increased in the presence of the QTL.

It is assumed for this study that the causative genes can be tested for and that all animals in the flock will inherit the gene in the predictive fashion. The linkage phase does not need to be determined under these circumstances. If a marker was used to test for the gene then the linkage phase would have to be determined to ensure that the marker is linked to the desired form of the QTL. Additionally, if markers were used then the effect of recombination would also have to be accounted for as recombination would break up the linkage phase. As the model only represents the first generation of the implementation of the QTL/gene there is no need to discriminate between whether the gene is dominant or has an additive gene action as only one copy of the gene will be present in the lambs and all will show the desired phenotype.

The effects of the Loin Max™ QTL, the myostatin gene and the Callipyge gene are limited to specific muscles. The Loin Max™ QTL, for example, increases the longissimus dorsi muscle which will affect the frenched rack and the strip loin cuts. However the percentage increase that is seen in the muscle will not be directly seen in the frenched rack cut as it contains muscle, fat, and bone. Therefore, a 5% increase in the muscle weight will result in a smaller increase in the whole cut. Increases in cut weight have been reported with the myostatin gene resulting in an increase in the hind limb and shoulder (Laville *et al.*, 2004; Marcq *et al.*, 2002). Additionally, increases in cut size have been documented in Callipyge and LoinMAX™ lambs. It was assumed for this model that the 5% increase in the muscle would result in a 5% increase in the entire cut. This assumption is made for all the muscle QTL/genes, even though the myostatin and Callipyge genes decrease fat and bone, as well as increasing muscle.

This will result in larger dollar gains in the model than would be seen if the QTL/gene was implemented into a flock.

### 3.4.1 Loin Max™ QTL

The first four Scenarios run through the model were based on the effect of the Loin Max™ QTL. The cuts modified in this scenario were the Frenched rack and the Strip Loin as the Loin Max™ QTL has been described as affecting the *Longissimus Dorsi* muscle. The first scenario involves a 5% increase in the relative size of the frenched rack and strip loin and an associated decrease in the relative size of the neck fillet, flap, boneless leg, boneless shoulder, fillet, and muscle trim. Fat trim and the bone measurements were not modified as the Loin Max™ QTL is shown to not have an effect on these carcass parts. Similarly the second, third, and four scenarios are also based on the Loin Max™ QTL but involve a 10, 15 and 20% increase in the relative size of the frenched rack and strip loin. There will also be an associated decrease in the neck fillet, flap, boneless leg, boneless shoulder, fillet, and muscle trim. The decrease in the relative size of these cuts will be directly related to the size of the increase in the frenched rack and strip loin. These values can be seen below in Table 3.5 the full tables for working out the yield proportions for scenario one to four can be seen in Appendix One.

**Table 3.5: Yield proportions for the base model, Loin Max™ 5%, Loin Max™ 10%, Loin Max™ 15%, and Loin Max™ 20%. There is a 5%, 10%, 15%, and 20%, increase in the frenched rack and strip loin for Scenario One to Four respectively.**

	Base Model	Loin Max™			
		5%	10%	15%	20%
Neck fillet	1.87	1.86	1.84	1.83	1.82
Flap	11.11	11.03	10.96	10.80	10.80
Frenched rack	5.29	5.55	5.82	6.08	6.35
Boneless leg	21.49	21.34	21.19	21.05	20.90
Boneless shoulder	14.52	14.42	14.32	14.22	14.12
Fillets	0.60	0.60	0.59	0.59	0.58
StripLoins	2.28	2.39	2.51	2.62	2.74
Muscle Trim	5.29	5.25	5.22	5.18	5.14
Fat Trim	7.36	7.36	7.36	7.36	7.36
Leg bone	6.49	6.49	6.49	6.49	6.49
Other bone	23.83	23.83	23.83	23.83	23.83

### 3.4.2 *Callipyge Gene*

Scenario five to eight were based on the Callipyge gene. As the Callipyge gene affects the semitendinosus, semimembranosus, the gluteus medius (leg muscles), and the longissimus dorsi (loin muscle) muscles of the lamb, there was an increase of 15%, 20%, 25% and 30% in the relative size of the boneless leg, frenched rack, strip loin, and fillet for scenario five to eight respectively. As the proportion of fat and bone is decreased in Callipyge lambs there were associated decreases in the neck fillet, flap, boneless shoulder, muscle trim, fat trim, leg bone, and other bone proportions. The yield proportions for all cuts for scenario five to eight can be seen in Table 3.6. In-depth tables with all the information showing how the yield proportions were generated for each scenario can be seen in Appendix One.

**Table 3.6: Yield proportions for the base model, Callipyge 15%, Callipyge 20%, Callipyge 25%, and Callipyge 30%. There is a 15%, 20%, 25%, and 30% increase in the boneless leg, frenched rack, strip loin, and fillet for Scenario Five to Eight respectively.**

	Base Model	Callipyge			
		15%	20%	25%	30%
Neck Fillet	1.87	1.75	1.71	1.67	1.63
Flap	11.11	10.41	10.17	9.94	9.71
Frenched rack	5.29	6.08	6.35	6.61	6.88
Boneless leg	21.49	24.71	25.79	26.86	27.94
Boneless shoulder	14.52	13.60	13.30	12.99	12.69
Fillets	0.6	0.69	0.72	0.75	0.78
StripLoins	2.28	2.62	2.74	2.85	2.96
Muscle Trim	5.29	4.96	4.84	4.73	4.62
Fat trim	7.36	6.90	6.74	6.59	6.43
Leg bone	6.49	6.08	5.94	5.81	5.67
Other bone	23.83	22.33	21.82	21.32	20.82

### 3.4.3 *Myostatin Gene*

Scenarios Nine to Twelve were based on the myostatin gene. The myostatin gene results in an increase in all muscle-containing cuts and a decrease in fat trim, leg bone, and the other bone of the carcass. The muscles cuts were increased by 10%, 15%, 20% and 25% for scenario nine to twelve respectively. The decrease in the other cuts was proportional to the size of the increase and the size of the cut to be decreased. The yield proportions for scenario nine to twelve can be seen below in Table 3.7. The full tables used to work out the yield proportions can be seen in Appendix One

**Table 3.7: Yield proportions for the base model, Myostatin 10%, Myostatin 15%, Myostatin 20%, Myostatin 25%. There is a 10%, 15%, 20%, and 25%, increase in the frenched rack and strip loin.**

	Base Model	Myostatin			
		10%	15%	20%	25%
Neck Fillet	1.87	2.06	2.15	2.24	2.34
Flap	11.11	12.22	12.78	13.33	13.89
Frenched rack	5.29	5.82	6.08	6.35	6.61
Boneless leg	21.49	23.64	24.71	25.79	26.86
Boneless shoulder	14.52	15.97	16.70	17.42	18.15
Filletts	0.6	0.66	0.69	0.72	0.75
StripLoins	2.28	2.51	2.62	2.74	2.85
Muscle Trim	5.29	5.82	6.08	6.35	6.61
Fat trim	7.36	6.14	5.53	4.92	4.31
Leg bone	6.49	5.41	4.88	4.34	3.80
Other bone	23.83	19.88	17.91	15.93	13.96

#### 3.4.4 Dressing out percentage QTL

Scenarios thirteen to sixteen were based on the effect of a QTL that increased dressing out percentage in lambs, which is an increase in carcass weight for a given liveweight. These scenarios were run because both the Callipyge gene and the myostatin gene increase the dressing out percentage. Scenario thirteen shows the effect of a 5% increase in the dressing out percentage resulting in an increase from 47.3% in the base model to 49.7%. A 10% increase was applied to the dressing out percentage in scenario fourteen raising it to 52.0%. Scenarios fifteen and sixteen had 15% and 20% increases in the dressing out percentage giving values of 54.4% and 56.8% respectively. Cut proportions were not altered and were therefore, the same as the base model.

### ***3.5 Comparison of base model to QTL/GENE effects***

The model was run five times and the average values from the five runs represented the base model. The model was run once for each QTL/gene effect (sixteen runs in total) and the outputs for each QTL/gene effect were compared to the base model. The outputs were grouped in fours, giving four QTL/gene effects with four magnitudes for each effect. The outputs compared to the base model were the per-lamb value to the processor for ram and ewe lambs for each QTL/gene effect. Additionally, the average values of the cuts to the processor for the ewe and ram lambs generated by the QTL/gene effect were compared with the corresponding values generated for the base model.

A sensitivity analysis was performed to show the effect of the processor paying different percentages of their profit to the farmer. Percentages of 65%, 70% and 75% were tested to see how the QTL/gene effects affected the farmer at the different payment levels. Tables were generated showing the base model compared to the different magnitudes within a QTL/gene effect and the different percentages paid to the farmer by the processor.

Comparison of the QTL/gene effects and the base model were performed by finding the absolute value difference between the base model and the effect of interest. The difference in the per-lamb income generated for the processor was evaluated against a figure of \$2.00 per lamb. An industry source suggested \$2.00 per lamb to be the minimum extra value that would be required to make the use of a QTL/gene profitable for both the farmer and the processor. The effect of the QTL/gene on the income to the farmer was evaluated by summing the per-lamb increase in income generated by the QTL/gene. This value was then given as the additional value available for the farmer to spend on rams that carry the gene of interest.

## 4 RESULTS

### 4.1 Base Model

#### 4.1.1 Model Validation

Lambs were drafted on four occasions, with two weeks between each drafting. Ram lambs were drafted for slaughter when they reached a minimum of 40kg liveweight and ewe lambs were drafted when they reached a minimum of 35kg liveweight. The base model was run five times to determine if similar results are obtained each time. Table 4.1 shows the averages for liveweight, carcass weight and processor income, for the five runs.

**Table 4.1: Comparison of the five runs of the base model to validate the model.**

		Draft Date					Average
		1 <sup>st</sup>	2 <sup>nd</sup>	3 <sup>rd</sup>	4 <sup>th</sup>	5 <sup>th</sup>	
Live weight	Rams	42.16	42.23	42.27	42.25	42.27	42.24
	Ewes	36.64	36.64	36.67	36.65	36.74	36.67
Carcass weight	Rams	17.86	17.71	17.85	17.82	17.69	17.79
	Ewes	15.46	15.36	15.40	15.41	15.40	15.41
Processor	Lamb	\$88.09	\$88.00	\$88.00	\$88.03	\$87.94	88.01

#### 4.1.2 Payment to farmers based on carcass weight and GR

The carcasses were all of a similar weight and were all assumed to be P grade for GR, therefore, the value paid per kilogram was the same for all the drafts. The value paid per kilogram was obtained from Richmond price schedule 19 for the week commencing 02/02/2003 and was \$3.77 per kilogram of carcass weight. Similarly, the prices paid to the processor were obtained by personal communication with Richmonds NZ ltd and were wholesale values for January 2003.

Table 4.2 shows the results of the base model when farmers are paid on the current system of carcass weight and GR. The average value per lamb to the farmer and processor decreased in the final draft due to all lambs being slaughtered at that date irrespective of their liveweight. Additionally, there was a higher proportion of ewe lambs in the final draft, which also contributed to the decrease in the average value.

The overall value paid to the farmer and processor per lamb was \$62.56 and \$88.01 respectively.

**Table 4.2: Base model: comparison of the income generated for farmers when paid on carcass weight and the income generated for processors paid on cut size.**

		Draft Date				
		12 Jan	26 Jan	9 Feb	23 Feb	Overall
No. Slaughtered		295	423	226	56	<b>1000</b>
Live weight	Rams	42.13	42.17	42.46	42.44	<b>42.24</b>
	Ewes	36.87	36.52	36.76	36.36	<b>36.67</b>
Carcass weight	Rams	17.82	17.93	17.89	16.12	<b>17.79</b>
	Ewes	15.42	15.37	15.52	15.11	<b>15.41</b>
Price \$/kg(cwt)		3.77	3.77	3.77	3.77	<b>3.77</b>
Farmer income	Per Lamb	\$62.65	\$62.76	\$62.98	\$58.87	<b>\$62.56</b>
Processor income	Per Lamb	\$89.37	\$88.43	\$86.51	\$83.63	<b>\$88.01</b>
Margin		\$26.72	\$25.66	\$23.54	\$24.75	<b>\$25.45</b>

Table 4.3 and Table 4.4 show the average value of the individual cuts for the processor at each draft, for ram lambs ewe lambs respectively. The average value received per ram lamb was \$94.31 (Table 4.3) and the average value per ewe lamb was \$81.71 (Table 4.4). Four cuts had a major effect on the carcass value with the boneless legs, frenched racks, boneless shoulders, and the striploins making up 37%, 20%, 17% and 11% of the carcass value respectively for both rams and ewes

**Table 4.3: The average value received by a processor per lamb and for individual cuts for ram lambs. Lambs were drafted at 40 kg liveweight and cut down into individual cuts.**

	Draft Date				Overall
	12 Jan	26 Jan	9 Feb	23 Feb	
<b>No. Slaughtered</b>	177	230	83	10	<b>500</b>
<b>Per Lamb value</b>	\$94.20	\$94.29	\$94.66	\$93.63	<b>\$94.31</b>
<b>Neck Fillets</b>	\$2.52	\$2.54	\$2.58	\$2.53	<b>\$2.54</b>
<b>Flaps</b>	\$4.11	\$4.16	\$4.15	\$4.23	<b>\$4.14</b>
<b>French racks</b>	\$18.80	\$18.67	\$18.75	\$18.59	<b>\$18.73</b>
<b>B/less Legs</b>	\$34.49	\$34.65	\$34.88	\$34.07	<b>\$34.62</b>
<b>B/less Shoulders</b>	\$15.75	\$15.75	\$15.81	\$15.61	<b>\$15.76</b>
<b>Fillets</b>	\$2.56	\$2.57	\$2.51	\$2.44	<b>\$2.55</b>
<b>Strip loins</b>	\$10.40	\$10.30	\$10.30	\$10.53	<b>\$10.33</b>
<b>Muscle trim</b>	\$2.74	\$2.76	\$2.80	\$2.74	<b>\$2.76</b>
<b>Fat trim</b>	\$1.37	\$1.39	\$1.39	\$1.41	<b>\$1.38</b>
<b>Leg bones</b>	\$0.64	\$0.64	\$0.64	\$0.64	<b>\$0.64</b>
<b>Other bones</b>	\$0.85	\$0.85	\$0.86	\$0.86	<b>\$0.85</b>

**Table 4.4: The average value received by a processor per lamb and for individual cuts for ewe lambs. Lambs were drafted at 35 kg liveweight and cut down into individual cuts.**

	Draft Date				Overall
	12 Jan	26 Jan	9 Feb	23 Feb	
<b>No. Slaughtered</b>	118	193	143	46	<b>500</b>
<b>Per Lamb value</b>	\$82.11	\$81.43	\$81.81	\$81.42	<b>\$81.71</b>
<b>Neck Fillets</b>	\$2.20	\$2.20	\$2.23	\$2.17	<b>\$2.21</b>
<b>Flaps</b>	\$3.58	\$3.57	\$3.56	\$3.50	<b>\$3.56</b>
<b>French racks</b>	\$16.33	\$16.22	\$16.29	\$16.21	<b>\$16.27</b>
<b>B/less Legs</b>	\$30.09	\$29.98	\$29.97	\$30.14	<b>\$30.02</b>
<b>B/less Shoulders</b>	\$13.71	\$13.50	\$13.69	\$13.60	<b>\$13.62</b>
<b>Fillets</b>	\$2.25	\$2.23	\$2.24	\$2.18	<b>\$2.23</b>
<b>Strip loins</b>	\$9.05	\$8.87	\$8.95	\$8.89	<b>\$8.94</b>
<b>Muscle trim</b>	\$2.40	\$2.36	\$2.40	\$2.30	<b>\$2.38</b>
<b>Fat trim</b>	\$1.20	\$1.20	\$1.18	\$1.15	<b>\$1.19</b>
<b>Leg bones</b>	\$0.56	\$0.55	\$0.55	\$0.55	<b>\$0.55</b>
<b>Other bones</b>	\$0.75	\$0.74	\$0.75	\$0.73	<b>\$0.74</b>

## 4.2 Loin Max™ QTL

The QTL effects for the Loin Max™ QTL were chosen to be 5%, 10%, 15%, and 20%. These values were chosen because the actual values for the effect of the Loin Max™ QTL have been estimated to be between 8% and 11%. The range from 5% to 20% gives a good coverage of the effects of the gene with values above and below the estimated effects of the actual gene.

### 4.2.1 Loin Max™ QTL with a 5% effect

In the first scenario there was a 5% increase in the frenched rack and strip loin and an associated decrease in the other cuts, excluding fat trim, leg bone and other bone. Table 4.5 shows the average liveweights and carcass weights for rams and ewes at each slaughter group. Ewes were slaughtered at greater than 35kg and rams were slaughtered at greater than 40kg, with drafting occurring at two week intervals. The average per-lamb income generated for the processor was \$88.81. The average per-lamb value for the last slaughter group is lower because of a higher proportion of ewe lambs, which have smaller live weights and therefore bring the average value down.

**Table 4.5: The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 5% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		319	404	214	63	<b>1000</b>
Live weight	Rams	42.11	42.29	42.64	42.60	<b>42.33</b>
	Ewes	36.61	36.58	36.80	36.15	<b>36.61</b>
Carcass weight	Rams	17.79	17.85	18.13	18.24	<b>15.29</b>
	Ewes	15.35	15.34	15.40	14.33	<b>17.92</b>
Processor	Lamb	\$90.05	\$88.88	\$88.71	\$82.41	<b>\$88.81</b>

Table 4.6 shows the average per-lamb value received by the processor in the base model and when there was a 5% increase in the frenched rack and strip loin. This increase resulted in a \$0.87 gain for rams and \$0.72 gain for ewes. The average values for the individual cuts are shown for ram lambs and ewe lambs for both the base model and a 5% increase in the above mentioned cuts.

**Table 4.6: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 5% effect and the difference (D) in per-lamb value and cut values between the two scenarios.**

	Average Value Received (\$)					
	Rams			Ewes		
	Base model	Loin Max™ 5%	D	Base model	Loin Max™ 5%	D
Value per lamb	\$94.31	\$95.18	\$0.87	\$81.71	\$82.43	\$0.72
Neck fillet	\$2.54	\$2.54	\$0.00	\$2.21	\$2.20	-\$0.01
Flap	\$4.14	\$4.13	-\$0.01	\$3.56	\$3.53	-\$0.03
Frenched rack	\$18.73	\$19.61	\$0.88	\$16.27	\$16.93	\$0.66
Boneless leg	\$34.62	\$34.32	-\$0.30	\$30.02	\$29.81	-\$0.21
Boneless shoulder	\$15.76	\$15.61	-\$0.15	\$13.62	\$13.63	\$0.01
Fillet	\$2.55	\$2.57	\$0.02	\$2.23	\$2.23	\$0.00
Strip loin	\$10.33	\$10.80	\$0.47	\$8.94	\$9.31	\$0.37
Muscle trim	\$2.76	\$2.74	-\$0.02	\$2.38	\$2.35	-\$0.03
Fat trim	\$1.38	\$1.38	\$0.00	\$1.19	\$1.15	-\$0.04
Leg bone	\$0.64	\$0.64	\$0.00	\$0.55	\$0.55	\$0.00
Other bone	\$0.85	\$0.85	\$0.00	\$0.74	\$0.74	\$0.00

#### 4.2.2 Loin Max™ QTL with a 10% Effect

In the second scenario there was a 10% increase in the frenched rack and strip loin and an associated decrease in the other cuts, excluding fat trim, leg bone and other bone. Table 4.7 shows the average liveweights and carcass weights for the rams and ewes at the slaughter dates. The per-lamb income generated for the processor was \$89.81.

**Table 4.7: The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 10% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		291	433	209	67	<b>1000</b>
Live weight	Rams	42.03	42.08	42.69	42.83	<b>42.24</b>
	Ewes	36.81	36.65	36.76	35.76	<b>36.66</b>
Carcass weight	Rams	17.87	17.87	18.09	17.08	<b>17.86</b>
	Ewes	15.46	15.50	15.46	14.05	<b>15.39</b>
Processor	Lamb	\$90.91	\$90.91	\$88.76	\$84.73	<b>\$89.81</b>

Table 4.8 shows the average values of the individual cuts to the processor for ewe and ram lambs for the base model and a 10% increase in the frenched rack and striploins. The average per-lamb value of ram lambs and ewe lambs to the processor in the base model and with a 10% increase in the aforementioned cuts are also shown. The 10% increase in these cuts resulted in a \$1.86 gain per ram lamb and a \$1.73 gain per ewe lamb.

**Table 4.8: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 10% effect and the difference (D) in per-lamb value and cut values between the two scenarios.**

	Average Value Received (\$)					
	Base model	Rams		D	Ewes	
		Loin Max™ 10%	D		Loin Max™ 10%	D
Value per lamb	\$94.31	\$96.17	\$1.86	\$81.71	\$83.44	\$1.73
Neck fillet	\$2.54	\$2.48	-\$0.06	\$2.21	\$2.20	-\$0.01
Flap	\$4.14	\$4.05	-\$0.09	\$3.56	\$3.48	-\$0.08
Frenched rack	\$18.73	\$20.45	\$1.72	\$16.27	\$17.77	\$1.50
Boneless leg	\$34.62	\$34.17	-\$0.45	\$30.02	\$29.55	-\$0.47
Boneless shoulder	\$15.76	\$15.57	-\$0.19	\$13.62	\$13.40	-\$0.22
Fillet	\$2.55	\$2.51	-\$0.04	\$2.23	\$2.25	\$0.02
Strip loin	\$10.33	\$11.35	\$1.02	\$8.94	\$9.95	\$1.01
Muscle trim	\$2.76	\$2.74	-\$0.02	\$2.38	\$2.36	-\$0.02
Fat trim	\$1.38	\$1.36	-\$0.02	\$1.19	\$1.18	-\$0.01
Leg bone	\$0.64	\$0.64	\$0.00	\$0.55	\$0.56	\$0.01
Other bone	\$0.85	\$0.86	\$0.01	\$0.74	\$0.74	\$0.00

### 4.2.3 Loin Max™ QTL with a 15% Effect

The third scenario involved a 15% increase in the frenched rack and strip loin and an associated decrease in the other cuts, excluding fat trim, leg bone and other bone. Table 4.9 shows the average ram and ewe liveweights and carcass weights for the four draft dates. Additionally it shows the average value per ram and ewe lamb paid to the processor and farmer at the four slaughter dates and overall. The per-lamb income generated for the processor was \$90.64.

**Table 4.9: The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 15% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		291	419	220	56	<b>1000</b>
Live weight	Rams	41.69	42.22	42.34	41.84	<b>42.07</b>
	Ewes	36.80	36.60	36.83	36.14	<b>36.68</b>
Carcass weight	Rams	17.54	17.92	18.07	16.50	<b>17.74</b>
	Ewes	15.65	15.39	15.51	14.78	<b>15.45</b>
Processor	Lamb	\$91.05	\$91.33	\$90.71	\$86.31	<b>\$90.64</b>

Table 4.10 shows the average value per lamb for ram and ewe lambs and the average values received per cut by the processor. Values for both the base model and a 15% increase in the frenched rack and strip loin are shown in the table. The result of the 15% increase was a \$2.68 gain for ram lambs and a \$2.58 gain for ewe lambs.

**Table 4.10: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 15% effect and the difference (D) in per-lamb value and cut values between the two systems.**

	Average Value Received (\$)					
	Base model	Rams	D	Base model	Ewes	D
		Loin Max™ 15%			Loin Max™ 15%	
Value per lamb	\$94.31	\$96.99	\$2.68	\$81.71	\$84.29	\$2.58
Neck fillet	\$2.54	\$2.50	-\$0.04	\$2.21	\$2.16	-\$0.05
Flap	\$4.14	\$4.01	-\$0.13	\$3.56	\$3.54	-\$0.02
Frenched rack	\$18.73	\$21.62	\$2.89	\$16.27	\$18.51	\$2.24
Boneless leg	\$34.62	\$33.64	-\$0.98	\$30.02	\$29.57	-\$0.45
Boneless shoulder	\$15.76	\$15.28	-\$0.48	\$13.62	\$13.25	-\$0.37
Fillet	\$2.55	\$2.54	-\$0.01	\$2.23	\$2.20	-\$0.03
Strip loin	\$10.33	\$11.86	\$1.53	\$8.94	\$10.30	\$1.36
Muscle trim	\$2.76	\$2.67	-\$0.09	\$2.38	\$2.32	-\$0.06
Fat trim	\$1.38	\$1.37	-\$0.01	\$1.19	\$1.16	-\$0.03
Leg bone	\$0.64	\$0.63	-\$0.01	\$0.55	\$0.55	\$0.00
Other bone	\$0.85	\$0.85	\$0.00	\$0.74	\$0.74	\$0.00

#### 4.2.4 Loin Max™ QTL with a 20% Effect

In the fourth scenario there was a 20% increase in the frenched rack and strip loin and an associated decrease in the other cuts, excluding fat trim, leg bone and other bone. Table 4.11 shows the overall liveweights and carcass weights for the ewes and rams and the average values at each slaughter dates. The per-lamb income generated for the processor was \$91.62.

**Table 4.11 : The number slaughtered, liveweights and carcass weights of rams and ewes, and per lamb value paid to the processor for four draft dates and overall when the Loin Max™ QTL has a 20% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		287	434	216	63	<b>1000</b>
Live weight	Rams	42.02	42.21	42.47	42.22	<b>42.21</b>
	Ewes	36.81	36.49	37.02	36.35	<b>36.69</b>
Carcass weight	Rams	17.89	17.93	17.84	16.29	<b>17.79</b>
	Ewes	15.66	15.31	15.51	14.45	<b>15.40</b>
Processor	Lamb	\$93.41	\$92.05	\$90.26	\$85.13	<b>\$91.62</b>

Table 4.12 shows the value of the individual cuts to the processor and the average per-lamb value. Figures are shown for both the base model and a 20% increase in the frenched rack and striploins, within those categories values are separated into rams and ewes. When the Loin Max™ effect is 20% there is a gain in carcass value of \$4.00 per ram lamb and a gain of \$3.22 per ewe lamb.

**Table 4.12: The average value received by the processor per lamb and for individual cuts in the base model and when the Loin Max™ QTL has a 20% effect and the difference (D) in per-lamb value and cut values between the two scenarios.**

	Average Value Received (\$)					
	Base model	Rams	D	Base model	Ewes	D
		Loin Max™ 15%			Loin Max™ 15%	
Value per lamb	\$94.31	\$98.31	\$4.00	\$81.71	\$84.93	\$3.22
Neck fillet	\$2.54	\$2.47	-\$0.07	\$2.21	\$2.15	-\$0.06
Flap	\$4.14	\$4.00	-\$0.14	\$3.56	\$3.41	-\$0.15
Frenched rack	\$18.73	\$22.42	\$3.69	\$16.27	\$19.38	\$3.11
Boneless leg	\$34.62	\$33.63	-\$0.99	\$30.02	\$29.13	-\$0.89
Boneless shoulder	\$15.76	\$15.44	-\$0.32	\$13.62	\$13.27	-\$0.35
Fillet	\$2.55	\$2.50	-\$0.05	\$2.23	\$2.12	-\$0.11
Strip loin	\$10.33	\$12.33	\$2.00	\$8.94	\$10.65	\$1.71
Muscle trim	\$2.76	\$2.64	-\$0.12	\$2.38	\$2.33	-\$0.05
Fat trim	\$1.38	\$1.37	-\$0.01	\$1.19	\$1.19	\$0.00
Leg bone	\$0.64	\$0.64	\$0.00	\$0.55	\$0.55	\$0.00
Other bone	\$0.85	\$0.85	\$0.00	\$0.74	0.75	\$0.01

### 4.3 Callipyge Gene

The Callipyge gene has variable effects on different muscles in the carcass the most affected muscles are the semitendinosus, semimembranosus, the gluteus medius, biceps femoris (leg muscles), and the longissimus dorsi muscle (loin muscle). Different percentage increases have been reported for different muscle from a 14% increase for the semitendinosus (Carpenter *et al.*, 1996) to 46% for the semimembranosus (Cockett *et al.*, 1999) and an approximately 30% increase in the weight of the longissimus dorsi (Carpenter *et al.*, 1996). Due to the large variation in the increase of the muscles a range of 15% to 30% was used to show the effects of the Callipyge gene on income.

#### 4.3.1 Callipyge gene with a 15% Effect

In the fifth scenario there was a 15% increase in the hind quarter cuts, which included the frenched rack, boneless leg, fillet and strip loin, and an associated decrease in all of the other cuts. Table 4.13 is an overview of the average liveweights and carcass weights for rams and ewes at each drafting date. Drafting dates were two weeks apart and ewes and rams were killed when they reached 35kg and 40kg respectively. Table 4.13 shows the per-lamb income generated for the processors was \$95.70. The average per-lamb value generated for the processor on the 23<sup>rd</sup> of February is smaller than the other draft dates because there was a larger proportion of ewe lambs with smaller liveweights, which brings the average value down.

**Table 4.13: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 15% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		323	417	195	65	1000
Live weight	Rams	42.19	42.24	42.61	42.21	42.29
	Ewes	36.67	36.51	36.63	36.48	36.58
Carcass weight	Rams	17.87	17.85	17.82	17.95	17.86
	Ewes	15.16	15.44	15.25	15.26	15.30
Processor	Lamb	\$96.65	\$96.33	\$94.10	\$91.76	\$95.70

Table 4.14 shows the average per-lamb value received by the processor in the base model and when there was a 15% increase in the frenched rack, boneless leg, fillet, and strip loin. The increase in these cuts generated a \$8.37 gain in the price paid per ram and a \$7.15 gain the price paid per ewe lamb. Table 4.14 also shows the average values

for the individual cuts for both ram and ewe lambs for the base model and a 15% increase in the aforementioned cuts.

**Table 4.14: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 15% effect and the difference (D) between the per-lamb value and cut values between the two scenarios.**

	Average Value Received by the processor(\$)						
	Base model	Rams			Ewes		
		Callipyge 15%	D		Base model	Callipyge 15%	D
Value per lamb	\$94.19	\$102.56	\$8.37	\$81.69	\$88.84	\$7.15	
Neck Fillets	\$2.54	\$2.38	-\$0.16	\$2.20	\$2.07	-\$0.13	
Flap	\$4.16	\$3.87	-\$0.29	\$3.55	\$3.34	-\$0.21	
Frenched rack	\$18.70	\$21.52	\$2.82	\$16.26	\$18.75	\$2.49	
Boneless legs	\$34.52	\$39.83	\$5.31	\$30.05	\$34.56	\$4.51	
Boneless shoulders	\$15.73	\$14.84	-\$0.89	\$13.63	\$12.73	-\$0.90	
Fillets	\$2.52	\$2.96	\$0.44	\$2.23	\$2.56	\$0.33	
Strip loins	\$10.38	\$11.92	\$1.54	\$8.94	\$10.30	\$1.36	
Muscle trim	\$2.76	\$2.56	-\$0.20	\$2.36	\$2.22	-\$0.14	
Fat trim	\$1.39	\$1.28	-\$0.11	\$1.18	\$1.09	-\$0.09	
Leg bone	\$0.64	\$0.59	-\$0.05	\$0.55	\$0.52	-\$0.03	
Other bone	\$0.85	\$0.81	-\$0.04	\$0.74	\$0.69	-\$0.05	

### 4.3.2 Callipyge gene with a 20% Effect

The sixth scenario showed a 20% increase in the frenched rack, boneless leg, fillet, and strip loin cuts and an associated decrease in the other cuts. The average liveweights and carcass weights for the rams and ewes at each slaughter date are shown in Table 4.15.

The per-lamb income generated for the processor was \$98.10.

**Table 4.15: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 20% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		291	454	197	98	1000
Live weight	Rams	42.22	42.35	42.31	42.67	42.32
	Ewes	37.08	36.46	36.70	36.40	36.68
Carcass weight	Rams	17.90	17.93	17.87	16.89	17.85
	Ewes	15.66	15.21	15.42	14.73	15.36
Processor	Lamb	\$100.08	\$98.26	\$96.17	\$93.49	\$98.10

Table 4.16 shows the average values of the individual cuts to the processor for ewes and rams for both the base model and a 20% increase in the frenched rack, boneless leg, fillet, and strip loin cuts. The average value obtained per lamb by the processor in the base model and when the Callipyge gene has a 20% effect is also shown in Table 4.16.

Ram lambs generated an extra \$10.92 when these cuts were increased, and ewe lambs generated an extra \$9.41 for the processor.

**Table 4.16: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 20% effect, and the difference (D) between the per-lamb value and cut values between the two scenarios.**

	Average Value Received by the processor(\$)						
	Base model	Rams			Ewes		
		Callipyge 20%	D		Base model	Callipyge 20%	D
Value per lamb	\$94.19	\$105.11	\$10.92	\$81.69	\$91.10	\$9.41	
Neck Fillets	\$2.54	\$2.34	-\$0.20	\$2.20	\$2.01	-\$0.19	
Flap	\$4.16	\$3.79	-\$0.37	\$3.55	\$3.28	-\$0.27	
Frenched rack	\$18.70	\$22.34	\$3.64	\$16.26	\$19.43	\$3.17	
Boneless legs	\$34.52	\$41.63	\$7.11	\$30.05	\$36.13	\$6.08	
Boneless shoulders	\$15.73	\$14.37	-\$1.36	\$13.63	\$12.35	-\$1.28	
Fillets	\$2.52	\$3.08	\$0.56	\$2.23	\$2.67	\$0.44	
Strip loins	\$10.38	\$12.42	\$2.04	\$8.94	\$10.75	\$1.81	
Muscle trim	\$2.76	\$2.51	-\$0.25	\$2.36	\$2.24	-\$0.12	
Fat trim	\$1.39	\$1.26	-\$0.13	\$1.18	\$1.07	-\$0.11	
Leg bone	\$0.64	\$0.58	-\$0.06	\$0.55	\$0.50	-\$0.05	
Other bone	\$0.85	\$0.78	-\$0.07	\$0.74	\$0.68	-\$0.06	

### 4.3.3 Callipyge gene with a 25% Effect

The seventh scenario involved a 25% increase in the frenched rack, boneless leg, fillet, and strip loin, with a decrease for all the other cuts. Table 4.17 shows the average liveweights and carcass weights for the ram lambs and ewe lambs at the four draft dates. Additionally, Table 4.17 shows the average per-lamb value for rams and ewes paid to the processor at the four slaughter dates and overall. The income generated for the processor per lamb was \$100.60.

**Table 4.17: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 25% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		286	406	244	64	1000
Live weight	Rams	42.04	42.31	42.64	41.70	42.27
	Ewes	36.78	36.57	36.78	35.81	36.63
Carcass weight	Rams	17.74	17.88	18.02	17.45	17.84
	Ewes	15.25	15.48	15.19	14.56	15.29
Processor	Lamb	\$102.39	\$101.16	\$99.54	\$93.15	\$100.60

Table 4.18 shows the average value per lamb for rams and ewes and the average values received for each cut by the processor. Values for both the base model and when the Callipyge gene has a 25% effect are shown. The effect of the Callipyge gene in this

scenario gave an extra \$13.41 and \$11.92 to the processor for ram and ewe lambs respectively.

**Table 4.18: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 25% effect and the difference (D) between in the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Rams			Ewes		
	Base model	Callipyge 25%	D	Base model	Callipyge 25%	D
Value per lamb	\$94.19	\$107.60	\$13.41	\$81.69	\$93.61	\$11.92
Neck Fillets	\$2.54	\$2.27	-\$0.27	\$2.20	\$1.97	-\$0.23
Flap	\$4.16	\$3.71	-\$0.45	\$3.55	\$3.21	-\$0.34
Frenched rack	\$18.70	\$23.39	\$4.69	\$16.26	\$20.41	\$4.15
Boneless legs	\$34.52	\$43.22	\$8.70	\$30.05	\$37.44	\$7.39
Boneless shoulders	\$15.73	\$13.86	-\$1.87	\$13.63	\$12.20	-\$1.43
Fillets	\$2.52	\$3.21	\$0.69	\$2.23	\$2.77	\$0.54
Strip loins	\$10.38	\$12.86	\$2.48	\$8.94	\$11.28	\$2.34
Muscle trim	\$2.76	\$2.51	-\$0.25	\$2.36	\$2.13	-\$0.23
Fat trim	\$1.39	\$1.22	-\$0.17	\$1.18	\$1.05	-\$0.13
Leg bone	\$0.64	\$0.58	-\$0.06	\$0.55	\$0.49	-\$0.06
Other bone	\$0.85	\$0.76	-\$0.09	\$0.74	\$0.66	-\$0.08

#### 4.3.4 Callipyge gene with a 30% Effect

In scenario eight there was a 30% increase in the frenched rack, boneless leg, fillet, and strip loin cuts and a decrease in the other cuts. Table 4.19 shows the overall liveweights and carcass weights for the ewe and ram lambs and the average values at each drafting date. The per-lamb income generated is also shown in Table 4.19 and was \$102.98 for the processor.

**Table 4.19: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Callipyge gene has a 30% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		296	412	232	60	1000
Live weight	Rams	41.93	42.20	42.43	42.13	42.17
	Ewes	36.76	36.44	36.62	36.13	36.56
Carcass weight	Rams	17.82	17.93	17.83	17.83	17.86
	Ewes	15.39	15.46	15.38	14.88	15.38
Processor	Lamb	\$104.01	\$103.51	\$102.20	\$97.27	\$102.98

The value of the individual cuts to the processor and the average per-lamb value are shown in Table 4.20. Values for both the base model and a 30% increase in the frenched rack, boneless leg, fillet, and strip loin cuts are shown for rams and ewes.

When the Callipyge gene effect was 30% there was an increase in the value paid per ram lamb of \$16.33 and increase of \$13.75 for ewe lambs.

**Table 4.20: The average value received by the processor per lamb, and for individual cuts in the base model and when the Callipyge gene has a 30% effect and the difference (D) between the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)						
	Base model	Rams			Ewes		
		Callipyge 25%	D		Base model	Callipyge 25%	D
Value per lamb	\$94.19	\$110.52	\$16.33	\$81.69	\$95.44	\$13.75	
Neck Fillets	\$2.54	\$2.23	-\$0.31	\$2.20	\$1.90	-\$0.30	
Flap	\$4.16	\$3.60	-\$0.56	\$3.55	\$3.12	-\$0.43	
Frenched rack	\$18.70	\$24.49	\$5.79	\$16.26	\$20.85	\$4.59	
Boneless legs	\$34.52	\$44.78	\$10.26	\$30.05	\$38.96	\$8.91	
Boneless shoulders	\$15.73	\$13.75	-\$1.98	\$13.63	\$11.80	-\$1.83	
Fillets	\$2.52	\$3.38	\$0.86	\$2.23	\$2.90	\$0.67	
Strip loins	\$10.38	\$13.39	\$3.01	\$8.94	\$11.64	\$2.70	
Muscle trim	\$2.76	\$2.37	-\$0.39	\$2.36	\$2.09	-\$0.27	
Fat trim	\$1.39	\$1.22	-\$0.17	\$1.18	\$1.05	-\$0.13	
Leg bone	\$0.64	\$0.56	-\$0.08	\$0.55	\$0.48	-\$0.07	
Other bone	\$0.85	\$0.74	-\$0.11	\$0.74	\$0.64	-\$0.10	

## 4.4 Myostatin Gene

The myostatin gene affects all muscles in the carcass, and Belgian Blue cattle with two copies of the non-functional myostatin gene have been reported to have 20% more muscle than animals with the normal gene (Kambadur *et al.*, 1997). In sheep a QTL assumed to be associated to the myostatin gene has been shown to increase muscle by 5-8% (Johnson, 2003). The percentage increases in muscle caused by the myostatin gene tested in the model is 5%, 10%, 15%, and 20%. These values were used to represent the effect of the myostatin gene.

### 4.4.1 Myostatin Gene with a 5% Effect

In scenario nine there was a 5% increase in all the muscle containing cuts and a decrease in the fat trim, leg bone and other bones. The drafting criterion for ewe lambs was 35kg and for ram lambs was 40kg, with drafting occurring every two weeks. Table 4.21 shows the overall liveweights and carcass weights for the ewe and ram lambs with average values given for each drafting date. The per-lamb income that was generated for the processor can be seen in Table 4.21 and for this scenario was \$92.20. The average per-lamb value decreased in the final drafting group due, to the number of rams in the final group being less than the number of ewes and the lower carcass weights of the ewes.

**Table 4.21: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the myostatin gene has a 5% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		298	417	226	59	1000
Live weight	Rams	42.22	42.25	42.41	41.86	42.25
	Ewes	36.81	36.48	36.83	36.33	36.65
Carcass weight	Rams	17.85	18.01	17.48	17.64	17.82
	Ewes	15.55	15.29	15.55	15.03	15.41
Processor	Lamb	\$93.62	\$92.96	\$90.19	\$87.29	92.20

The value of the individual cuts to the processor and the average value generated per lamb are shown in Table 4.22. Values for rams and ewe, for both the base model and a 5% increase in the aforementioned cuts, are also shown. When the myostatin gene

effect was 5% there was an increase in the value paid per ram lamb of \$4.13 and an increase of \$3.83 for ewe lambs.

**Table 4.22: The average value received by the processor per lamb, and for individual cuts in the base model and when the myostatin gene has a 5% effect and the difference (D) between the per-lamb value and cut values between the two scenarios.**

	Average Value Received by the processor(\$)						
	Base model	Rams			Ewes		
		Myostatin 5%	D		Base model	Myostatin 5%	D
Value per lamb	\$94.19	\$98.32	\$4.13	\$81.69	\$85.52	\$3.83	
Neck Fillets	\$2.54	\$2.71	\$0.17	\$2.20	\$2.31	\$0.11	
Flap	\$4.16	\$4.17	\$0.01	\$3.55	\$3.79	\$0.24	
Frenched rack	\$18.70	\$19.38	\$0.68	\$16.26	\$17.01	\$0.75	
Boneless legs	\$34.52	\$36.46	\$1.94	\$30.05	\$31.58	\$1.53	
Boneless shoulders	\$15.73	\$16.50	\$0.77	\$13.63	\$14.39	\$0.76	
Fillets	\$2.52	\$2.69	\$0.17	\$2.23	\$2.32	\$0.09	
Strip loins	\$10.38	\$10.90	\$0.52	\$8.94	\$9.42	\$0.48	
Muscle trim	\$2.76	\$2.87	\$0.11	\$2.36	\$2.43	\$0.07	
Fat trim	\$1.39	\$1.25	-\$0.14	\$1.18	\$1.10	-\$0.08	
Leg bone	\$0.64	\$0.59	-\$0.05	\$0.55	\$0.50	-\$0.05	
Other bone	\$0.85	\$0.79	-\$0.06	\$0.74	\$0.68	-\$0.06	

#### 4.4.2 Myostatin Gene with a 10% Effect

Scenario ten showed a 10% increase in all the muscle containing cuts and a decrease in the fat trim, leg bone, and other bones. Table 4.23 shows the average liveweights and carcass weights for rams and ewes on each slaughter date. The per-lamb income generated for the processor for this scenario was \$96.00.

**Table 4.23: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the myostatin gene has a 10% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		298	405	226	49	1000
Live weight	Rams	42.03	42.28	42.45	42.63	42.27
	Ewes	36.91	36.48	36.72	36.26	36.65
Carcass weight	Rams	17.78	18.02	17.84	16.55	17.80
	Ewes	15.42	15.15	15.51	14.18	15.31
Processor	Lamb	\$97.00	\$97.06	\$93.66	\$93.17	\$96.00

The average per-lamb value received by the processor is shown in Table 4.24 for both the base model and when the myostatin gene effect was 10%. The effect of the gene resulted in an increase of \$8.71 paid for the rams and \$7.41 paid for the ewe lambs.

Table 4.24 also shows the average values for individual cuts for both the base model and the gene effect, for rams and ewes.

**Table 4.24: The average value received by the processor per lamb, and for individual cuts in the base model and when the Myostatin gene has a 10% effect and the difference (D) between the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Rams			Ewes		
	Base model	Myostatin 10%	D	Base model	Myostatin 10%	D
Value per lamb	\$94.19	\$102.90	\$8.71	\$81.69	\$89.10	\$7.41
Neck Fillets	\$2.54	\$2.80	\$0.26	\$2.20	\$2.46	\$0.26
Flap	\$4.16	\$4.60	\$0.44	\$3.55	\$3.96	\$0.41
Frenched rack	\$18.70	\$20.62	\$1.92	\$16.26	\$18.08	\$1.82
Boneless legs	\$34.52	\$38.16	\$3.64	\$30.05	\$32.83	\$2.78
Boneless shoulders	\$15.73	\$17.22	\$1.49	\$13.63	\$14.85	\$1.22
Fillets	\$2.52	\$2.83	\$0.31	\$2.23	\$2.44	\$0.21
Strip loins	\$10.38	\$11.27	\$0.89	\$8.94	\$9.77	\$0.83
Muscle trim	\$2.76	\$3.02	\$0.26	\$2.36	\$2.64	\$0.28
Fat trim	\$1.39	\$1.14	-\$0.25	\$1.18	\$0.99	-\$0.19
Leg bone	\$0.64	\$0.53	-\$0.11	\$0.55	\$0.46	-\$0.09
Other bone	\$0.85	\$0.72	-\$0.13	\$0.74	\$0.61	-\$0.13

#### 4.4.3 Myostatin Gene with a 15% Effect

The eleventh scenario had a 15% increase in all the muscle containing cuts and a decrease in the fat trim, leg bone, and other bones. Table 4.25 shows the average carcass weights and liveweights for each slaughter group for both rams and ewes. The income generated for the processor per lamb at each draft is also shown in Table 4.25, and the overall per-lamb income generated was \$99.69.

**Table 4.25: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the myostatin gene has a 15% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		287	438	221	54	1000
Live weight	Rams	42.05	42.30	42.41	42.57	42.27
	Ewes	36.83	36.47	36.74	36.37	36.63
Carcass weight	Rams	17.79	17.91	18.02	16.51	17.83
	Ewes	15.36	15.42	15.50	15.03	15.40
Processor	Lamb	\$101.00	\$100.30	\$98.19	\$94.00	\$99.69

Table 4.26 shows the average values of the individual cuts to the processors for ewes and rams for both the base model and a 15% increase in all the muscle containing cuts. The average value to the processor per lamb is also shown in Table 4.26, with the additional value per ram being \$12.82 and per ewe being \$10.69.

**Table 4.26: The average value received by the processor per lamb, and for individual cuts in the base model and when the myostatin gene has a 15% effect and the difference (D) between in the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Base model	Rams		Base model	Ewes	
		Myostatin 15%	I		Myostatin 15%	I
Value per lamb	\$94.19	\$107.01	\$12.82	\$81.69	\$92.38	\$10.69
Neck Fillets	\$2.54	\$2.95	\$0.41	\$2.20	\$2.55	\$0.35
Flap	\$4.16	\$4.81	\$0.65	\$3.55	\$4.13	\$0.58
Frenched rack	\$18.70	\$21.47	\$2.77	\$16.26	\$18.51	\$2.25
Boneless legs	\$34.52	\$39.59	\$5.07	\$30.05	\$34.31	\$4.26
Boneless shoulders	\$15.73	\$18.07	\$2.34	\$13.63	\$15.55	\$1.92
Fillets	\$2.52	\$2.98	\$0.46	\$2.23	\$2.52	\$0.29
Strip loins	\$10.38	\$11.88	\$1.50	\$8.94	\$10.19	\$1.25
Muscle trim	\$2.76	\$3.13	\$0.37	\$2.36	\$2.72	\$0.36
Fat trim	\$1.39	\$1.00	-\$0.39	\$1.18	\$0.90	-\$0.28
Leg bone	\$0.64	\$0.48	-\$0.16	\$0.55	\$0.42	-\$0.13
Other bone	\$0.85	\$0.64	-\$0.21	\$0.74	\$0.57	-\$0.17

#### 4.4.4 Myostatin Gene with a 20% Effect

Scenario Twelve involves a 20% increase in all the muscle containing cuts and a decrease in the fat trim, leg bone, and other bones. Table 4.27 shows the average liveweights and carcass weights for ram and ewe lambs over the four slaughter groups and overall. Additionally, Table 4.27 also shows the average value paid to the processor per lamb for ram and ewe lambs at the four draft dates. The income generated for the processor per lamb was \$104.16.

**Table 4.27: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the Myostatin gene has a 20% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		302	416	230	52	1000
Live weight	Rams	42.21	42.16	42.44	42.09	42.23
	Ewes	37.01	36.54	36.81	36.26	36.73
Carcass weight	Rams	17.93	17.81	17.94	16.31	17.80
	Ewes	15.64	15.44	15.53	15.25	15.51
Processor	Lamb	\$106.15	\$103.91	\$103.23	\$98.68	\$104.16

Table 4.28 shows the average value per lamb for ram and ewe lambs, plus the average value received by the processor for each cut. Values for both the base model and when the myostatin gene effect is 20% are shown. The myostatin gene effect resulted in an additional \$17.32 per ram lamb and \$15.11 per ewe lamb.

**Table 4.28: The average value received by the processor per lamb, and for individual cuts in the base model and when the myostatin gene has a 20% effect and the difference (D) between the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Rams			Ewes		
	Base model	Myostatin 20%	D	Base model	Myostatin 20%	D
Value per lamb	\$94.19	\$111.51	\$17.32	\$81.69	\$96.80	\$15.11
Neck Fillets	\$2.54	\$3.06	\$0.52	\$2.20	\$2.64	\$0.44
Flap	\$4.16	\$4.92	\$0.76	\$3.55	\$4.27	\$0.72
Frenched rack	\$18.70	\$22.57	\$3.87	\$16.26	\$19.56	\$3.30
Boneless legs	\$34.52	\$41.49	\$6.97	\$30.05	\$36.00	\$5.95
Boneless shoulders	\$15.73	\$18.81	\$3.08	\$13.63	\$16.37	\$2.74
Fillets	\$2.52	\$3.05	\$0.53	\$2.23	\$2.66	\$0.43
Strip loins	\$10.38	\$12.33	\$1.95	\$8.94	\$10.75	\$1.81
Muscle trim	\$2.76	\$3.36	\$0.60	\$2.36	\$2.88	\$0.52
Fat trim	\$1.39	\$0.92	-\$0.47	\$1.18	\$0.82	-\$0.36
Leg bone	\$0.64	\$0.43	-\$0.21	\$0.55	\$0.36	-\$0.19
Other bone	\$0.85	\$0.58	-\$0.27	\$0.74	\$0.49	-\$0.25

## 4.5 Dressing Out Percentage QTL

Both the Callipyge gene and the myostatin gene have an affect on dressing out percentage as well as an affect on muscle size. The size of the effect caused by the myostatin gene is undocumented but it has been noted that there has been an increase in the dressing out percentage of cattle associated with the myostatin gene. Two studies have given a modest figure of approximately 4% for the increase in dressing out percentage seen in Callipyge lambs (Cockett *et al.*, 1996; Freking *et al.*, 1998b). The increases in dressing out percentage were selected to be 5%, 10%, 15% and 20%. Although this scenario is based on both the Callipyge and myostatin gene, no variation in cut distribution was added.

### 4.5.1 Dressing Out Percentage QTL with a 5% Effect

Scenario thirteen showed the effect of a 5% increase in the dressing out percentage of the lambs. Table 4.29 is an overview of the average liveweights and carcass weights for rams and ewes on each slaughter date. Drafting occurred every two weeks and ewes and rams were slaughtered when they were heavier than 35kg and 40kg respectively. The value generated for the processor per lamb was \$91.57 and can be seen in Table 4.29. The average per-lamb value decreased in the final draft due to the increased proportion of ewe lambs with smaller liveweights, resulting in a decrease in the average value.

**Table 4.29: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 5% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		268	464	202	66	1000
Live weight	Rams	41.81	42.13	42.55	42.18	42.13
	Ewes	36.65	36.44	36.78	36.30	36.55
Carcass weight	Rams	18.65	18.85	19.06	18.99	18.85
	Ewes	16.16	16.05	16.48	15.76	16.15
Processor	Lamb	\$92.89	\$91.85	\$90.61	\$87.27	\$91.57

Table 4.30 shows the average per-lamb value received by the processor for both the base model and when the dressing out percentage is increased by 5%. The effect of this was an increase of \$3.99 paid for ram lambs and \$3.28 paid for ewe lambs. Table 4.30

also shows the average values for individual cuts for both the base model the 5% increase in the dressing out percentage, for both rams and ewes.

**Table 4.30: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 5% effect and the difference (D) between the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Base model	Rams		Base model	Ewes	
		DO% 5%	D		DO% 5%	D
Value per lamb	\$94.19	\$98.18	\$3.99	\$81.69	\$84.97	\$3.28
Neck Fillets	\$2.54	\$2.64	\$0.10	\$2.20	\$2.28	\$0.08
Flap	\$4.16	\$4.34	\$0.18	\$3.55	\$3.74	\$0.19
Frenched rack	\$18.70	\$19.22	\$0.52	\$16.26	\$16.53	\$0.27
Boneless legs	\$34.52	\$36.30	\$1.78	\$30.05	\$31.50	\$1.45
Boneless shoulders	\$15.73	\$16.49	\$0.76	\$13.63	\$14.23	\$0.60
Fillets	\$2.52	\$2.66	\$0.14	\$2.23	\$2.29	\$0.06
Strip loins	\$10.38	\$10.55	\$0.17	\$8.94	\$9.22	\$0.28
Muscle trim	\$2.76	\$2.91	\$0.15	\$2.36	\$2.54	\$0.18
Fat trim	\$1.39	\$1.51	\$0.12	\$1.18	\$1.31	\$0.13
Leg bone	\$0.64	\$0.66	\$0.02	\$0.55	\$0.57	\$0.02
Other bone	\$0.85	\$0.90	\$0.05	\$0.74	\$0.78	\$0.04

#### 4.5.2 Dressing Out Percentage QTL with a 10% Effect

The fourteenth scenario had a 10% increase in the dressing out percentage of the lambs. Table 4.31 shows the average carcass weights and liveweights at each slaughter group for ram and ewe lambs. The income generated per-lamb for the processor at each draft date and overall is also shown in Table 4.31. The overall per-lamb income generated for the processor was \$96.12.

**Table 4.31: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 10% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		285	450	216	49	1000
Live weight	Rams	42.16	42.31	42.52	42.31	42.31
	Ewes	37.04	36.46	36.82	36.30	36.70
Carcass weight	Rams	19.83	20.02	20.05	19.84	19.96
	Ewes	17.05	17.10	17.17	16.04	17.05
Processor	Lamb	\$96.76	\$96.82	\$94.97	\$90.90	\$96.12

The average values of the individual cuts to the processor for ewe and ram lambs for both the base model and a 10% increase in the dressing out percentage is seen in Table

4.32. Table 4.32 also shows the average value generated for the processor per lamb. The additional value per ram and ewe lamb is \$8.58 and \$7.77 respectively.

**Table 4.32: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 10% effect and the difference (D) between the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Base model	Rams		Base model	Ewes	
		DO% 10%	D		DO% 10%	D
Value per lamb	\$94.19	\$102.77	\$8.58	\$81.69	\$89.46	\$7.77
Neck Fillets	\$2.54	\$2.72	\$0.18	\$2.20	\$2.37	\$0.17
Flap	\$4.16	\$4.62	\$0.46	\$3.55	\$3.94	\$0.39
Frenched rack	\$18.70	\$19.76	\$1.06	\$16.26	\$17.40	\$1.14
Boneless legs	\$34.52	\$38.24	\$3.72	\$30.05	\$33.18	\$3.13
Boneless shoulders	\$15.73	\$17.34	\$1.61	\$13.63	\$15.07	\$1.44
Fillets	\$2.52	\$2.71	\$0.19	\$2.23	\$2.36	\$0.13
Strip loins	\$10.38	\$10.98	\$0.60	\$8.94	\$9.60	\$0.66
Muscle trim	\$2.76	\$3.14	\$0.38	\$2.36	\$2.69	\$0.33
Fat trim	\$1.39	\$1.61	\$0.22	\$1.18	\$1.42	\$0.24
Leg bone	\$0.64	\$0.69	\$0.05	\$0.55	\$0.60	\$0.05
Other bone	\$0.85	\$0.97	\$0.12	\$0.74	\$0.84	\$0.10

### 4.5.3 Dressing Out Percentage QTL with a 15% Effect

Scenario fifteen involves a 15% increase in the dressing out percentage of the lambs. Table 4.33 shows the average liveweights and carcass weights for ram and ewe lambs over four slaughter groups and overall. Additionally, Table 4.33 shows the average value paid to the processor per lamb at the four draft dates for ram and ewe lambs. The per-lamb income generated for the processor was \$100.00.

**Table 4.33: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 15% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		300	427	211	62	1000
Live weight	Rams	42.08	42.18	42.52	42.91	42.27
	Ewes	36.98	36.55	36.90	36.66	36.76
Carcass weight	Rams	20.78	20.86	21.14	21.22	20.92
	Ewes	18.07	17.91	18.15	18.23	18.03
Processor	Lamb	\$100.49	\$100.59	\$99.29	\$95.89	\$100.00

Table 4.34 shows the average value paid to the processor per cut and also the average value paid for ram and ewe lambs. In Table 4.34 the values for both the base model and when the dressing out percentage is increased by 15% are presented. The 15% increase

in the dressing out percentage resulted in an additional \$12.66 per ram lamb and \$11.45 per ewe lamb

**Table 4.34: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 15% effect and the difference (D) between the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Base model	Rams		Base model	Ewes	
		DO% 15%	D		DO% 15%	D
Value per lamb	\$94.19	\$106.85	\$12.66	\$81.69	\$93.14	\$11.45
Neck Fillets	\$2.54	\$2.78	\$0.24	\$2.20	\$2.41	\$0.21
Flap	\$4.16	\$4.86	\$0.70	\$3.55	\$4.21	\$0.66
Frenched rack	\$18.70	\$20.20	\$1.50	\$16.26	\$17.89	\$1.63
Boneless legs	\$34.52	\$40.02	\$5.50	\$30.05	\$34.90	\$4.85
Boneless shoulders	\$15.73	\$18.46	\$2.73	\$13.63	\$15.87	\$2.24
Fillets	\$2.52	\$2.79	\$0.27	\$2.23	\$2.43	\$0.20
Strip loins	\$10.38	\$11.11	\$0.73	\$8.94	\$9.53	\$0.59
Muscle trim	\$2.76	\$3.24	\$0.48	\$2.36	\$2.85	\$0.49
Fat trim	\$1.39	\$1.68	\$0.29	\$1.18	\$1.53	\$0.35
Leg bone	\$0.64	\$0.70	\$0.06	\$0.55	\$0.62	\$0.07
Other bone	\$0.85	\$1.02	\$0.17	\$0.74	\$0.89	\$0.15

#### 4.5.4 Dressing Out Percentage QTL with a 20% Effect

In scenario sixteen there was a 20% increase in the dressing out percentage of the lambs. Table 4.35 shows the average liveweights and carcass weights for each slaughter group and overall. The per-lamb income generated for the processor is also shown in Table 4.35 and was \$102.68 for this scenario.

**Table 4.35: The number of lambs slaughtered, liveweights and carcass weights of rams and ewes, and the per-lamb value paid to the processor for four draft dates and overall when the dressing out percentage QTL has a 20% effect.**

		Draft Date				Overall
		12 Jan	26 Jan	9 Feb	23 Feb	
No. Slaughtered		301	430	205	64	1000
Live weight	Rams	42.06	42.33	42.52	42.84	42.32
	Ewes	36.59	36.55	36.73	36.63	36.60
Carcass weight	Rams	21.79	21.86	21.37	22.37	21.77
	Ewes	18.82	18.66	18.85	18.56	18.74
Processor	Lamb	\$104.12	\$103.26	\$100.91	\$97.66	\$102.68

The average values of the individual cuts to the processor and the average value generated per lamb are shown in Table 4.36. Values for both the base model and a 20% increase in the dressing out percentage are shown. When the dressing out percentage was increased by 20% the increase in the value per ram was \$15.10 and per ewe was \$14.38.

**Table 4.36: The average value received by the processor per lamb, and for individual cuts in the base model and when the dressing out percentage QTL has a 20% effect and the difference (D) between the per-lamb value and cut values between the two systems.**

	Average Value Received by the processor(\$)					
	Rams			Ewes		
	Base model	DO% 20%	D	Base model	DO% 20%	D
Value per lamb	\$94.19	\$109.29	\$15.10	\$81.69	\$96.07	\$14.38
Neck Fillets	\$2.54	\$2.89	\$0.35	\$2.20	\$2.43	\$0.23
Flap	\$4.16	\$5.13	\$0.97	\$3.55	\$4.43	\$0.88
Frenched rack	\$18.70	\$20.24	\$1.54	\$16.26	\$18.22	\$1.96
Boneless legs	\$34.52	\$41.24	\$6.72	\$30.05	\$36.11	\$6.06
Boneless shoulders	\$15.73	\$18.88	\$3.15	\$13.63	\$16.59	\$2.96
Fillets	\$2.52	\$2.82	\$0.30	\$2.23	\$2.55	\$0.32
Strip loins	\$10.38	\$11.25	\$0.87	\$8.94	\$9.65	\$0.71
Muscle trim	\$2.76	\$3.22	\$0.46	\$2.36	\$2.94	\$0.58
Fat trim	\$1.39	\$1.82	\$0.43	\$1.18	\$1.61	\$0.43
Leg bone	\$0.64	\$0.72	\$0.08	\$0.55	\$0.63	\$0.08
Other bone	\$0.85	\$1.09	\$0.24	\$0.74	\$0.91	\$0.17

## 5 Discussion

### 5.1 Loin Max™ QTL

The first four scenarios were based on the Loin Max™ QTL, which was originally named the Carwell QTL as it was found in the offspring of Poll Dorset rams from the Carwell stud in Australia (Jopson *et al.*, 2001). The Loin Max™ QTL has been shown to increase the eye muscle area by 10% (Jopson *et al.*, 2001) and the weight by 8% (Nicoll *et al.*, 1998). The eye muscle is cut out to the frenched racks and strip loins and therefore scenario one to four show the effect of a 5%, 10%, 15%, and 20% increase in these cuts.

**Table 5.1: Comparison of the base model with Loin Max™ 5%, 10%, 15% and 20%**

		Base model		Loin Max™						
			5%	D	10%	D	15%	D	20%	D
Live weight (kg)	Rams	42.24	42.33		42.24		42.07		42.21	
	Ewes	36.67	36.61		36.66		36.68		36.69	
Carcass weight (kg)	Rams	17.79	17.92		17.86		17.74		17.79	
	Ewes	15.41	15.29		15.39		15.45		15.40	
Income (\$)	Lamb	\$88.01	\$88.81	\$0.80	\$89.81	\$1.80	\$90.64	\$2.63	\$91.62	\$3.61

D = the difference in value between the per-lamb value for rams and ewes when Loin Max™ has a 5%, 10%, 15% and 20% effect and the corresponding values for the base model

#### 5.1.1 Processor

From Table 5.1 it can be determined that the processor received an additional \$0.80, \$1.80, \$2.63, \$3.61, per lamb compared to the base model when the QTL effect was 5%, 10%, 15%, and 20% respectively. This money is available to be redistributed between the farmer and the processor. The amount that will be paid to the farmer will be decided by the processor and will determine whether it will be economic for the farmer to incorporate the QTL into his/her flock.

As the Loin Max™ QTL results in the increase in the eye muscle weight by approximately 8% (Nicoll *et al.*, 1998), scenario one and two closely mimic the real effect of the Loin Max™ QTL. This means that a likely increase in the value generated for the processor per lamb would be between \$0.80 and \$1.80. An industry source (pers. comm.) has suggested that an increase of \$2.00 per lamb would be required to

make the extra gain generated by a QTL sufficiently worthwhile for the processor to pass on to the farmer. If this is the case a 5% to 10% increase in the frenched rack and strip loin (increase of \$0.80 and \$1.80, respectively) would not generate sufficient extra income for the processor to pass on to the farmers and to retain some additional income for themselves. If a QTL was found that affected these two cuts but increased their weight by 15% or 20%, giving an extra gain of \$2.63 and \$3.61 respectively, the increase in price would be sufficient to pass on to the farmer.

These results do not, however, completely mimic the real situation, as the Loin Max™ QTL only increases the eye muscle. Therefore, the increase would not be in the complete cut but only in the muscle part of the cut. For example the frenched rack contains muscle, fat (depending on whether it is cap on or cap off), and bone as part of the cut so only the muscle portion would be increased. For this reason the effect of the QTL would be less than shown in the results here and an even larger effect may be required to make the use of the QTL profitable.

### 5.1.2 Farmer

**Table 5.2: Price paid to the farmer and the difference (D) compared to the base model when they are paid at 65, 70 and 75% of the value received by the processor**

	Base Model	Percentage of Processor income paid to farmer							
		5%		10%		15%		20%	
			D		D		D		D
Processor	\$88.01	\$88.81	\$0.80	\$89.81	\$1.80	\$90.64	\$2.63	\$91.62	\$3.61
65%	\$57.21	\$57.73	\$0.52	\$58.38	\$1.17	\$58.92	\$1.71	\$59.55	\$2.35
70%	\$61.61	\$62.17	\$0.56	\$62.87	\$1.26	\$63.45	\$1.84	\$64.13	\$2.53
75%	\$66.01	\$66.61	\$0.60	\$67.36	\$1.35	\$67.98	\$1.97	\$68.72	\$2.71

Table 5.2 shows that when the farmer is paid 65, 70 and 75% of what the processor receives, a 5, 10, 15 and 20% increase in the frenched rack and strip loin the range of extra value generated per lamb is \$0.52 to \$2.71.

For farmers to produce lambs with the Loin Max™ QTL they must buy in rams with the QTL from a nucleus flock. A commercial farmer might use a ram for two seasons, therefore, if one ram can mate with approximately 100 ewes, with a lambing percentage of 125%, then in two seasons the ram could produce 250 offspring. The range of extra gains that were generated by the Loin Max™ QTL were from \$0.52, when the farmer

was paid 65% on the 5% QTL, to \$2.71, when the farmer was paid 75% on a 20% QTL. Of the 125 lambs that would be produced by the ram approximately 33 ewe lambs would be retained as replacements each year. Therefore, 92 lambs would be available to be slaughtered each year and 184 would be slaughtered over two seasons. The range of extra value generated per ram brought onto the farm would be from \$96.68 to \$498.64. This would be the additional income a farmer would have available to spend on buying a ram with the Loin Max™ QTL.

If all the extra money generated by the use of the Loin Max™ QTL was put into buying the ram then the farm would not profit from the use of the QTL. This means that the farm is not better off from using the QTL than it was when the QTL had not been imported. Additionally, it is unknown what costs are associated with the Loin Max™ QTL and therefore the economic influence of the QTL effect cannot be precisely explored at the current time. For the implementation of the Loin Max™ QTL to be favourable for the farmer the resulting extra gain needs to be enough to cover the costs of buying the ram with the QTL, cover any extra costs associated with growing the animals, and give the farmer extra profit.

## 5.2 Callipyge Gene

The effect of the Callipyge gene is variable within the carcass and some muscles are affected more than others. The most affected muscles are those in the hind end of the animal and include the semitendinosus, the semimembranosus, the biceps femoris (leg muscles), and the longissimus dorsi (loin muscle). These muscles are affected differently, with the largest increase seen in the semimembranosus with an increase of 46%, followed by an increase of 42.1% in the biceps femoris, 30% in the longissimus dorsi, and 14% in the semitendinosus. The cuts that are affected by the Callipyge gene are, therefore, the boneless leg, frenched rack, strip loin and fillet. Estimates of the overall increase in muscle weight in Callipyge lambs are 27.6%(Koochmaraie *et al.*, 1995), 32.2%(Cockett *et al.*, 1994), and 42%(Jackson *et al.*, 1997c).

### 5.2.1 Processor

When the Callipyge gene effect is 15%, 20%, 25%, and 30% the additional value per lamb when compared to the base model is \$7.69, \$10.09, \$12.59, and \$14.79 respectively (Table 5.3). Some of this money will be paid to the farmer; the size of the portion rewarded to the farmer will be decided by the processor. Whether it is economically viable for the farmer to incorporate the gene into his/her flock will be dependant on the proportion paid by the processor.

**Table 5.3: Comparison of the base model with Callipyge 15%, 20%, 25% and 30%**

		Base model			Callipyge					
			15%	D	20%	D	25%	D	30%	D
Live weight (kg)	Rams	42.24	42.29		42.32		42.27		42.17	
	Ewes	36.67	36.58		36.68		36.63		36.56	
Carcass weight (kg)	Rams	17.79	17.86		17.85		17.84		17.86	
	Ewes	15.41	15.30		15.36		15.29		15.38	
Income (\$)	Lamb	\$88.01	\$95.70	\$7.69	\$98.10	\$10.09	\$100.60	\$12.59	\$102.98	\$14.97

D = the difference in value between the per-lamb value for rams and ewes when Callipyge has a 15%, 20%, 25% and 30% effect and the corresponding values for the base model

The scenarios that best mimics the real affects of the Callipyge gene is when the cuts are increased by 25% and 30%. When the gene effect was this size the additional income generated per lamb was \$12.59 and \$14.97. This is larger than the \$2.00 suggested by an industry source (pers. comm.) that would the minimum additional income generated per lamb to sufficiently worthwhile for the farmer to pass on to the farmer. From these

results it can be said that the increase in muscle yield that results from the Callipyge gene would be sufficient to make the use of the <sup>gene</sup> profitable for processors. Unfortunately, the tenderness issue that is associated with the Callipyge gene currently makes it undesirable to consumers and therefore not practical for farmers to introduce into their flocks. If however, the tenderness problem can be overcome through the use of post mortem treatments, then the use of the Callipyge gene would be advantageous for processors.

### 5.2.2 Farmers

The additional income generated for the farmer ranges from \$5.00, when the Callipyge gene effect is 15% and the farmer is paid 65% of the processor income, to \$11.23, when the proportion paid by the processor is 75% and the gene effect is 30% (Table 5.4).

**Table 5.4: Price paid to the farmer when they are paid at 65, 70 and 75% of the value received by the processor**

	Base Model	Percentage of Processor income paid to farmer							
		Callipyge gene							
		15%	D	20%	D	25%	D	30%	D
Processor	\$88.01	\$95.70	\$7.69	\$98.10	\$10.09	\$100.60	\$12.59	\$102.98	\$14.97
65%	\$57.21	\$62.21	\$5.00	\$63.77	\$6.56	\$65.39	\$8.18	\$66.94	\$9.73
70%	\$61.61	\$66.99	\$5.38	\$68.67	\$7.06	\$70.42	\$8.81	\$72.09	\$10.48
75%	\$66.01	\$71.78	\$5.77	\$73.58	\$7.57	\$75.45	\$9.44	\$77.24	\$11.23

To generate this additional income, farmers would have to buy and use a ram that carried the Callipyge gene. The ram may be able to produce 184 offspring for slaughter over two seasons (refer to section 5.1.2). The range of additional income generated per lamb with the Callipyge gene was \$5.00 to \$11.23. For each ram with the Callipyge the farmer would earn an additional \$920 to \$2066. This additional income is the money that could be spent on a Callipyge ram and added to the profit of the farm. As stated previously in section 5.2.1, the effects of the Callipyge gene are best represented by a 25% and 30% increase in the frenched rack, boneless leg, strip loin, and the fillet. As at February 2003 the proportion of the processor income paid to the farmer was 0.72, therefore if a Callipyge ram was used to produce lambs for that market then the farmer would generate approximately \$1621 to \$1928 additional income per ram used.

### 5.3 *Myostatin Gene*

The myostatin gene <sup>a</sup>ffects all the muscle, fat and bone in a lamb carcass. The proportion of muscle in the carcass is increased and the proportion of fat and bone in the carcass is decreased. The percentage increase in muscle in sheep carrying the myostatin gene has been reported by Johnson (2003) to be 5-8%.

#### 5.3.1 *Processor*

The use of the myostatin gene by farmers could be advantageous to processors. The model has shown that when the effect of the myostatin gene ranges from 5% to 20% the extra income generated for the processor ranges from \$4.19 to \$16.15. The decision on how much of this extra income is paid to the farmer is made by the processor and will impact on how much advantage the farmer gets from the use of the gene.

**Table 5.5: Comparison of the base model with Myostatin 5%, 10%, 15%, and 20%**

		Base model			Myostatin gene					
			5%	D	10%	D	15%	D	20%	D
Live weight (kg)	Rams	42.24	42.25		42.27		42.27		42.23	
	Ewes	36.67	36.65		36.65		36.63		36.73	
Carcass weight (kg)	Rams	17.79	17.82		17.80		17.83		17.80	
	Ewes	15.41	15.41		15.31		15.40		15.51	
Income (\$)	Lamb	\$88.01	92.20	\$4.19	\$96.00	\$7.99	\$99.69	\$11.68	\$104.16	\$16.15

D = the difference in value between the per-lamb value for rams and ewes when the myostatin gene has a 5%, 10%, 15%, and 20% effect and the corresponding values for the base model

As the myostatin effect has been documented as being 5%-8% in sheep the scenarios that best mimic the real effect of the gene are when all the muscle cuts are increased by 5% and 10%. In these scenarios the extra income generated for the processor was \$4.19 and \$7.99 respectively. This additional income would not be profit as a proportion of it would be paid to the farmer. An industry source suggested that an additional gain of \$2.00 would be required to make the use of a QTL/gene in a sheep flock worth while for the processor and enable them to pass some of the additional income back to the farmer. The values generated by the model for the myostatin gene are greater than this value and therefore could be advantageous for farmers to introduce into their flocks.

### 5.3.2 Farmer

The proportion of the per-lamb income generated for the farmer will be determined by the processor and Table 5.6 shows a sensitivity analysis of the effect of different proportions paid to the farmer. The range of extra value generated for the farmer is from \$2.72, when the gene effect is 5% and the farmers are paid 65% of the processor income, to \$12.11, when the gene effect is 20% and farmers are paid 75% of the processor income.

**Table 5.6: Price paid to the farmer when they are paid at 65, 70 and 75% of the value received by the processor**

	Base Model	Percentage of Processor income paid to farmer																																					
		Myostatin gene																																					
		5%		D		10%		D		15%		D		20%		D																							
Processor	\$88.01	\$92.20	\$4.19	\$96.00	\$7.99	\$99.69	\$11.68	\$104.16	\$16.15	65%	\$57.21	\$59.93	\$2.72	\$62.40	\$5.19	\$64.80	\$7.59	\$67.70	\$10.50	70%	\$61.61	\$64.54	\$2.93	\$67.20	\$5.59	\$69.78	\$8.18	\$72.91	\$11.31	75%	\$66.01	\$69.15	\$3.14	\$72.00	\$5.99	\$74.77	\$8.76	\$78.12	\$12.11

To generate the additional value seen in Table 5.6 the farmer first needs to buy in a ram carrying the myostatin gene. If one ram could produce 184 lambs for slaughter over two seasons (refer to section 5.1.2) then the additional value generated by one ram would range from \$500, when the gene effect is 5% and the farmer is paid 65%, to \$2,228, when the farmer is paid 75% and the gene effect is 20%. This additional money generated would be divided into the money paid for the ram and the money that becomes profit for the farmer. If the ratio of farmer income to processor income is 0.72, as it was in 2003, and the myostatin gene effect is 5% and 10% the farmer has the potential to make an additional \$539 to \$1,028 per lamb under these circumstances.

ram

## 5.4 Dressing out percentage QTL

Both the myostatin gene and the Callipyge gene have an affect on the dressing out percentage of the lambs that carry the genes. The myostatin gene has been reported to decrease the amount of skin, alimentary tract and other internal organs, which would result in an increase in the dressing out percentage. Correspondingly, the Callipyge gene results in an increase in the dressing out percentage of 4%.

### 5.4.1 Processor

The additional value generated for the processor was \$3.56, \$8.11, \$11.99 and \$14.67 when the dressing out percentage when the dressing out percentage QTL effect is 5%, 10%, 15% and 20% respectively. This extra income will be divided up between the processor and the farmer, the size of the portion allocated to the farmer will be dependent on the processor.

**Table 5.7: Comparison of the base model with a dressing out percentage QTL of 5%, 10%, 15% and 20%.**

		Base model		Dressing out percentage QTL						
			5%	D	10%	D	15%	D	20%	D
Live weight (kg)	Rams	42.24	42.13		42.31		42.27		42.32	
	Ewes	36.67	36.55		36.70		36.76		36.60	
Carcass weight (kg)	Rams	17.79	18.85		19.96		20.92		21.77	
	Ewes	15.41	16.15		17.05		18.03		18.74	
Income (\$)	Lamb	\$88.01	\$91.57	\$3.56	\$96.12	\$8.11	\$100.00	\$11.99	\$102.68	\$14.67

D = the difference in value between the per-lamb value for rams and ewes when the dressing out percentage QTL has a 5%, 10%, 15% and 20% effect and the corresponding values for the base model

As there is no information of the size of the effect of the myostatin gene on dressing out percentage the best information for the real effect of a dressing out percentage QTL is the 8% reported for the effect of the Callipyge gene on dressing out percentage. The scenario that mimics the real effect of a dressing out percentage QTL is the 5% increase, which resulted in an additional \$3.56 generated for the processor. Compared to a minimum of \$2.00 suggested by an industry source (pers. comm.) the \$3.56 additional income is large enough to be sufficiently worthwhile for the processor to pass on to the farmer.

### 5.4.2 Farmer

The range of additional income obtained by the farmer with a dressing out percentage QTL is from \$2.31, when the QTL effect is 5% and the farmer is paid 65% of the processor income, to \$11.00, when the QTL effect is 20% and the farmer is paid 75% of the processor income. This equates to a range of \$425 to \$2,024 additional dollars income per ram carrying the dressing out percentage QTL, when he produces 184 lambs for slaughter (refer to section 5.1.2). This additional money would be spent on buying the ram carrying the QTL and what remains after the purchase of the ram will be extra profit for the farm.

**Table 5.8: Price paid to the farmer when they are paid at 65, 70 and 75% of the value received by the processor**

	Base Model	Percentage of Processor income paid to farmer							
		Dressing out percentage QTL							
		5%	D	10%	D	15%	D	20%	D
Processor	\$88.01	\$91.57	\$3.56	\$96.12	\$8.11	\$100.00	\$11.99	\$102.68	\$14.67
65%	\$57.21	\$59.52	\$2.31	\$62.48	\$5.27	\$65.00	\$7.79	\$66.74	\$9.54
70%	\$61.61	\$64.10	\$2.49	\$67.28	\$5.68	\$70.00	\$8.39	\$71.88	\$10.27
75%	\$66.01	\$68.68	\$2.67	\$72.09	\$6.08	\$75.00	\$8.99	\$77.01	\$11.00

The scenario that best mimics a real effect of a dressing out percentage QTL is the 5% increase in the dressing out percentage. At February 2003 the farmers were paid 72% of the income generated by the processor. Under these two conditions, a 5% increase in dressing out percentage and the farmer being paid approximately 72% of the processor income, a ram carrying the QTL would generate an additional \$458 for the farmer.

## 5.5 General discussion

There are few published reports on the economic effects on selecting for QTL/genes in animal populations. Although a lot of work has occurred in the past decade to identify markers and QTL/genes, the commercial use of these QTL/genes appears to be limited to date. Livestock Improvement Corporation (LIC) in New Zealand currently genotype all progeny tested bulls, and their daughters for 25 markers that characterise six QTL (Spelman, 2002). In addition, the introgression of the Booroola gene into Awassi and Assaf dairy flocks in Israel to increase lamb production has been documented by Gootwine *et al.* (2001). An example of the successful use of MAS to introgress QTL in plant populations has been reported in Lacape *et al.* (2005) where fibre quality traits were introgressed from one cotton cultivar to another.

Theoretical evaluation of the economic effect of using MAS and MAI have been reported by several authors (Amer *et al.*, 1998; Brascamp *et al.*, 1993; Gootwine *et al.*, 2001). Brascamp *et al.* (1993) documented the economic effect of improving milk yield in cattle and reported that the use of marker information generated additional financial returns of between \$7.00 and \$21.00 with costs of \$1.00 per cow for genotyping. Gootwine *et al.* (2001) found that the introgression of the Booroola gene into Awassi flocks generated a negative net present value (NPV) when homozygous backcross 2 rams were used. The project was only marginally profitable when the United States meat prices were high (4.0 US\$/kg) (Gootwine *et al.*, 2001).

The introduction of muscle QTL/genes in this study resulted in an increase in income for all the scenarios. The additional income generated for the processor was between \$0.80 and \$1.80 per lamb for the LoinMAX™ QTL, \$12.59 and \$14.97 per lamb when the Callipyge gene was selected on, \$4.19 and \$7.99 per lamb for the myostatin gene, and \$3.56 per lamb for a QTL that affects dressing percent. The extra income generated for farmers was estimated to be approximately 70% of the value generated for the processor, based on the comparison of the prices paid to the processor and the farmer in 2003. Due to the variation in the prices paid to the processor and the farmer this value is likely to change, and therefore only represents that point in time.

Costs associated with using muscle QTL/genes have not been incorporated into the current model. Therefore, the profit from the above scenarios will be somewhat less than the increases in income mentioned above. Costs that may be associated with the use of QTL/genes are the additional costs of purchasing a ram carrying the QTL/gene, additional costs that may be associated with producing animals with the QTL/gene, and the costs of processing the carcasses at the processing plant. It is also possible that there are increased animal feed and health costs.

There is still disagreement in the literature as to whether the redistribution of muscle, fat, and bone growth is practically possible. There is evidence in lambs carrying the Callipyge gene that the muscle is redistributed <sup>in</sup> these lambs. Jackson *et al.* (1997) reported that in a 54.5kg ram lamb the proportion of leg and loin muscle will be greater in a Callipyge lamb than a normal lamb. In addition, Freking *et al.* (1998b) reported that the percentage of carcass protein deposited in the anterior, middle, and posterior sections of a normal lamb were 34.8, 28.0, and 37.2% respectively, compared to values of 33.3, 28.3, and 38.4% respectively in a Callipyge lamb. Both of these reports suggest that a redistribution of muscle is possible within a lamb carrying a muscle QTL/gene. If the QTL/gene effect is that of redistribution then there will be a biological limit to the change that can be made using these QTL/genes because animals can not become excessively disproportionate, without some harm to their form and function.

Care must be taken to ensure that problems that have occurred in other industries, with the generation of animals that are not anatomically balanced, do not occur in sheep. In the chicken industry, broiler chickens have been selected so intensely for growth that sound broiler chickens spend 76% of their time lying down and lame chickens spend 86% of their time lying down due to their increased body weight (Weeks *et al.*, 2000). Additionally, intensely farmed turkeys cannot breed naturally due to selection on increased breast size (Weaver, 1998). The benefits of New Zealand sheep farming is that lambs can be produced on pasture providing New Zealand with a clean green reputation. If lambs were being produced with the problems seen in the poultry industry sheep farming in New Zealand would be severely compromised. In addition to the negative effects on the animal of increasing certain cuts too much, there is also the limitation to the size of cuts that consumers want. A leg roast that had been increased in

size too much will not be purchased by a consumer as they would be unable to cook it due to domestic oven sizes.

The price that might be paid for a ram carrying muscle QTL/genes is as yet unknown. The cost of testing and the additional income that could be obtained by the commercial farmer would affect the extra price that may be charged for a ram with the QTL/gene as opposed to a ram without the QTL/gene. An issue with pricing such rams is that the cost of testing rams could be greater than the benefit that the farmer would obtain by using the ram. Additionally, the producers of rams carrying desired QTL/genes may believe that they are worth more than just the additional costs of testing the rams. For example the cost of testing may be \$50 per ram but the producer may believe that the ram is worth \$200 more than a ram without the QTL/gene. However, whatever the scenario the additional price that can be asked for a ram with the QTL/gene must be less than the extra gain generated for the commercial farmer through the use of the ram. The extra income generated for the commercial farmer should cover the additional cost of buying the ram and generate extra profit for the farmer.

The results of this model do not completely mimic the real situation because it has been assumed that the effect of the QTL/gene affects the entire cut. In reality the muscle QTL/genes only increase muscle in the carcass and therefore, the effect of the QTL/gene on the entire cut will not be as large as it is for the muscle. However, increases in the size of cuts as well as the size of muscles have been reported for the myostatin gene, Callipyge gene and the LoinMAX™ QTL (Laville *et al.*, 2004; Marcq *et al.*, 2002) Additionally, the Callipyge and myostatin genes decrease fat and bone as well as increasing muscle. For cuts such as the frenched rack, this increase in the muscle portion of the cut may be offset by the decrease in the bone and fat, which may result in the weight of the cut staying the same or even decreasing. However, the weight of muscle is greater than the weight of fat therefore it is unlikely that a decrease in the fat content of the cut will offset the increase in muscle. The effect of the assumption that the QTL/gene affects the entire cut will be that the income generated for most of the scenarios will be overestimated and the real effect of the QTL/gene will be less than that shown in this study.

The costs of processing the carcasses are currently in bands, similar to payment on carcass weight, so it is assumed that carcasses within a weight range will cost the same to process. This causes an averaging effect, the same that is seen with payment on carcass weight, where a large carcass within the band will cost more to process than a small carcass within the band; however the average cost of processing is used. The additional costs of processing lambs carrying muscle QTL/genes are currently unknown. If the increased cuts do cost more to process then the extra income generated by the use of the QTL/gene may be, either in part or fully, used up to pay for the additional costs. Depending on the costs, it may make the use of QTL/genes in a flock not profitable.

The results of this study rely on payment to the farmers changing from payment on carcass weight and GR to farmers being paid for individual cuts. This change is required because the muscle QTL/genes do not increase the size of the carcass but increase the proportion of certain muscles within the carcass. For example, currently farmers producing carcasses showing muscle hypertrophy only benefit from the increase in the dressing out percentage seen in these animals and not from the increase in muscle in the individual cuts. However if farmers were paid on the cuts from the double-muscled cattle they would benefit more from producing these animals. Progressive Meats Ltd is currently changing their processing plant to enable farmers to be paid on individual cuts (pers. comm. Craig Hickson). Additionally, the Alliance group are utilising the VIAscan® imagine scanning equipment to pay farmers on yield of lean meat (Chalmers, 2003). Payment on individual cuts allows the processor to give market signals to farmers to produce lambs that have larger specific cuts. If an increased proportion is paid for one cut then the proportion paid for other cuts would have to decrease.

An additional affect of the use of QTL/genes is the effect they have on other economically important traits, such as fertility. An example of the negative effects of utilising a QTL/gene is the increased incidence of dystocia in Belgian Blue cattle, carrying the myostatin gene, due to the increased size of the calves at birth. Approximately 85% of cows homozygous for the myostatin gene experience extreme dystocia and 62% of cows require caesarean section to have their calves (Menissier, 1982). Additionally, the increase in muscle in Callipyge lambs is associated with a

decrease in tenderness of some of the hypertrophied muscles (Duckett *et al.*, 2000). These negative effects of the QTL/genes on other traits can have a large impact on the profitability of the QTL/genes when total costs are taken into account. Callipyge lamb is not desired by consumers due to the toughness, and the costs of caesarean births in Belgian Blue cattle would reduce the profitability of the myostatin gene.

### **5.6 Limitations of the study**

This study used a model that followed the growth of 1000 lambs from weaning to slaughter and then through the processing of the lambs down to individual cuts and payment to the processor. The income generated for the farmer was determined in a sensitivity analysis. The model did not take into account the cost associated with the production of lambs for slaughter, or the costs of processing the lambs.

The dressing out percentage equation used in the model used a percentage of 47.3%, which is relatively high for New Zealand, and the figure was this high because the liveweight measurements used in Garrick *et al.* (1986) were taken after a nights fasting and therefore represented the empty liveweight of the sheep. Generally, farmers in New Zealand want a dressing out percentage that relates to the full liveweight of the lamb. A dressing out percentage using the full weight of the lamb will be smaller than when the empty weight it used.

## **6 Conclusion**

From this study it can be concluded that the size of the QTL/gene effect and the aspect of the carcass that it affects has a large impact on the additional income generated by the QTL/gene. QTL/genes that have larger effects and affect more of the carcass, or specifically high value cuts will result in a greater additional income for both farmers and processors. Under the conditions stipulated in this research all QTL/genes tested increased the income of the farmers and the processors, even when only small increases were tested. However the increase in income generated for the processor by the LoinMAX™ QTL was marginal and may not be sufficiently large enough for the processor to pass some benefit on to the farmer.

Additionally, it can be concluded that the use of QTL/genes under the current method of paying farmers for lamb meat, using carcass weight and GR, would not generate an advantage for the farmers. For farmers to see a benefit of using muscle QTL/genes processors would be required to pay farmers on individual cuts.

Further study is required to determine the effect of the LoinMAX™ QTL, Callipyge gene, and myostatin gene on the meat cuts as well as the effects on the carcass composition of the animal. Additionally, more research is needed in the area of the costs of growing and processing lambs that carry QTL/genes for carcass traits, in order to determine the profit generated by the use of the QTL/gene. Finally, the effect of carcass QTL/genes on other economically important traits needs to be determined to see if the improvement in carcass traits results in the decrease in other important traits such as fertility.

## 7 Reference List

- Amer, P.R., McEwan, J. C., Dodds, K. G., and Davis, G. H., (1998) Cost benefit analysis of commercial use of the Inverdale prolificacy gene. *Proceedings of the New Zealand Society of Animal Production*. **58: 157-160.**
- Anon, (1995) New Zealand Meat: Guide to lamb and mutton carcass classification.
- Anon, (1996) New Zealand Meat: Guide to beef carcass classification.
- Anon. (2001) New Zealand Meat: Trade Guide. New Zealand Meat Producers Board, New Zealand.
- Anon, (2003) Lamb yield payment for Alliance plants by 2005-06: *Country-Wide Northern*, v. **August**,
- Arendonk, J. A. M. Van., Tier, B., and Kinghorn, B.P., (1994) Use of multiple genetic markers in prediction of breeding values. *Genetics*. **137: 319-329.**
- Arranz, J.-J., Coppieters, W., Berzi, P., Canbisano, N., Grisart, B., Karim, L., Marcq, F., Riquet, J., Simon, P., Vanmanshoven, P., Wagenaar, D., and Georges, M., (1998) A QTL affecting milk yield and composition maps to chromosome 20: A conformation. *Animal Genetics*. **29: 107-115.**
- Aurther, P. F., (1995) Double muscling in cattle: a review. *Australian Journal of Agricultural Research*. **46: 1493-1515.**
- Berry, C., Thomas, M., Langley, B., Sharma, M., and Kambadur, R., (2002) Single cysteine to tyrosine transition inactivates the growth inhibitory function of Piedmontese myostatin. *American Journal of Physiology*. **283: C135-C141**
- Brascamp, E.W., Arendonk, J. A. M. Van., and Groen, A.F., (1993) Economic appraisal of the utilization of genetic markers in dairy cattle breeding. *Journal of Dairy Science*. **76: 1204-1213.**
- Bray, A.R., (1984) Lamb live weights at slaughter and carcass grades. *Proceedings of the New Zealand Society of Animal Production*. **44: 223-225.**
- Carpenter, C. E., Rice, O. D., Cockett, N. E., and Snowden, G. D., (1996) Histology and composition of muscles from normal and Callipyge lambs. *Journal of Animal Science*. **74: 388-393.**
- Casas, E., Keele, J. W., Shackelford, S. D., Koohmaraie, M., Sonstegard, T. S., Smith, T. P. L., Kappes, S. M., and Stone, R. T., (1998) Association of Muscle Hypertrophy Locus with Carcass Traits in Beef Cattle. *Journal of Animal Science*. **76: 468-473.**

- Casas, E., Shackelford, S. D., Keele, J. W., Stone, R. T., Kappes, S. M., and Koohmaraie, M., (2000) Quantitative trait loci affecting growth and carcass composition of cattle segregating alternate forms of myostatin. *Journal of Animal Science*. **78**: 560-569.
- Chalmers, H., (2003) Alliance yield payments not for 3 years: *Rural News*, v. **July**,
- Charlier, C., Segers, K., Wagenaar, D., Karim, L., Berghmans, S., Jaillon, O., Shay, T., Weissenbach, J., Cockett, N. E., Gyapay, G., and Georges, M., (2001) Human-ovine comparative sequencing of a 250-kb imprinted domain encompassing the Callipyge (*clpg*) locus and identification of six imprinted transcripts: *DLK1*, *DAT*, *GTL2*, *PEG11*, *antiPEG11*, and *MEG8*. *Genome Research*. **11**: 850-862.
- Clarke, R. D., Kirton, A. H., Bartle, C. M., and Dobbie, P. M., (1999) Application of dual-energy x-ray absorptiometry for ovine carcass evaluation. *Proceedings of the New Zealand Society of Animal Production*. **59**: 272-274.
- Cockett, N. E., (1999) Genomics of Sheep. *AgBiotechNet*. **1**: 1-5.
- Cockett, N. E., Jackson, S. P., Shay, T. L., Nielsen, D., Moore, S. S., Steel, M. M., Barendse, W., Green, R. D., and Georges, M., (1994) Chromosomal localization of the Callipyge gene in sheep (*Ovis aries*) using bovine DNA markers. *Proceedings of the National Academy of Science*. **91**: 3019-3023.
- Cockett, N. E., Jackson, S. P., Snowden, G. D., and Carpenter, C. E. (1996) Characterization of the Callipyge trait in sheep. *Proceedings of the 49th Annual Reciprocal Meats Conference*. AMSA:
- Cockett, N. E., Jackson, S. P., Snowden, G. D., Shay, T. L., Berghmans, S., Beaver, J. E., Carpenter, C., and Georges, M., (1999) The Callipyge phenomenon: Evidence for unusual genetic inheritance. *Journal of Animal Science*. **77**: 221-227.
- Coppieters, W., Riquet, J., Arranz, J. J., Berzi, P., Canbisano, N., Grisart, B., Karim, L., Marcq, F., Moreau, L., Nezer, C., Simon, P., Vanmanshoven, P., Wagenaar, D., and Georges, M., (1998) A QTL with major effect on milk yield and composition maps to bovine Chromosome 14. *Mammalian Genome*. **9**: 540-544.
- Cunningham, E.P., (1999) The application of biotechnologies to enhance animal production in different farming systems. *Livestock Production Science*. **58**: 1-24.
- Davidson, R.M., (2000) Genetic improvement and importance to sheep and beef farming. *Proceedings of the New Zealand Society of Animal Production*. **60**: 184-188.
- Davis, G. H., McEwan, J. C., Fennessy, P. F., Dodds, K. G., and Farquhar, P. A., (1991) Evidence for the presence of a major gene influencing ovulation rate on the X chromosome in sheep. *Biology of Reproduction*. **44**: 620-624.

- Davis, G. H., McEwan, J. C., Fennessy, P. F., Dodds, K. G., and O, W.-S., (1992) Infertility due to bilateral ovarian hyperplasia in sheep homozygous (FecX1 FecX1) for the Inverdale prolificacy gene located on the X-chromosome. *Biology of Reproduction*. **46: 636-640.**
- Davis, G. P. and DeNise, S. K., (1998) The impact of genetic markers on selection. *Journal of Animal Science*. **76: 2331-2339.**
- Dekkers, J. C. M., (1999) Breeding Values for Identified Quantitative Trait Loci Under Selection. *Genetics, Selection, Evolution*. **31: 421-436.**
- Dekkers, J. C. M., (2004) Commercial application of marker- and gene-assisted selection in livestock: Strategies and lessons. *Journal of Animal Science*. **82 (E. suppl.): E313-E328**
- Dentine, M. R., (1990) Using molecular biology to improve the accuracy of selection. *Proceedings of the 4th World Congress on Genetics Applied to Livestock Production*. **XIV: 35-43.**
- Dooley, A. E., (2002) *Milk segregation on dairy farms*. Massey University. Palmerston North, New Zealand
- Duckett, S. K., Snowden, G. D., and Cockett, N. E., (2000) Effect of the Callipyge gene on muscle growth, calpastatin activity, and tenderness of three muscles across the growth curve. *Journal of Animal Science*. **78: 2836-2841.**
- Elson, J., (2003) Utilization of genomic information in livestock improvement. *Outlook on Agriculture*. **32: 241-245.**
- Falconer, D. S. and Mackay, T. F. C., (1996) *Introduction to Quantitative Genetics*. Longman, Harlow., UK
- Fernando, R. L., (1998) Genetic evaluation and selection using genotypic, phenotypic and pedigree information. *Proceedings of the 6th World Congress on Genetics Applied to Livestock Production*. **26: 329-335.**
- Flanagan, S. and O'Riordan, E. G., (1993) Sheep production from New Zealand grasslands. *Irish Grassland and Animal Production Association Journal*. **27: 125-132.**
- Flynn, G. *Marketing lambs 'over-the-hooks'*:  
<http://www.dpi.vic.gov.au/dpi/nrenfa.nsf/FID/-67B48BEDBA0208D2CA256C72001A8042?OpenDocument> 3/7/2005
- Freking, B. A., Keele, J. W., Beattie, C. W., Kappes, S. M., Smith, T. P. L., Sonstegard, T. S., Nielsen, M. K., and Leymaster, K. A., (1998a) Evaluation of the ovine *Callipyge* locus: I. Relative chromosomal position and gene action. *Journal of Animal Science*. **76: 2062-2071.**

- Freking, B. A., Keele, J. W., Nielsen, M. K., and Leymaster, K. A., (1998b) Evaluation of the ovine *Callipyge* locus: II. Genotypic effects on growth, slaughter, and carcass traits. *Journal of Animal Science*. **76**: 2549-2559.
- Freking, B. A., Murphy, S. K., Wylie, A. A., Rhodes, S. J., Keele, J. W., Leymaster, K. A., Jirtle, R. L., and Smith, T.P.L., (2002) Identification of the single base change causing the Callipyge muscle hypertrophy phenotype, the only known example of polar overdominance in mammals. *Genome Research*. **12**: 1496-1506.
- Garrick, D.J., Purchas, R.W., and Morris, S.T., (1986) Consideration of alternative lamb drafting strategies. *Proceedings of the New Zealand Society of Animal Production*. **46**: 49-53.
- Georges, M., (1999) Towards marker-assisted selection in livestock. *Reproduction, Nutrition, Development*. **39**: 555-562.
- Gootwine, E., Zenu, A., Bor, A., Yossafi, S., Rosov, A., and Pollat, G.E., (2001) Genetic and economic analysis of introgression the B allele of the FecB (Booroola) gene in the Awassi and the Assaf dairy sheep breeds. *Livestock Production Science*. **71**: 49-58.
- Gray, L., (2004) Announcing gene discovery the turning point: *Country-Wide Southern*, v. **June**.
- Greenwood, P. L., Hunt, A. S., Hermason, J. W., and Bell, A. W., (1998) Effects of birth weight and postnatal nutrition on neonatal sheep: I. Body growth and composition, and some aspects of energetic efficiency. *Journal of Animal Science*. **76**: 2354-2367.
- Groen, A.F. and Smith, C., (1995) A stochastic simulation study of the efficiency of marker-assisted introgression in livestock. *Journal of Animal Breeding and Genetics*. **112**: 161-170.
- Haley, C. S., (1995) Livestock QTLs - bringing home the bacon? *Trends in Genetics*. **11**: 488-492.
- Haley, C. S. and Visscher, P., (1999) Annual Report - Roslin Institute (No. 1998/99): Edinburgh: University of Edinburgh.
- Hanset, R. and Michaux, C., (1985a) On the genetic determinism of muscular hypertrophy in the Belgium White and Blue cattle breed I. Experimental data. *Genetics, Selection, Evolution*. **17**: 359-368.
- Hanset, R. and Michaux, C., (1985b) On the genetic determinism of muscular hypertrophy in the Belgium White and Blue cattle breed I. Population data. *Genetics, Selection, Evolution*. **17**: 369-385.

- Hayes, B. and Goddard, M. E., (2001) The distribution of the effects of genes affecting quantitative traits in livestock. *Genetics, Selection, Evolution*. **33**: 209-229.
- Jackson, S. P., Green, R. D., and Miller, M. F., (1997a) Phenotypic characterisation of Rambouillet sheep expressing the *Callipyge* gene: I. Inheritance of the condition and production characteristics. *Journal of Animal Science*. **75**: 14-18.
- Jackson, S. P., Miller, M. F., and Green, R. D., (1997b) Phenotypic characterisation of Rambouillet sheep expressing the *Callipyge* gene: II. Carcass characteristics and retail yield. *Journal of Animal Science*. **75**: 125-132.
- Jackson, S. P., Miller, M. F., and Green, R. D., (1997c) Phenotypic characterisation of Rambouillet sheep expressing the *Callipyge* gene: III. Muscle weights and muscle weight distribution. *Journal of Animal Science*. **75**: 133-138.
- Johnson, P. L., (2003) *A directed search for QTL affecting carcass composition traits in Texel sheep*. Massey University. Palmerston North
- Johnson, P. L., McEwan, J. C., Dodds, K. G., Purchas, R. W., and Blair, H. T., (2005) QTL affecting carcass traits in Texel sheep: A directed search for quantitative trait loci affecting carcass traits in Texel sheep. *Journal Of Animal Science* .
- Johnson, P.L., Purchas, R.W., and Blair, H.T., (2002) Ranking Romney sires on carcass value from a progeny test. *Proceedings of the New Zealand Society of Animal Production*. **62**: 183-187.
- Jones, H. E., Lewis, R. M., and Warkup, C. C., (2003) Market requirements for lamb. *British Food Journal*. **105**: 364-379.
- Jopson, N.B., Nicoll, G.B., Stevenson-Barry, J. M., Duncan, S., Greer, G. J., Bain, W. E., Gerard, E. M., Glass, B. C., Broad, T. E., and McEwan, J. C., (2001) Mode of inheritance and effects on meat quality of the rib-eye muscling (*REM*) QTL in sheep. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics*. **14**: 111-114.
- Kambadur, R., Sharma, M., Smith, P. P. L., and Bass, J. J., (1997) Mutations in the *myostatin* (*GDF8*) in Double-Muscled Belgian Blue and Piedmontese Cattle. *Genome Research*. **7**: 910-915.
- Kim, J.J. and Park, Y.I, (2001) Current status of quantitative trait locus mapping in livestock species. *Asian-Australasian Journal of Animal Sciences*. **14**: 587-596.
- Kinghorn, B., Arendonk, J. A. M. Van., and Hetzel, J., (1994) Detection and use of major genes in animal breeding. *AgBiotech News and Information*. **6**: 297-302.

- Kirton, A. H., (1989) Principles of classification and grading: *in Meat production and processing*. Purchas, R.W., Butler-Hogg, B. W., and Davies, A. S. eds New Zealand Society of Animal Production (Inc): Hamilton, New Zealand.
- Kirton, A.H., Carter, A.H., Clarke, J.N., and Duganzich, D.M., (1984) Dressing percentages of lambs. *Proceedings of the New Zealand Society of Animal Production*. **44**: 231-233.
- Kirton, A. H., Duganzich, D. M., Feist, C. L., Bennett, G. L., and Woods, E. G., (1985) Prediction of lamb carcass composition from GR and carcass weight. *Proceedings of the New Zealand Society of Animal Production*. **45**: 63-65.
- Koohmaraie, M., (1988) Relationships between growth rate, carcass composition, feed intake, feed conversion ratio and income in four biological types of cattle. *Proceedings* . **19**: 225-248.
- Koohmaraie, M., Shackelford, S. D., Wheeler, T. L., Lonergan, S. M., and Doumit, M. E., (1995) A muscle hypertrophy condition in lamb (Callipyge): Characterization of effects on muscle growth and meat quality traits. *Journal of Animal Science*. **73**: 3596-3607.
- Koudande, O.D., Iraqi, F., Thomson, P.C., Teale, A.J., and Arendonk, J. A. M. Van., (2000) Strategies to optimise marker assisted introgression of multiple unlinked QTL. *Mammalian Genome* . **11**: 145-150.
- Lacape, J. M., Nguyen, T. B., Hau, B., and Giband, M. *Targeting introgression of cotton fibre quality QTLs using molecular markers*:  
<http://www.fao.org/biotech/docs/Giband.pdf> 22/2/2005
- Landcorp Farming Ltd. *Sire breeding programmes*:  
<http://www.landcorp.co.nz/BreedingProgrammes.htm> 2/8/2005
- Lande, R. and Thompson, R., (1990) Efficiency of marker assisted selection in the improvement of quantitative traits. *Genetics*. **124**: 743-756.
- Laville, E., Bouix, J., Sayd, T., Bibe, B., Elsen, J. M., Larzul, C., Eychenne, F., Marcq, F., and Georges, M., (2004) Effects of a quantitative trait locus for muscle hypertrophy from Belgium Texel sheep on carcass conformation and muscularity. *Journal of Animal Science*. **82**: 3128-3137.
- Lin, C. Y., Sasaki, O., and Sabour, M. P., (1997) Incorporation of genetic markers into animal breeding programs. *Sabrao Journal*. **29**: 1-20.
- Lirette, A., Seoane, J. R., Minvielle, F., and Froehlich, D., (1984) Effects of breed and castration on conformation, classification, tissue distribution, composition and quality of lamb carcasses. *Journal of Animal Science*. **58**: 1343-1357.

- Marchitelli, C., Savarese, M. C., Crisa, A., Nardone, A., Marsan, P. A., and Valentini, A., (2003) Double muscling in Marchigiana beef breed is caused by a stop codon in the third exon of myostatin gene. *Mammalian Genome*. **14**: 392-395.
- Marcq, F., Larzul, C., Marot, V., Eychenne, F., Laville, E., Bibe, B., Leyroy, P. L., Georges, M., and Elsen, J. M., (2002) Preliminary results of a whole-genome scan targeting QTL for carcass traits in a Texel x Romanov intercross. *Proceedings of the 7th World Congress on Genetics Applied to Livestock Production*. **2-14**:
- Marle-Koster, E. van. and Nel, L.H., (2003) Genetic markers and their application in livestock breeding in South Africa: A review. *South African Journal of Animal Science*. **33**: 1-10.
- Mateescu, R. G. and Thonney, M. L., (2002) Genetic expression in sexually dimorphic muscles in sheep. *Journal of Animal Science*. **80**: 1879-1887.
- McCracken, T. O., Kainer, R. A., and Spurgeon, T. L., (1999) *Spurgeon's colour atlas of large animal anatomy. The essentials*. Lippincott Williams & Wilkins, United States of America
- McLaren, D., McEwan, J. C., For, R., Glass, B. C., Broad, T. E., Greer, G. J., and Nicoll, G. B., (2003) Recombination breakpoint mapping of the Carwell locus for rib-eye muscling in sheep. *International Congress on Genetics*. (Abstract)
- McMahon, C. D., Popovic, L., Jeanplong, F., Oldham, J. M., Kirk, S. P., Osepchook, C. C., Wong, K. W. Y., Sharma, M., Kambadur, R., and Bass, J. J., (2003) Sexual dimorphism is associated with decreased expression of processed myostatin in males. *American Journal of Physiology*. **284**: 377-381.
- Meat New Zealand, (2003) Forging New Horizons: Annual Report 2002-2003: New Zealand: Meat New Zealand.
- Menissier, F., (1982) General survey of the effect of double muscling on cattle performance: in *Muscle hypertrophy of genetic origin and its use to improve beef production*. King, J. W.B. and Menissier, F. eds 23-53. Martinus Nijhoff Publishers: The Hague.
- Meuwissen, T. H. E. and Arendonk, J. A. M. Van., (1992) Potential improvements in rate of genetic gain from marker assisted selection in dairy cattle breeding schemes. *Journal of Dairy Science*. **75**: 1651-1659.
- Meuwissen, T. H. E. and Goddard, M. E., (1996) The use of marker haplotypes in animal breeding schemes. *Genetics, Selection, Evolution*. **28**: 161-176.
- Mitchell, A. D., Soloman, M. B., and Rumsey, T. S., (1997) Composition analysis of beef rib sections by dual-energy x-ray absorptiometry. *Meat Sciences*. **47**: 115-124.

- Moore, S. S. and Hansen, C., (2003) Genomics: Delivering added value to the beef industry? *Outlook on Agriculture*. **32**: 247-252.
- Moore, S. W., Field, R. A., Riley, M. L., and Russell, W. C., (1998) Consumer evaluation of cuts from normal and Callipyge lambs. *Sheep & Goat Research Journal*. **14**: 202-205.
- Muir, P., (2004) Answers coming on multiple lamb survival: *Country Wide*, (June):
- Nicoll, G. B., Burkin, H. H, Broad, T. E., Jopson, N. B., Greer, G. J., Bain, W. E., Wright, C. S., Dodds, K. G., Fennessy, P. F., and McEwan, J. C., (1998) Genetic linkage of microsatellite markers to the Carwell locus for rib-eye muscling in sheep. *Proceedings of the 6th World Congress on Genetics Applied to Livestock Production*. **26**: 529-532.
- Piper, L. R. and Bindon, B. M., (1982) Genetic segregation for fecundity in Booroola merino sheep. *Proceedings of the 1st World Congress on Sheep and Beef Cattle Breeding*. **1**: 395-400.
- Reisz-Porszasz, S., Bhasin, S., Artaza, J. N., Shen, R. Q., Sinha-Hikim, I., Hogue, A., Fielder, T. J., and Gonzalez-Cadavid, N. F., (2003) Lower skeletal muscle mass in male transgenic mice with muscle-specific overexpression of myostatin. *American Journal of Physiology*. **285**: E876-E888
- Rios, R. , Carneiro, I. , Arce, V. V., and Devesa, J., (2002) Myostatin is an inhibitor of myogenic differentiation. *American Journal of Physiology*. **282**: 993-999.
- Ross, I. (2005) Viascan. *Lambline*. **January 2005(5)**. WAMMCO International, Western Australia.  
<http://www.wammco.com.au/documents/newsletter/32/Lambline%20January%202005.pdf>
- Ruane, J. and Colleau, J. J., (1996) Marker-assisted selection for a sex-limited character in a nucleus breeding population. *Journal of Dairy Science*. **79**: 1666-1678.
- Schwerin, M., (2001) Structural and functional genomics in domestic animals: the way to understand the phenotype. *Journal of Applied Genetics*. **42**: 293-308.
- Shackelford, S. D., Wheeler, T. L., and Koohmaraie, M., (1997) Effect of the Callipyge phenotype and cooking method on tenderness of several major lamb muscles. *Journal of Animal Science*. **75**:
- Shahin, K. A. and Berg, R. t., (1985) Growth patterns of muscle, fat, and bone, and carcass composition of double muscled and normal cattle. *Canadian Journal of Animal Science*. **65**: 279-293.

- Simm, G., (1998) *Genetic improvement of cattle and sheep*. Farming Press, Miller Freeman UK Ltd, Ipswich, UK
- Smith, C., (1967) Improvement of metric traits through specific genetic loci. *Animal Production*. **9**: 349-358.
- Smith, C. and Simpson, S. P., (1986) The use of genetic polymorphisms in livestock improvement. *Journal of Animal Breeding and Genetics*. **103**: 205-217.
- Sorenson, J. T., (1998) Modeling and simulation in applied livestock production science: *in Agricultural systems modeling and simulation*. Anonymous, eds **475-494**. Marcel Dekker Inc: New York, USA.
- Spedding, C. R. W., (1998) *An introduction to agricultural systems*. Elsevier Applied Science Publishers Ltd, Essex, England
- Spelman, R. J., (2002) Utilisation of molecular information in dairy cattle breeding. *Proceedings of the 7th World Congress on Genetics Applied to Livestock Production*. **22-02**:
- Spelman, R. J. and Arendonk, J. A. M. Van., (1997) Effect of inaccurate parameter estimates on genetic response to marker-assisted selection in an outbred population. *Journal of Dairy Science*. **80**: 3399-3410.
- Spelman, R.J and Bovenhuis, H., (1998) Moving from QTL experimental results to the utilization of QTL in breeding programmes. *Animal Genetics*. **29**: 77-84.
- Spelman, R. J., Coppieters, W., Grisart, B., Blott, S., and Georges, M., (2001) Review of QTL mapping in the New Zealand and Dutch Dairy cattle populations. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics*. **14**: 11-16.
- Spelman, R. J., Coppieters, W., Karim, L., Arendonk, J. A. M. Van., and Bovenhuis, H., (1996) Quantitative trait loci analysis for five milk production traits on chromosome six in the Dutch Holstein-Friesian Population. *Genetics*. **144**: 1799-1808.
- Spelman, R. J., Ford, C. A., Gregory, G. C., and Snell, R. G., (2002) Characterisation of the DGAT1 gene in the New Zealand dairy population. *Journal of Dairy Science*. **85**: 3514-3517.
- Spelman, R. J. and Garrick, D., (1997) Utilisation of marker assisted selection in the commercial dairy cow population. *Livestock Production Science*. **47**: 139-147.
- Swatland, H. *Major muscles of the carcass*:  
<http://www.clues.abdn.ac.uk:8080/mirrors/growth/ch4.1.html> 3/8/2005

Tortora, G. J. and Grabowski, S. R., (2000) *Principles of anatomy and physiology*. John Wiley and Sons, Inc, United States of America

Van Eenennaam, A. (2004) Marker-assisted selection in beef cattle. University of California, California.  
[http://respositories.cdlib.org/anrrec/2004\\_marker\\_assisted\\_selection\\_in\\_beef\\_cattle](http://respositories.cdlib.org/anrrec/2004_marker_assisted_selection_in_beef_cattle)

Waaij, E. H. Van Der and Arendonk, J. A. M. Van., (1999) Introgression of genes responsible for disease resistance in a cattle population selected for production: Genetic and economic consequences. *Animal Science*. **70**: 207-220.

Weaver, T., (1998) Spotting top notch toms: *Agricultural Research*, v. **July** ,

Weeks, C. A., Danbury, T. D., Davies, H. C., Hunt, P., and Kestin, S. C., (2000) The behaviour of broiler chickens and its modification of lameness. *Applied Animal Behaviour Science*. **67**: 111-125.

Weller, J. I., (2001) Marker-Assisted Introgression: in *Quantitative Trait Loci Analysis in Animals*. Weller, J. I. eds Cromwell Press: Trowbridge, U.K.

Wylie, A.R.G, Chestnutt, D.M.B, and Kirkpatrick, D.J., (1997) Growth and carcass characteristics of heavy slaughter weight lambs: effects of sire breed and size of lambs and relationships to serum metabolites and IGF-1. *Animal Science*. **64**: 309-318.

Zgur, S., Cividini, A., Kompan, D., and Birtic, D., (2003) The effect of live weight at slaughter and sex on lambs carcass traits and meat characteristics. *Agriculturae Conspectus Scientificus (Poljoprivredna Znanstvena Smotra)*. **68**: 155-159.

## 8 Appendix One: Calculations to determine yield proportions for each of the scenarios investigated.

QTL Scenario One							
LoinMAX™ QTL							
	Original value	QTL effect	First change			Decrease	Adjusted value
NF	1.87	0	1.87	1.87	0.03	0.013	1.86
F	11.11	0	11.11	11.11	0.20	0.077	11.03
FR	5.29	0.2645	5.55	0.00	0.00	0.000	5.55
BL	21.49	0	21.49	21.49	0.39	0.148	21.34
BS	14.52	0	14.52	14.52	0.26	0.100	14.42
FI	0.6	0	0.60	0.60	0.01	0.004	0.60
ST	2.28	0.114	2.39	0.00	0.00	0.000	2.39
MT	5.29	0	5.29	5.29	0.10	0.036	5.25
FT	7.36	0	7.36	0.00	0.00	0.000	7.36
LB	6.49	0	6.49	0.00	0.00	0.000	6.49
BN	23.83	0	23.83	0.00	0.00	0.000	23.83
	100.13		100.51	54.88	1.00		100.13
			<b>Difference</b>	0.38			

QTL Scenario Two							
LoinMAX™ QTL							
	Original value	QTL effect	First change			Decrease	Adjusted value
NF	1.87	0	1.87	1.87	0.03	0.026	1.84
F	11.11	0	11.11	11.11	0.20	0.153	10.96
FR	5.29	0.529	5.82	0.00	0.00	0.000	5.82
BL	21.49	0	21.49	21.49	0.39	0.296	21.19
BS	14.52	0	14.52	14.52	0.26	0.200	14.32
FI	0.6	0	0.60	0.60	0.01	0.008	0.59
ST	2.28	0.228	2.51	0.00	0.00	0.000	2.51
MT	5.29	0	5.29	5.29	0.10	0.073	5.22
FT	7.36	0	7.36	0.00	0.00	0.000	7.36
LB	6.49	0	6.49	0.00	0.00	0.000	6.49
BN	23.83	0	23.83	0.00	0.00	0.000	23.83
	100.13		100.89	54.88	1.00		100.13
			<b>Difference</b>	0.76			

QTL Scenario Three							
LoinMAX™ QTL							
	Original value	QTL effect	First change			Decrease	Adjusted value
NF	1.87	0	1.87	1.87	0.03	0.039	1.83
F	11.11	0	11.11	11.11	0.20	0.230	10.88
FR	5.29	0.7935	6.08	0.00	0.00	0.000	6.08
BL	21.49	0	21.49	21.49	0.39	0.445	21.05
BS	14.52	0	14.52	14.52	0.26	0.300	14.22
FI	0.6	0	0.60	0.60	0.01	0.012	0.59
ST	2.28	0.342	2.62	0.00	0.00	0.000	2.62
MT	5.29	0	5.29	5.29	0.10	0.109	5.18
FT	7.36	0	7.36	0.00	0.00	0.000	7.36
LB	6.49	0	6.49	0.00	0.00	0.000	6.49
BN	23.83	0	23.83	0.00	0.00	0.000	23.83
	100.13		101.27	54.88	1.00		100.13
			<b>Difference</b>	1.14			

<b>QTL Scenario Four</b>							
<b>LoinMAX™ QTL</b>				20%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0	1.87	1.87	0.03	0.052	1.82
F	11.11	0	11.11	11.11	0.20	0.306	10.80
FR	5.29	1.058	6.35	0.00	0.00	0.000	6.35
BL	21.49	0	21.49	21.49	0.39	0.593	20.90
BS	14.52	0	14.52	14.52	0.26	0.401	14.12
FI	0.6	0	0.60	0.60	0.01	0.017	0.58
ST	2.28	0.456	2.74	0.00	0.00	0.000	2.74
MT	5.29	0	5.29	5.29	0.10	0.146	5.14
FT	7.36	0	7.36	0.00	0.00	0.000	7.36
LB	6.49	0	6.49	0.00	0.00	0.000	6.49
BN	23.83	0	23.83	0.00	0.00	0.000	23.83
	100.13		101.64	54.88	1.00		100.13
			<b>Difference</b>	1.51			

<b>QTL Scenario Five</b>							
<b>Callipyge Gene</b>				15%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0	1.87	1.87	0.03	0.118	1.75
F	11.11	0	11.11	11.11	0.16	0.701	10.41
FR	5.29	0.7935	6.08	0.00	0.00	0.000	6.08
BL	21.49	3.2235	24.71	0.00	0.00	0.000	24.71
BS	14.52	0	14.52	14.52	0.21	0.917	13.60
FI	0.6	0.09	0.69	0.00	0.00	0.000	0.69
ST	2.28	0.342	2.62	0.00	0.00	0.000	2.62
MT	5.29	0	5.29	5.29	0.08	0.334	4.96
FT	7.36	0	7.36	7.36	0.10	0.465	6.90
LB	6.49	0	6.49	6.49	0.09	0.410	6.08
BN	23.83	0	23.83	23.83	0.34	1.504	22.33
	100.13		104.58	70.47	1.00		100.13
			<b>Difference</b>	4.45			

<b>QTL Scenario Six</b>							
<b>Callipyge Gene</b>				20%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0	1.87	1.87	0.03	0.157	1.71
F	11.11	0	11.11	11.11	0.16	0.935	10.17
FR	5.29	1.058	6.35	0.00	0.00	0.000	6.35
BL	21.49	4.298	25.79	0.00	0.00	0.000	25.79
BS	14.52	0	14.52	14.52	0.21	1.222	13.30
FI	0.6	0.12	0.72	0.00	0.00	0.000	0.72
ST	2.28	0.456	2.74	0.00	0.00	0.000	2.74
MT	5.29	0	5.29	5.29	0.08	0.445	4.84
FT	7.36	0	7.36	7.36	0.10	0.620	6.74
LB	6.49	0	6.49	6.49	0.09	0.546	5.94
BN	23.83	0	23.83	23.83	0.34	2.006	21.82
	100.13		106.06	70.47	1.00		100.13
			<b>Difference</b>	5.93			

<b>QTL Scenario Seven</b>							
<b>Callipyge Gene</b>				25%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0	1.87	1.87	0.03	0.197	1.67
F	11.11	0	11.11	11.11	0.16	1.169	9.94
FR	5.29	1.3225	6.61	0.00	0.00	0.000	6.61
BL	21.49	5.3725	26.86	0.00	0.00	0.000	26.86
BS	14.52	0	14.52	14.52	0.21	1.528	12.99
FI	0.6	0.15	0.75	0.00	0.00	0.000	0.75
ST	2.28	0.57	2.85	0.00	0.00	0.000	2.85
MT	5.29	0	5.29	5.29	0.08	0.557	4.73
FT	7.36	0	7.36	7.36	0.10	0.774	6.59
LB	6.49	0	6.49	6.49	0.09	0.683	5.81
BN	23.83	0	23.83	23.83	0.34	2.507	21.32
	100.13		107.55	70.47	1.00		100.13
			<b>Difference</b>	7.41			

<b>QTL Scenario Eight</b>							
<b>Callipyge Gene</b>				30%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0	1.87	1.87	0.03	0.236	1.63
F	11.11	0	11.11	11.11	0.16	1.403	9.71
FR	5.29	1.587	6.88	0.00	0.00	0.000	6.88
BL	21.49	6.447	27.94	0.00	0.00	0.000	27.94
BS	14.52	0	14.52	14.52	0.21	1.833	12.69
FI	0.6	0.18	0.78	0.00	0.00	0.000	0.78
ST	2.28	0.684	2.96	0.00	0.00	0.000	2.96
MT	5.29	0	5.29	5.29	0.08	0.668	4.62
FT	7.36	0	7.36	7.36	0.10	0.929	6.43
LB	6.49	0	6.49	6.49	0.09	0.819	5.67
BN	23.83	0	23.83	23.83	0.34	3.009	20.82
	100.13		109.03	70.47	1.00		100.13
			<b>Difference</b>	8.90			

<b>QTL Scenario Nine</b>							
<b>Myostatin Gene</b>				10%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0.187	2.06	0.00	0.00	0.000	2.06
F	11.11	1.111	12.22	0.00	0.00	0.000	12.22
FR	5.29	0.529	5.82	0.00	0.00	0.000	5.82
BL	21.49	2.149	23.64	0.00	0.00	0.000	23.64
BS	14.52	1.452	15.97	0.00	0.00	0.000	15.97
FI	0.6	0.06	0.66	0.00	0.00	0.000	0.66
ST	2.28	0.228	2.51	0.00	0.00	0.000	2.51
MT	5.29	0.529	5.82	0.00	0.00	0.000	5.82
FT	7.36	0	7.36	7.36	0.20	1.220	6.14
LB	6.49	0	6.49	6.49	0.17	1.076	5.41
BN	23.83	0	23.83	23.83	0.63	3.950	19.88
	100.13		106.38	37.68	1.00		100.13
			<b>Difference</b>	6.25			

<b>QTL Scenario Ten</b>							
<b>Myostatin Gene</b>				15%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0.2805	2.15	0.00	0.00	0.000	2.15
F	11.11	1.6665	12.78	0.00	0.00	0.000	12.78
FR	5.29	0.7935	6.08	0.00	0.00	0.000	6.08
BL	21.49	3.2235	24.71	0.00	0.00	0.000	24.71
BS	14.52	2.178	16.70	0.00	0.00	0.000	16.70
FI	0.6	0.09	0.69	0.00	0.00	0.000	0.69
ST	2.28	0.342	2.62	0.00	0.00	0.000	2.62
MT	5.29	0.7935	6.08	0.00	0.00	0.000	6.08
FT	7.36	0	7.36	7.36	0.20	1.830	5.53
LB	6.49	0	6.49	6.49	0.17	1.613	4.88
BN	23.83	0	23.83	23.83	0.63	5.924	17.91
	100.13		109.50	37.68	1.00		100.13
			<b>Difference</b>	9.37			

<b>QTL Scenario Eleven</b>							
<b>Myostatin Gene</b>				20%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0.374	2.24	0.00	0.00	0.000	2.24
F	11.11	2.222	13.33	0.00	0.00	0.000	13.33
FR	5.29	1.058	6.35	0.00	0.00	0.000	6.35
BL	21.49	4.298	25.79	0.00	0.00	0.000	25.79
BS	14.52	2.904	17.42	0.00	0.00	0.000	17.42
FI	0.6	0.12	0.72	0.00	0.00	0.000	0.72
ST	2.28	0.456	2.74	0.00	0.00	0.000	2.74
MT	5.29	1.058	6.35	0.00	0.00	0.000	6.35
FT	7.36	0	7.36	7.36	0.20	2.440	4.92
LB	6.49	0	6.49	6.49	0.17	2.151	4.34
BN	23.83	0	23.83	23.83	0.63	7.899	15.93
	100.13		112.62	37.68	1.00		100.13
			<b>Difference</b>	12.49			

<b>QTL Scenario Twelve</b>							
<b>Myostatin Gene</b>				25%			
	<b>Original value</b>	<b>QTL effect</b>	<b>First change</b>			<b>Decrease</b>	<b>Adjusted value</b>
NF	1.87	0.4675	2.34	0.00	0.00	0.000	2.34
F	11.11	2.7775	13.89	0.00	0.00	0.000	13.89
FR	5.29	1.3225	6.61	0.00	0.00	0.000	6.61
BL	21.49	5.3725	26.86	0.00	0.00	0.000	26.86
BS	14.52	3.63	18.15	0.00	0.00	0.000	18.15
FI	0.6	0.15	0.75	0.00	0.00	0.000	0.75
ST	2.28	0.57	2.85	0.00	0.00	0.000	2.85
MT	5.29	1.3225	6.61	0.00	0.00	0.000	6.61
FT	7.36	0	7.36	7.36	0.20	3.050	4.31
LB	6.49	0	6.49	6.49	0.17	2.689	3.80
BN	23.83	0	23.83	23.83	0.63	9.874	13.96
	100.13		115.74	37.68	1.00		100.13
			<b>Difference</b>	15.61			