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UTILISATION OF MARKER ASSISTED SELECTION
IN THE NEW ZEALAND DAIRY INDUSTRY

A thesis presented in partial fulfilment of the requirements for the degree of
Master of Agricultural Science
in Animal Breeding and Genetics
at Massey University

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ABSTRACT

The genetic and economic benefits of marker assisted selection (MAS) to the New Zealand dairy industry were evaluated. The genetic marker was assumed to be the additive quantitative trait loci (QTL) itself and thus no recombination existed between the marker and QTL. Three sizes of QTL were evaluated; 0.1, 0.3 and 0.5 genetic standard deviations (σ_G), at three starting QTL frequencies; 0.01, 0.10 and 0.35. Three MAS strategies were evaluated and compared to the current New Zealand breeding scheme that had no genotypic knowledge of the QTL (control). The economic benefits, for the three MAS strategies, were calculated from the returns of extra milk produced, resultant from superior rates of increase in QTL frequency, less the costs of identifying the QTL linked genetic markers and subsequent genotyping.

The size of the QTL had a major effect on the economic viability of the MAS strategies. For a 0.1 σ_G QTL, the most profitable strategy to utilise the QTL was to ignore it and continue with the current breeding scheme. For a single additive QTL of size 0.3 σ_G , it had to be at the 0.35 starting frequency for the MAS strategy of progeny testing only homozygous and heterozygous QTL bulls, to be more profitable than the current breeding scheme. This same MAS strategy at the 0.5 σ_G sized QTL was the most profitable for the range of QTL starting frequencies evaluated.

The MAS strategy where only homozygous QTL bulls were progeny tested, was not economically viable for any of the QTL sizes and frequencies. This was due to the reduced selection differential on the cow to bull and bull to bull pathways. The third MAS strategy investigated utilised the current breeding scheme but included knowledge of the QTL genotype for the active cows and bulls. Superior rates of genetic gain were achieved at all QTL sizes and frequencies, but it was only economically profitable for a 0.5 σ_G QTL with a starting frequency of 0.35. Selection on large QTL with this strategy resulted in short-term genetic gain, but long-term loss. This was due to less selection intensity being applied to the quantitative background, in comparison to the control.

MAS is a long-term selection strategy as the earliest returns from extra milk production, were received ten years after the selection decisions on bulls entering the progeny test system were made. The increase in the QTL frequency was not immediate and thus the benefits of the increased QTL frequency were received in the later years of analysis.

The size and frequency of the QTL have to be ascertained before a decision on how to utilise the QTL can be made. The use of MAS in the present New Zealand breeding scheme may be profitable for a single additive QTL of size $0.5 \sigma_G$, with the degree of profitability being influenced by the starting QTL frequency.

Further study is required on the effect of; dominant QTL, multiple QTL, recombination between marker and QTL, use of multiple ovulation and embryo transfer and the utilisation of MAS in breeding schemes other than those based on progeny testing.

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CHAPTER ONE

INTRODUCTION

Selection for production traits has altered the genotype of domestic animals over time. To date this selection has been based on the phenotype, without a great deal of knowledge of what and how the gene frequency has been altered by this action.

Recent advances in molecular biology and genetics, will enable animal breeders and quantitative geneticists to be in the position of having a better understanding of the locations, sizes, actions and interactions, of major loci that contribute to variation in quantitative traits.

The most recent advance in technology has been the ability to identify regions of deoxyribonucleic acid (DNA) that affect production traits. Identification of DNA regions that affect the performance of the animal relies on DNA polymorphisms being located and amplified. A DNA polymorphism being a piece of DNA that is in a different form to that of another animal's. Amplification of a polymorphism may be undertaken by a procedure called the polymerase chain reaction (PCR).

The polymorphisms, which are called genetic markers, are not likely to be the pieces of DNA that affect animals performance, known as quantitative trait loci (QTL), but they may be linked to them.

The utilisation of genetic markers and phenotypic observations could provide more information on the genetic merit of the animal than phenotypic information alone. Combining marker and phenotypic information is referred to as marker assisted selection (MAS). Marker data may be collected early in the life of the animal, allowing selection at an early age, and in this respect, MAS is similar to juvenile indicator traits (Meuwissen and Van Arendonk, 1992).

Various studies have looked at the use of MAS in animal breeding schemes, (Smith, 1967; Soller, 1978; Smith and Simpson, 1986; Stam, 1986; Kashi et al, 1990; Lande and Thompson, 1990; Massey and Georges, 1992; Meuwissen and Van Arendonk, 1992; Brascamp et al, 1993; Gibson, 1994, Van Arendonk et al, 1994; Van der Beek and Van Arendonk, 1994). The theoretical responses calculated in these studies have varied from minimal improvement in annual genetic gain to selection responses of up to forty percent.

The objective of this study is to evaluate the genetic and economic benefits of MAS in the New Zealand dairy industry. The study will look at using genetic markers within Livestock Improvement's breeding scheme for the Holstein-Friesian breed. The genetic marker is assumed to be the QTL itself. Genetic markers are identified through genotyping and are used in the selection of parents and sampling bulls such that only bulls with the QTL are progeny tested. The rate of genetic gain is measured and compared to a selection programme that has no knowledge of the QTL. The economic benefit is calculated from the returns of extra milk produced, resultant from superior rates of increase in QTL frequency, less the cost of the initial research of identifying the QTL linked genetic markers and subsequent genotyping to identify QTL animals.

CHAPTER TWO

REVIEW OF THE LITERATURE

.1 Introduction

deuwissen and Van Arendonk (1992) described four steps in the development and application of genetic markers to a breeding scheme:

-) Search for genetic markers.
-) Establishment of a linkage map of the markers.
-) Detection of associations between markers and QTL.
-) Use of marker-QTL associations in the breeding scheme.

Each of these steps will be expanded in the following section, after describing the basis of the PCR reaction, common to many modern DNA applications.

2 Polymerase Chain Reaction

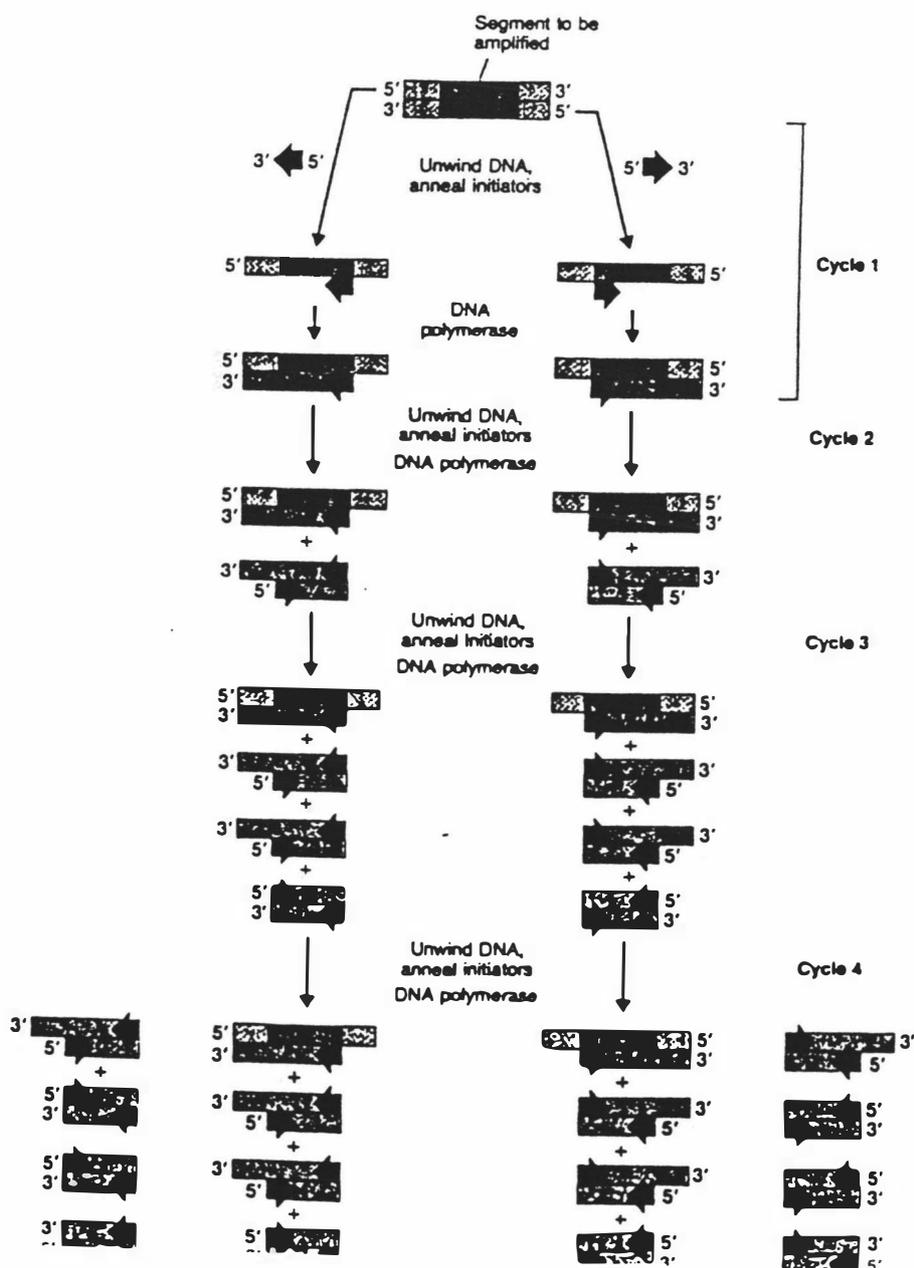
The polymerase chain reaction has become one of the most valuable techniques in molecular biology and underlies most of the advances made in recent years (Williams et al., 1993). This technique is used to make millions of copies of DNA fragments in a matter of hours. The amplification of DNA fragments is often used in the identification of genetic markers. To undertake PCR, a specific sequence of DNA has to be selected to be amplified. Construction of complementary short strands of nucleotides (four building blocks of DNA) that flank either end of the desired sequence is undertaken. These short strands are called primers.

Figure 1 outlines the procedure. The DNA is heated which forces it to denature (unwind from the double helix into single strands) in the presence of a large excess of the two primers. The primers anneal (join) to the DNA and DNA polymerase is added which

tiates DNA replication from the primers. The mixture is heated again for the DNA to separate again and then cooled for the primers to anneal to their complementary sequence and the cycle continues (Benz, 1989).

Initially synthesis will go beyond the sequence complementary to the other primer, as shown in cycle one. In each subsequent cycle the amount of DNA in the region of interest (flanked by each primer) will increase exponentially whilst longer sequences will only accumulate in linear fashion, providing the amount of starting DNA is limiting. This is observed over the four cycles in figure 1. After several cycles the region of interest will be predominant (Taylor, 1991).

Figure 1: Amplifying defined segments of DNA using PCR. (Berg and Singer, 1992)



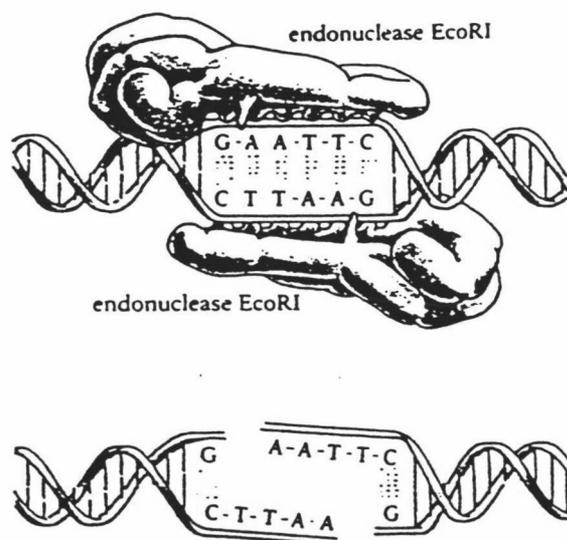
The requirements of the reaction are; deoxynucleotides to provide the energy and nucleotides for DNA synthesis, DNA polymerase, primers and template (DNA of interest), (Benz, 1989).

2.3 Genetic Markers

2.3.1 Restriction Fragment Length Polymorphisms

There are many types of genetic markers. One type is known as restriction fragment length polymorphisms (RFLP's). These are produced when restriction enzymes, which splice DNA (cut the DNA at a specified sequence of nucleotides), reduce the DNA to fragments of different sizes. In figure 2, the endonuclease named EcoRI, identifies and cuts the DNA at the nucleotide sequence of Adenosine (A), Guanine (G).

Figure 2: The action of restriction enzymes. (Keeton and Gould, 1993)



The DNA fragments, which are negatively charged, are placed at one end of a gel and an electrical current is applied. The smaller fragments move faster than the larger ones and thus the DNA pieces are spread out along a narrow path or 'lane' in the gel. The DNA fragments are then transferred to a thin membrane, denatured and exposed to a

radioactive or fluorescent dye. This produces a lane that appears as a series of bands (Lee, 1993). This process is called "Southern blotting".

Two types of DNA variations represent the basis of RFLP's; single base alterations and repeated sequences. In some cases the RFLP has components of both (Feldman, 1990).

The genetic variability of human and animal DNA is low and it has been estimated that one per one hundred base pairs is polymorphic in humans, although only one percent of these are detectable by Southern blot techniques. Only one percent are detected as the variants cannot be separated. The RFLP genetic markers are the most common, but have the disadvantage of being mainly two allele systems. Therefore many individuals will be homozygous, limiting the use of these markers for pedigree and paternity analysis (Edwards and Caskey, 1991; Prokop, 1990).

2.3.2 Variable Number Of Tandem Repeats

In addition to simple polymorphisms detected by the presence or absence of a restriction enzyme cleavage site, variable number of tandem repeats (VNTR's) provide another major source of polymorphic variation. VNTR's are tandemly repeated DNA sequences, characterised by variation in the number of repeat units at a particular chromosomal location. The size of different repeated units varies from a single nucleotide up to tens of nucleotides (Williams et al, 1993).

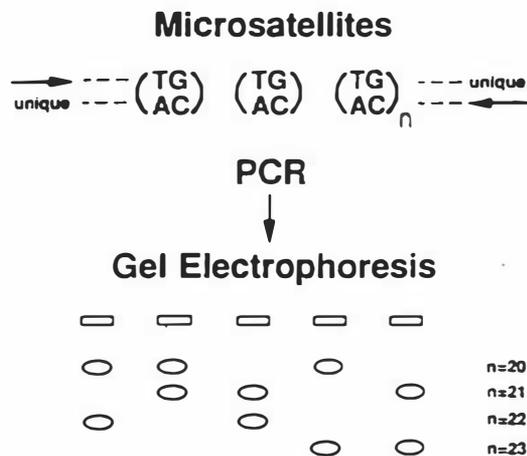
The major advantage of VNTR's (also known as minisatellites), over RFLP's is that VNTR markers show multi-allelic variation. Rather than just two alleles, there is a great variation in the size of each VNTR within the genome of different individuals (Williams et al, 1993). Although VNTR's have increased polymorphism content, VNTR loci have not been found on all chromosome arms and eighty percent of those found are often situated near telomeres (end of the chromosome arm), leaving large regions of the genome out of reach of multiallelic marker loci (Litt, 1991).

2.3.3 Short Tandem Repeats

VNTR's consisting of repeats of 1-4 nucleotides are termed short tandem repeats (STR's) or microsatellites (Williams et al, 1993). The most frequent STR's are dimeric (two nucleotide) [AC] sequences, that are found every twenty to thirty kilobases in genomic DNA. Trimeric (three nucleotides) and tetrameric (four nucleotides) sequences, are found every 300-500 kilobases. Dimeric STR's with greater number of repeats, eg. [AC]₂₀ compared to [AC]₁₀, are more likely to be polymorphic and have higher heterozygote frequency than STR's with few repeats (Edwards and Caskey, 1991).

STR's are detected using PCR as shown in figure 3. The repeats are embedded in unique sequences in genomic DNA. The unique sequences can be used as primers for the PCR to amplify the repeat region. Gel electrophoresis reveals polymorphism in size of the PCR product, a function of the number of times that the motif is repeated (Womack, 1993).

Figure 3: Microsatellite analysis. (Womack, 1993)



One problem with dimeric STR's, when interpreting the banding locus with microsatellites, is the two base pair ladder effect seen after gel electrophoresis from insertion or deletion of one of the repeats. With an incomplete PCR reaction, the difference may be only one base pair, which can make identification of an allele at a particular locus difficult. It is less of a problem with trimeric and tetrameric sequences

(Edwards and Caskey, 1991). Individual alleles are therefore sometimes pooled into 'buckets', each bucket representing a range in the number of repeats.

The total number of STR's in the genome is thought to be in orders of magnitude higher than that of minisatellites, and they appear to be distributed randomly across the genome unlike longer sequence VNTR markers (Williams et al, 1993).

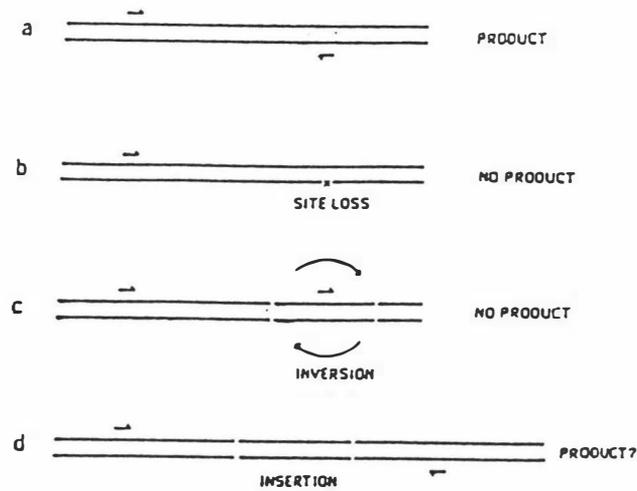
The relative ease that STR's can be amplified, the potential for sequence based allelic identification and high heterozygosity, makes them good genetic markers. With the higher numbers and increased precision of identification, their use will be widespread (Edwards and Caskey, 1991).

2.3.4 Randomly Amplified Polymorphic DNA

Another class of marker, which is being used in *pinus radiata* breeding programmes in New Zealand, is based on a modified form of the PCR being used to amplify a region of genomic DNA. Randomly Amplified Polymorphic DNA (RAPD) markers result from a variant type of PCR, using shorter primers of arbitrary sequence, usually 8-10 bases in size and 50-80 percent Guanine and Cytosine. The rationale for the RAPD procedure is that within the genome, there is a certain distribution of annealing sites for any single, arbitrary primer. The distribution is thought to result mainly from chance (Anderson, 1993).

Theoretically, the number of amplified fragments generated by PCR depends on the length of the primer and the size of the target genome. RAPD's are based on the probability that a given DNA sequence (complementary to that of the primer) will occur in the genome, on opposite DNA strands, in opposite orientation within a distance that is readily amplifiable by PCR (figure 4), (Waugh and Powell, 1992).

Figure 4: Polymorphisms in a genomic region of four haploid individuals that result in the loss of a RAPD product. (Anderson, 1993)



The products are easily separated by standard electrophoretic techniques and do not require Southern blotting or radioactive probes (Anderson, 1993).

The DNA quality can be lower for RAPD's, in contrast to the relatively pure DNA needed for RFLP's, VNTR's and STR's. Other advantages for RAPD's are that they do not need radioactive isotopes and the probes are random nine or ten primer nucleotides compared to the species specific complementary DNA clones needed for RFLP, VNTR and STR work.

The use of RAPD's enables the identification and application of the marker in one step, whereas when using RFLP's, VNTR's and STR's, the markers need to be identified first and then applied. Therefore in the short-term, RAPD's are a quicker technique, but once the RFLP, VNTR or STR marker has been identified, there is no difference in speed of application between the different markers.

The major disadvantage of RAPD analysis, is that reactions can be extremely sensitive to conditions such as the concentrations of reaction components, contaminants in the target DNA preparation, enzyme source, and especially the temperature cycling profile (Waugh and Powell, 1992). Great care must be taken to show that the RAPD markers

are repeatable in fully independent experiments. Given proper controls, the RAPD technique can be extremely powerful (Anderson, 1993).

The genetic markers are thought to be in areas that are 'silent' phenotypically, though some no doubt affect gene regulation in various subtle ways, thereby contributing to quantitative variation in the phenotype. The important role of these DNA polymorphisms in quantitative genetics is to provide markers for the mapping of the QTL, but a few of them could be QTL themselves (Fincham, 1994).

2.4 Genetic Maps

There are two types of genome maps; physical maps and linkage maps. Physical maps are derived mainly from chemical measurements made on the DNA molecules that form the genome. Genetic linkage maps describe the arrangements of genes and DNA markers on the basis of the pattern of their inheritance (National Research Council, 1988).

2.4.1 Physical Maps

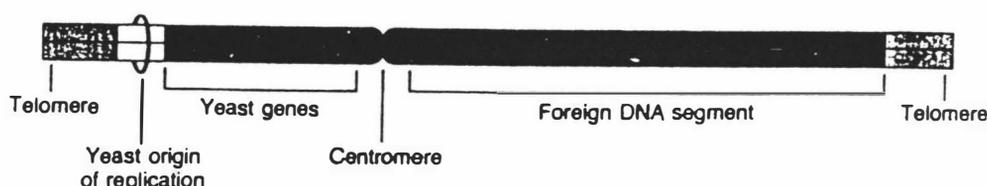
Mapping can be facilitated by making a recombinant DNA library (a collection of DNA fragments cloned from a particular organism) with the DNA from an isolated chromosome (Fincham, 1994). Physical maps of the cloned segments can then be made. Clones that contain overlapping segments of the chromosome's DNA can be used to reconstruct the order of the cloned regions on the chromosomes (Berg and Singer, 1992).

Cloning systems using bacterial plasmids or phage vectors, known as bacterial artificial chromosomes (BAC's), have the limitations of; the upper limit of the clone being 40 kilobases (kb) and the occurrence of uncloned regions at an average distance of every 100-200 kb. Because of these two deficiencies, overlapping clones require a number of walking steps to achieve as much as 200 kb of coverage and rarely extended much further before encountering a gap (Schlessinger and Kere, 1992). With the bovine

genome being in the order of three billion kb, the formation of a physical map would be a labour intensive exercise.

Using recombinant DNA methods, DNA molecules have been constructed that contain a yeast centromere segment, an origin of replication functional in yeast, a few yeast genes and the yeast telomeric segments at the ends (figure 5). When introduced into yeast cells, these molecules behave like normal chromosomes in mitosis and meiosis. The constructions are yeast artificial chromosomes (YAC's), (Berg and Singer, 1992).

Figure 5: Yeast artificial chromosome. (Berg and Singer, 1992)



Yeast artificial chromosomes can hold up to twenty times more foreign DNA than the largest BAC's and have been proven to clone more than ninety-nine percent of human DNA in a number of regions (Schlessinger and Kere, 1992). Thus, YAC's have become an important host vector system for cloning large regions of the genome (Berg and Singer, 1992).

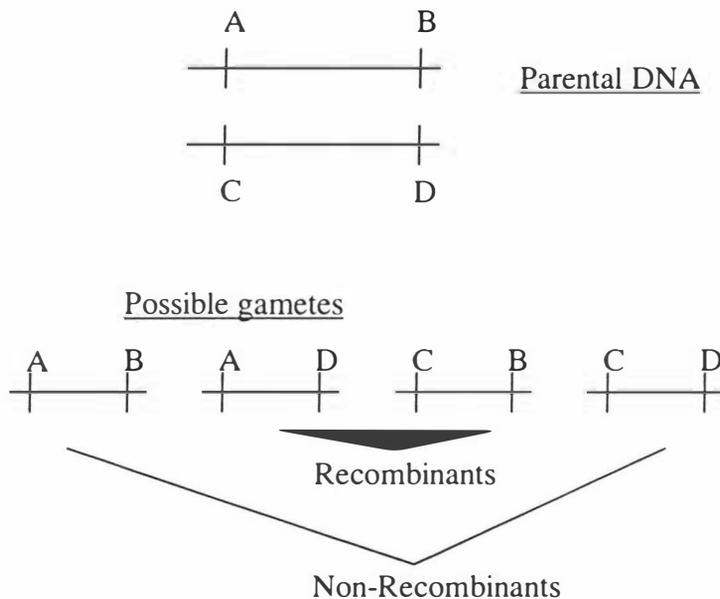
2.4.2 Linkage Maps

Genes that are inherited together (ie. linked) are close together on linkage maps and those inherited independently are distant (eg. different chromosomes). Genes on the same chromosome can be tightly linked, loosely linked or unlinked, presumably depending on their proximity.

If the loci are far apart on the same chromosome, a cross-over between the two is very likely; the traits will occur separately in each of the recombinants but together in the non-recombinants (Connor and Ferguson-Smith, 1993). In figure 6, the two copies (strands) of parental DNA are heterozygous at the two loci. At the first loci there are two alleles, A and C and at the second loci, B and D. In sexual reproduction only one copy of the parental DNA is passed on to the offspring. The single copy is termed

gametic DNA, which is formed in a process called meiosis. In figure 6, there are four possible gametes from the parental DNA, with respect to the two loci. When recombination is rare, as may occur when the loci are close together, the gametes will predominantly be non-recombinants.

Figure 6: Recombinants and Non-recombinants.



The relationship between the recombination fraction and the actual physical distance between loci, depends upon several factors. A recombination fraction of ten percent corresponds approximately to a map distance of 10 centimorgans (cM), but with increasing distance apart, the apparent recombination fraction falls due to occurrence of double cross-overs. The measurement of recombination rates between markers, can be used to identify the order and distance between markers and thus allow construction of a linkage map.

The total bovine map is thought to be in the vicinity of 2500-3000 cM (on average 1cM equals 1Mb). In practice it is difficult to detect linkages between loci more than 25 cM apart and thus the construction of a bovine linkage map requires a minimum of 100 well-spaced polymorphic markers (Womack, 1993).

Genetic linkage maps use RFLP's, VNTR's and STR's in their construction. Heterozygosity allows genes to be tracked through families and enables the detection of linkage. An 'ideal' genetic marker is one that exists in so many distinct forms that every individual is heterozygous and unrelated individuals are heterozygous for different forms. The marker can then be traced unambiguously from grandparent to parent to offspring in all families, allowing the inheritance of linked genes in the family to be traced accurately and efficiently. The markers that come closest to the 'ideal' are the STR's (microsatellites).

Genetic linkage maps allow those genes with no known cellular or molecular effects to be located on the genome, whereas physical maps describe the DNA molecules in chromosomes. RFLP, VNTR and STR markers can be placed on genetic linkage maps and they are also DNA molecules and thus their position on the map can be determined. This allows the partial alignment of physical and genetic linkage maps.

Chromosomal maps are sufficiently developed to identify chromosomal conservation with other mammals, which is especially useful for the extrapolation of data to cattle from the better developed maps of mice and humans (Womack, 1993).

2.5 Associations Between Markers and QTL

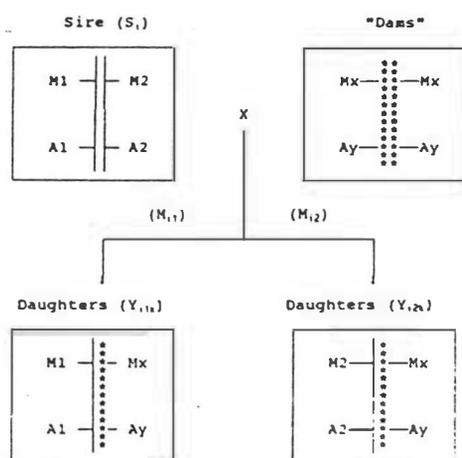
Mapping of QTL by means of genetic markers is based on the expectation that if an individual is heterozygous at a marker locus and a linked QTL, then recombination excepted, progeny receiving a particular marker allele will also tend to receive the linked QTL allele. Consequently when progeny are grouped according to the marker allele received from the heterozygous parent, the presence of alternative alleles at the linked QTL will tend to generate a difference in mean quantitative value between the two progeny groups. Conversely, a significant difference in mean quantitative value of the progeny groups, receiving alternative marker alleles from their common parent, will be indicative of the presence of a linked QTL near the marker (Weller et al, 1990).

The genotyping of a segment of the population to identify marker-QTL associations may be undertaken in various experimental settings including the so-called 'daughter' or 'granddaughter' designs.

a) Daughter design

This design is based upon daughters of sires heterozygous for markers being genotyped for the markers and evaluated for the quantitative traits of interest (figure 7). M1 and M2 are marker alleles from the sire and Mx the marker allele from the dams. The QTL alleles for the sire are A1 and A2 and the QTL allele for the dam is Ay. The sire markers are traced to his daughters and recombination excepted, the daughters will receive linked QTL. In simplified terms, a test of significance is undertaken on the mean quantitative values (Y_{i1k} and Y_{i2k}), for the two marker daughter groups. If a significant difference exists, this indicates the presence of a linked QTL near the marker (Weller et al, 1990).

Figure 7: Daughter design. (Weller et al, 1990)

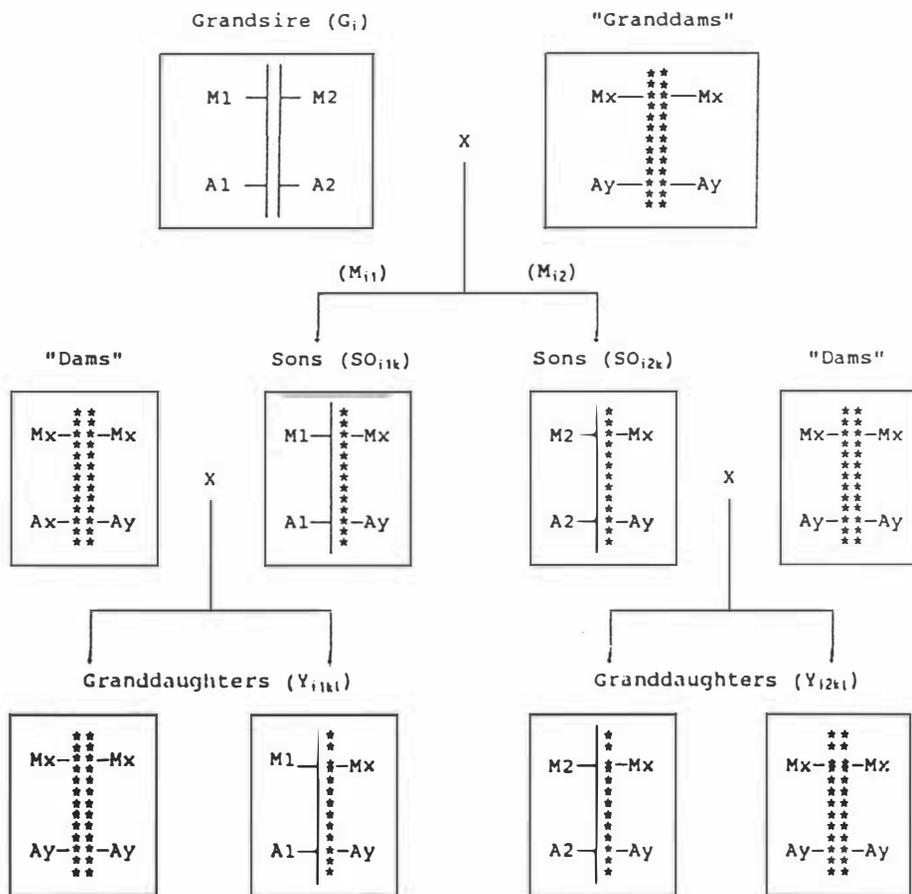


It is possible to test for the presence of a QTL linkage in the offspring of a single sire, but in many cases, it is useful to pool data across a number of sires. This will be desirable, in order to increase the power of the experiment, in cases where there are only a limited number of daughters per sire. Also, in a segregating population a sire may be heterozygous for a marker but not heterozygous for the linked QTL (Weller et al, 1990).

b) Granddaughter design

The granddaughter design involves genotyping a number of sons of a heterozygous sire and evaluating the granddaughters for the quantitative trait (figure 8). The heterozygous sire in this design is termed 'grandsire', his sons are termed 'sons' and the daughters of the sons termed 'granddaughters'. M1 and M2 are marker alleles from the grandsire and Mx the marker alleles from the granddams and dams. A1 and A2 are the QTL alleles from the grandsire and Ay the QTL from granddams and dams. In this design the marker associated effects are half those measured in the daughter generation (Weller et al, 1990).

Figure 8: Granddaughter design. (Weller et al, 1990)



Another method is the mapping of polygenic sources of variation, eg. protein yield. Polygenically or quantitatively determined sources of variation are characterised by continuous range of variation. Thus members at the extreme of the distribution, eg. high

and low protein yields, are expected to differ at most of the loci controlling protein yield. These genotypes are likely to be the most informative since the alleles (increasing and decreasing) are expected to be highly associative. Bulk samples comprising the extreme members of the distribution may be screened with markers. The objective is to find markers that are present in the high yield group but not in the low yield group and vice versa (Waugh and Powell, 1992).

It has been advocated by Smith and Smith (1993), that once an association has been identified there should be a direct search for DNA markers closer to the QTL. With a close linkage, selection on the QTL will be able to be across the population rather than only within specific families. A YAC library will facilitate such a search.

Once the linked markers have been identified, they can be used in a breeding scheme. It is generally thought that MAS will not replace the traditional approaches of phenotypic measurements, but will be integrated with them to increase the rate of improvement. Two reasons for this are:

a) Although there may be loci with large effects, the majority of the genetic variance may be controlled by many genes with small effects. It is too difficult for these small genes to be mapped, therefore traditional methods, such as progeny testing, will be needed to identify the effect of these genes.

b) Single genes of large effects may have deleterious pleiotropic effects or be tightly linked to another gene with detrimental effects. This has been seen with the Weaver gene in the Brown Swiss dairy cattle breed. This gene is associated with extra milk production but also with a condition that affects the animal's nervous system. Monitoring of the offspring's phenotype will have to continue (Lande and Thompson, 1990).

2.6 Genetic And Economic Responses To MAS

Smith (1967), reported that known genetic loci, ones that can be typed, may be useful in livestock improvement when normal selection methods are not very effective, such as low heritability or when indirect selection on relatives is necessary. The increased response due to the known loci, depends on the proportion of the additive variance that is due to the known loci relative to heritability of the trait concerned and on the form of selection practised. Soller (1978), stated that if known loci affecting milk production could be found, using the information on selection of young males before entry into progeny testing would be the area where it could have an effect on genetic gain.

Soller and Beckmann (1982), evaluated the gains in response from pre-selection of dairy progeny test bulls using QTL via MAS. The gains over conventional progeny testing were 46 percent for direct selection on 20 identified QTL (which accounted for half the genetic variance in milk yield) and 15 and 8 percent respectively for MAS with 30 QTL loci (accounting for 0.75 of the genetic variance and with zero and 10 percent crossing over respectively). Stam (1986), looked at the theoretical ideal circumstances for MAS sib-selection and found that the expected gain in selection response is approximately forty percent. Smith and Simpson (1986), reported factors that reduce effectiveness of MAS of progeny test bulls. The main factors were the effect of recombination between marker and QTL, and homozygosity at the marker locus which limits possibilities for identifying marker alleles. They also raised the difficulty of tracing specific marker alleles from sire to progeny. However, the use of closely linked groups of markers (haplotypes) can be traced between generations more effectively than single markers.

Kashi et al (1990), also looked at the gains from pre-selection of progeny test bulls with the markers identified in a daughter design. They reported that MAS based on the use of a single diallelic marker in linkage to a QTL will only have a negligible effect on the rate of genetic progress. However, increases of 15 to 20 percent in the rate of genetic gain can be obtained by the use of single polyallelic markers, and increases of 20 to 30 percent can be obtained by utilising haplotypes of diallelic or polyallelic markers.

Meuwissen and Van Arendonk (1992), studied the effects of inclusion of marker information in the estimation of the breeding value in both progeny testing and multiple ovulation and embryo transfer nucleus breeding schemes. It was found that prediction of within-family deviations accounted for by markers, hardly improved rates of genetic gain in conventional progeny testing due to a considerable amount of the within-family variances being explained by individual or progeny performance. However, in the nucleus schemes, in which selection is mainly on pedigree and sib performance the genetic gain was improved by up to twenty five percent. The difference in responses for MAS in progeny testing between Kashi et al (1990), and Meuwissen and Van Arendonk (1992), are due to Kashi et al (1990) using a fixed number of bulls entering the progeny test compared to Meuwissen and Van Arendonk (1992) who had the number of bulls born annually restricted. In addition, Brascamp et al (1993) noted that Kashi et al (1990) assumed incorrectly that the accuracy of estimated breeding values of young bulls was zero without marker information.

Brascamp et al (1993), evaluated the benefits of MAS on the basis of increased milk production and increased semen sales if a breeding organisation used MAS for twenty years and its competitors did not. The returns from the use of MAS in an open nucleus scheme were greater than those from conventional progeny testing. The returns from increased semen sales to an organisation were found to be substantial.

2.7 New Zealand Dairy Breeding Scheme

In the 1992-93 season there were 237 dairy bulls progeny tested in New Zealand; 157 Holstein-Friesian bulls, 68 Jersey, 7 Ayrshire and 5 from other breeds (Livestock Improvement, 1994). Approximately seventy percent of the bulls were progeny tested by Livestock Improvement.

Livestock Improvement annually progeny tests approximately 95 Holstein-Friesian bulls, 55 Jersey bulls and 8 Ayrshires. A review undertaken by Livestock Improvement has recommended that from 1996, the target number of bulls to be progeny tested increase by approximately fifty percent.

The process of a bull being progeny tested begins with the selection of the top 'active cows' ranked on aggregate economic merit. An active cow in New Zealand is currently defined as being one that has three generations of identified artificial breeding to one breed (at least seven-eighths pure-bred), and is being herd-tested. The top ranked cows are inspected by staff and representatives of Livestock Improvement for conformation. The cows that don't meet the conformation criteria are rejected and take no further place in the breeding of progeny test bulls. The elite cows are then contracted by Livestock Improvement to be mated to the elite bulls.

The bulls used by Livestock Improvement to sire the next crop of bulls may have been bred in New Zealand or overseas. The New Zealand bulls are selected on their assessed total merit and the overseas bull on conversion breeding indexes. Predominantly two New Zealand bulls are used as sires of sons with a group of overseas bulls being classed as the 'third bull'. A group of overseas bulls are used in preference to one bull, as the conversion breeding indexes have low reliabilities, and thus using a team of bulls increases the reliability of the 'third bull'.

The resulting offspring of the contract matings make up approximately fifty percent of the bulls to be progeny tested. The balance is made up of bulls that result from imported embryos, bulls from active cows that have moved into the elite bracket and are already in-calf to elite bulls, and a small number of bulls that are nominated by the respective breed associations.

The bulls are randomly mated as yearlings to produce offspring for progeny test. The progeny testing of the bulls takes place in approximately four hundred herds, dispersed through-out New Zealand. These herds are contracted to Livestock Improvement. At least eighty percent of the herd or eighty cows, whichever is the greater, must be mated to the progeny test bulls. These herds comprise the Sire Proving Scheme (SPS). The liquid semen from the SPS bulls is distributed at random in the progeny test herds, with the Holstein-Friesian bulls predominantly being mated to Holstein-Friesian cows and likewise for the other breeds. The scheme aims to produce eighty five, sixty and fifty daughters in milk per Holstein-Friesian, Jersey and Ayrshire bull respectively. This is

achieved by inseminating approximately six cows to produce each two year old daughter in milk.

The bulls are retained until their daughters have completed their first lactation as a two year old. The SPS daughters are herd tested at least four times in their first lactation; farmer assessed for milking speed, temperament and acceptability; and assessed by representatives of the breed associations for conformation traits. These phenotypic observations are used in the calculation of the breeding indexes. Approximately ten percent of the bulls are retained for further use. Of the ten percent retained, approximately half of them are used on a widespread basis. The bulls can be utilised in a team of proven bulls known as Premier Sires or the farmer(s) can nominate the bull(s) they want to use. The proven bulls are retained in Premier Sires for up to three years until superseded by the next crop of bulls. The bulls in Premier Sires have liquid semen distributed and therefore an individual can have over 250,000 inseminations per year. Bulls used for nominated matings are distributed via deep frozen semen.

2.8 Measurement of Genetic Gain

Genetic gain can be predicted by calculating the theoretical response in the four pathways as demonstrated by Rendel and Robertson (1950):

$$\Delta G = \frac{I_{cc} + I_{cb} + I_{bb} + I_{bc}}{L_{cc} + L_{cb} + L_{bb} + L_{bc}} \quad [1]$$

where I is the estimated genetic superiority of the selected animals over their contemporaries in the base group born in the same year, and L is the average age of the selected animals when their offspring were born (Van Tassell and Van Vleck, 1991). These parameters are separately estimated for the four pathways; bull to bull pathway (bb), bull to cow pathway (bc), cow to cow pathway (cc) and cow to bull pathway (cb).

The estimated genetic superiority (I) is calculated as:

$$I = r_{\hat{g}g} i \sigma_G \quad [2]$$

where $r_{\hat{g}g}$ is the accuracy of evaluation (reliability figures published by Livestock Improvement are $r_{\hat{g}g}^2$), i is the selection intensity and σ_G is the genetic standard deviation (Van Vleck et al, 1987).

Rendel and Robertson's (1950) equation calculates an asymptotic rate of genetic gain for the stated conditions. When short term gain is of interest, the asymptotic genetic gain may be inadequate for comparisons of breeding plans (Ducrocq and Quaas, 1988). In the first few years of initialising a new breeding plan there can be fluctuations in selection response. Ducrocq and Quaas (1988) used the genetic merit of the newly born females to calculate the yearly genetic gain and found that fluctuations of the yearly genetic gain of the newborn females around the asymptotic value, do not stabilise before twenty to thirty years of repeated and identical selection in cattle.

CHAPTER THREE

BREEDING SCHEME MODEL

3.1 Introduction

A deterministic simulation model was programmed using a computer software package called; A Programmers Language (APL, 1982). The model was based around bull and cow populations from which animals were selected.

3.2 Bull and Cow Populations

The simulation was based on the New Zealand Holstein-Friesian population. The bull population comprised 140 bulls to be progeny tested as yearlings and receiving their proofs as five year olds. Eighty-five daughters were generated per bull. The loss rate for the bull population was two percent (three bulls) per year.

The active cow population was estimated to be 200,000 for the 1994/95 season by extrapolating two years from the data presented in the Macdonald Committee Report (1992). The active cow population from the Macdonald Committee Report (1992), was assumed to be for cows aged two years and older. The active cow population for the simulation model includes animals aged between two and seven years old. The population size for the model was 169,000 (Appendix I). The number of cows in each age group was calculated from the age structure of 1.5 million herd tested cows as presented by Livestock Improvement (1994). Population figures were also established for heifer calves and yearlings (Appendix I).

3.3 Selection of Animals

Selection of animals for the four pathways was undertaken by truncation of sub-populations based on normal distribution theory:

a) Cow to cow pathway

It was assumed that no selection took place in the choice of cows to breed cows. The age structure of the cow population was assumed to be identical to that of the active cow population. In practice this was not correct as animals older than seven years of age are used as cow dams. The effect of this was that the generation interval for this pathway was under-estimated and the mean parental cow breeding value was over-estimated, but this would have little effect on the results as it was the same in all scenarios. It was also assumed that thirty-five percent of the yearling heifers were artificially mated and replacements were kept from them.

b) Cow to bull pathway

It takes on average, 3.25 cows to breed each progeny test bull (Appendix II). To generate the required 140 bulls, 455 cows are required to be contracted mated. Selection was among all active cows with lactation records. It was assumed that all bulls progeny tested were the result of contract matings. The active cow population size and age structure were kept stable over time.

It was assumed that the cows selected had the progeny test bulls the year after selection. In reality, the animals selected for contract mating have contract calves two years later, for example, cow selected as two year old, contract mated as three year old and the contract calf born when four year old. However, not all of the progeny test bulls are generated through contract mating. Some of the cows at the time of selection are already in calf to elite sires and thus a prospective progeny test bull is born a year later. In addition, yearling heifers are selected, whereas they were not in this study. In practice the interval between selection and progeny test bull born is probably between one and two years. For modelling ease the interval was taken as one year and therefore, the generation interval for the cow to bull pathway was under-estimated.

) Bull to cow pathway

Ten proven bulls were selected each year. Bulls were eligible for selection in the first three years after receiving a progeny test proof. Selection was only from bulls that were alive at time of proof.

f) Bull to bull pathway

Three proven bulls were selected each year. Bulls were eligible for selection in their first two years after receiving a progeny test proof. Although there were bull losses while the bulls awaited proof, selection was from the initial 140 bulls as enough deep frozen semen was retained from each bull to generate sons.

Selection was assumed to be on an index of pedigree and performance records combined using selection index techniques, conforming to the additive infinitesimal model. The breeding values were assumed to be normally distributed. Selection of animals from the four pathways would ideally take place on true breeding value, with the best being selected. However, the true breeding values were unknown and therefore selection was on estimated breeding values (EBV's), calculated from phenotypic records.

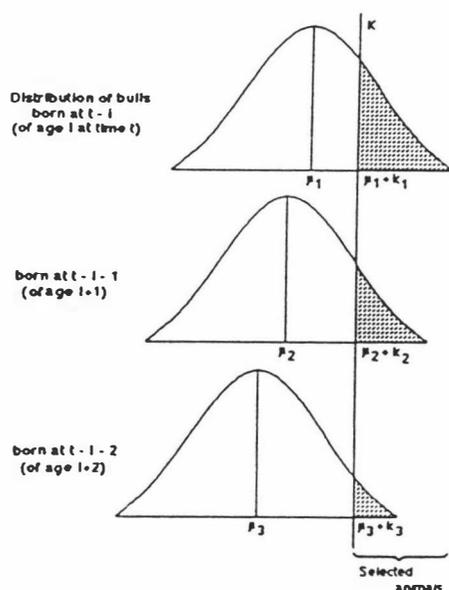
Where all adults have a single strictly limited period of reproduction, and are replaced by their offspring, the generations remain quite distinct in the population. When reproduction in one or both sexes continues for a long period relative to the age at first breeding, then the generations will no longer remain discrete, but will overlap (Richard et al, 1973). When generations overlap, the estimated genetic merit of potential candidates for selection cannot be considered as belonging to a distinct distribution, if genetic trend exists in the population, and if the precision of the evaluation increases as a candidate gets older (Ducrocq and Quaas, 1988).

The means between the different age groups in both the cow and bull population differ by the rate of genetic gain for those years (figure 9). The variance of the EBV's for the age groups increase as the animals get more records:

$$\sigma_{EBV}^2 = r_{gg}^2 \sigma_G^2 \quad - \quad [3]$$

where r_{gg}^2 is the square of the accuracy of evaluation and σ_G^2 is additive genetic variance (Bichard et al, 1973). For convenience, the simulation was based on a genetic variance standardised to unity.

Figure 9: Selection across age groups. (Ducrocq and Quaas, 1988)



Selection is performed by truncation (figure 9), with the truncation point chosen so that the animals represented at the right hand side of the populations, truncating across all age groups, are as required. All active animals, whatever their age, whose genetic evaluation is larger than the unique threshold K are selected. Therefore the probability of an animal being selected depends on the mean and variance of its evaluation (Ducrocq and Quaas, 1988).

Given the truncation point, the number of animals, selection superiority and mean EBV of the animals selected from each age group can be ascertained. Generation interval and the afore-mentioned parameters can then be calculated for the overall population.

Truncation selection was undertaken for all of the pathways with the exception of the cow to cow, for which all animals were selected.

The expected (true) breeding value of the selected group was taken to be the mean EBV, as it was assumed that the prediction error variance was random with mean zero. Thus the true mean breeding value of the male and female offspring was calculated from the mean EBV's of the parents.

Once the mean breeding values of the progeny were calculated, the population EBV means moved down an age group, ie. the five year olds became six year olds, the seven year olds dropped out of the population and the new crop of animals joined the population. Selection on the population (one year older) took place, and the above procedure was re-iterated.

3.4 Calculation of r_{gg}

The r_{TI} 's for the bulls were calculated from combining ancestry information and information from daughters progeny tested using selection index principles. Likewise for cows, ancestry and lactation records were combined in the same method.

The ancestry r_{gg} for a bull calf born from a selected proven bull and a selected cow was calculated as follows (Van Vleck et al, 1987):

$$r_{gg} \text{ calf} = \frac{1}{4} (r_{gg} \text{ sire} + r_{gg} \text{ cow}) \quad [4]$$

The sires were selected from the population of live proven bulls. The variance and r_{gg} of the selected sires was less than that for the population. The cows were selected from

the active cow population and also exhibited less variation as a group in comparison to the cow population. The variance of the selected groups was calculated as:

$$\sigma^2 (1 - i(i - t)) \quad [5]$$

where σ^2 is the population variance, i is the selection intensity and t is the truncation point.

From equation [5] the r_{gg} of the selected sires and cows were calculated to be 0.08 and 0.12 respectively. Therefore using equation [4], the r_{gg} of the male offspring was 0.05. If the r_{gg} for the bull and cow populations were used (0.92 and 0.62), the r_{gg} for the group of bull calves would be approximately 0.4. This implies that if selection took place on the yearling bulls, there would be sufficient variance of EBV's to select the best bulls within this group. This is incorrect in practice as the EBV's of bulls entering progeny test have very little variance and thus scope for selection, as shown in the calculated r_{gg} of 0.05.

Consider the population of heifer calves whose sires were selected, but whose dams were not and thus showed the full population variance. The r_{gg} for the heifer calves, using equation [4] and 0.08 for the sire r_{gg} and 0.62 for the dam r_{gg} , was 0.18.

This ancestry r_{gg} component was combined with progeny test information for the bulls and lactation records for the cows using selection index procedures to calculate the r_{gg} for each age group (Appendix I).

3.5 Setting up starting values for the populations

The simulation model was run for sixty years in order to generate the situation where the population had been under the influence of selection for a long time and the rate of genetic gain was stable. The population EBV means generated from this simulation were used as the starting values for the QTL analysis and show an asymptotic genetic gain of $0.29 \sigma_G$ per year (Appendix I).

3.6 Inclusion of a QTL

A single bi-allelic locus with pre-defined genotype effects was added to the additive infinitesimal model which increased the genetic variance to σ^2_G plus the QTL effect. It was assumed that the QTL was detectable by DNA-based tests, ie. the marker for the QTL was the QTL itself, such that no recombination could occur between the marker and the QTL. Thus selection for the favourable marker allele always resulted in selection for the favourable QTL allele. This is not the case in reality, where the genetic marker is usually tightly linked to the QTL and therefore selection for the favourable marker allele does not always result in the selection of the favourable QTL. The genetic marker being the QTL meant that the degree of association between the QTL and marker was the same for all sire-families. This again is not the case in reality, where it has been found that marker-QTL associations can be family specific. This assumption had the effect of over-estimating the QTL response from MAS.

3.6.1 Cow and Bull Populations

The presence of the QTL in the cow and bull populations meant that the respective populations were split into three; homozygous QTL (QQ), heterozygous QTL (Q+) and homozygous normal (++). The starting gene frequency of the QTL determined the number of animals that were in the three sub-populations, as determined by Hardy-Weinberg laws:

$$p + q = 1 \quad [6]$$

where p is the gene frequency of the QTL. Thus the frequency of the QQ sub-population was p^2 , Q+ sub-population $2pq$ and the ++ sub-population q^2 . It is unlikely in practice that the QTL would be in Hardy-Weinberg equilibrium as selection for the traits that included the 'introduced' QTL would result in the QTL genotype frequency departing from Hardy-Weinberg equilibrium.

3.6.2 QTL effect

The action of the QTL was additive, with the size of the QTL, measured in genetic standard deviations, being the difference between the two homozygotes. The QTL had

the effect of increasing the mean of the sub-populations that contained the QTL but had no effect on the r_{gg} .

The effect of the QTL on the mean of each sub-population depended on whether the animals had been genotyped. If they had, the mean of the sub-population increased by the pre-defined homozygous or heterozygous QTL effect. Where the animal had not been genotyped, the QTL was expressed in the phenotypic records of progeny test daughters for a bull, or lactation records for a cow. By the QTL being expressed in the phenotypic records, the QTL was also expressed in the animal's EBV, but in a regressed manner. The amount expressed in the EBV was calculated in the following manner.

If the QTL effect was σ_G then the phenotypic effect was also σ_G , as the environmental effects were taken to be random with mean zero. The heritability (h^2) of the index was assumed to be 0.25 and the square root of the heritability (0.5) being equal to:

$$h = \frac{\sigma_G}{\sigma_P} \quad [7]$$

where σ_P is the phenotypic standard deviation and h is the square root of the heritability.

By σ_G being set to one, equation [7] becomes:

$$0.5 = \frac{1}{\sigma_P} \quad [8]$$

and thus σ_P is equal to two, twice σ_G . Therefore if an animal has a QTL that has the effect of increasing production by one genetic standard deviation, for example fifteen kilograms, the phenotypic effect will also be an increase of fifteen kilograms, which is half a phenotypic standard deviation.

For an animal being QQ compared to another animal that is of the same genetic merit, except that the animal is ++ for the QTL, the difference in their production figures

for this example (with QTL size being σ_G) will be fifteen kilograms. The estimated breeding value difference between the two animals, based on one lactation record will be:

$$\text{EBV diff} = 0.25 \times 15 = 3.75 \text{ kg} \quad [9]$$

which is equivalent to:

$$\text{EBV diff} = h^2 \frac{1}{2} \sigma_P \quad [10]$$

being the h^2 multiplied by the QTL effect. This is equivalent to the selection index weighting factor multiplied by the QTL effect where the selection index weighting factor (b) for a cow is:

$$b = kh^2/[1+(k-1)r] \quad [11]$$

where k is the number of lactation records and r is the repeatability of the trait.

The selection index weighting factor (b) for a bull based on daughters performance is:

$$b = \frac{1}{2}nh^2/[1+(n-1)r] \quad [12]$$

where n is the number of daughters in the bull's progeny test.

This holds true for k lactation records and for a sire with n progeny. Thus as the cows or bulls got more records, more of the QTL effect was expressed in their EBV's.

Therefore the difference between the EBV means for QQ sub-population and ++ sub-population was the full QTL effect for genotyped animals and that expressed in the EBV for non-genotyped animals.

3.6.3 Selection of animals

Selection was undertaken by truncation across the sub-populations of eligible age groups. As previously explained the mean EBV of the animals selected was calculated and this was expected to be the average true breeding value. However, this did not hold true with the introduction of the QTL. When a QQ or Q+ animal was selected on EBV, its EBV was biased, as not all of the QTL was being accounted for and therefore the true genetic merit of the animal was under-estimated. Thus the part of the QTL that had not been accounted for in the EBV, had to be added on to the mean EBV of the selected animals. This was achieved through the following equation:

$$\text{QTL effect unaccounted} = (1 - \text{selection index weighting factor}) \times \text{QTL effect} \quad [13]$$

The deterministic model selected fraction of animals, eg. 34.35 QQ cows. This obviously is impractical. Using fraction of animals smoothed the rate of genetic gain out over time as it assumed, for example, that 0.2 of a QQ bull was used per year over five years, instead of one QQ bull in one of the five years. Monte Carlo simulations could have been undertaken to derive 'whole animals' for the pathways.

3.6.4 Progeny means

The mean progeny breeding value was calculated from the average of the selected parental means. The parental means contained some of the QTL effect. Equation [10] did not hold for the progeny, as they already had some of the QTL expressed in their EBV's (ancestral). Thus a new weighting had to be calculated to combine the ancestral QTL component and that expressed in the records. The new weighting factors depended on how much of the QTL was contained in the ancestry component. To avoid calculating new weighting factors for each iteration, it was decided that ancestral QTL effects would be ignored and not included in the ancestry component of the animals EBV.

To remove the QTL effect from ancestry EBV's, the QTL component in the parental means were calculated. This was done by calculating the proportion of QQ and Q+ animals selected from the population. Multiplying the proportion of QQ animals by the

QTL size and the Q+ proportion by half the QTL size, the QTL component was calculated. The QTL component was deducted from the mean of the selected animals:

$$\text{Mean EBV minus } (\% \text{“QQ”} \times \text{QTL size} + \% \text{“Q+”} \times \frac{1}{2} \text{QTL size}) \quad [14]$$

Equation [14] was applied to both sires and dams. The adjusted parental means were then used as the ancestral BV's for the three sub-populations. As the animals received lactation or progeny records, the QTL was expressed in the EBV (equations [10], [11] and [12]).

3.6.5 Number of animals in each sub-population

The percentage of animals selected from each sub-population was calculated from a single truncation point across sub-populations. This information was used to calculate the QTL frequency in offspring. The number of progeny in each sub-population of the next generation was calculated from mating rules presented in table 1.

Table 1: Frequency of progeny in each sub-population resultant from matings.

Parents		Offspring		
Male	Female	QQ	Q+	++
QQ	QQ	1	-	-
QQ	Q+	½	½	-
QQ	++	-	1	-
Q+	QQ	½	½	-
Q+	Q+	¼	½	¼
Q+	++	-	½	½
++	QQ	-	1	-
++	Q+	-	½	½
++	++	-	-	1

For example, if the bulls selected were 20% QQ, and the cows were randomly mated to the cow population that was 50% Q+, one would expect that 10% of the total matings

would be QQ(sire)/Q+(dam). Half of the progeny from these matings would be QQ and the other half Q+.

The gene frequencies for the male and female offspring were calculated separately, as the QTL gene frequency in the cows for the cow to bull pathway was higher than the frequency in the cows for the cow to cow pathway. This was due to the QTL having the effect of increasing the mean EBV of the sub-population, and in the cow to bull pathway, cows were selected on EBV in comparison to the cow to cow pathway where there was no selection pressure.

Once the mean and QTL frequency of both progeny sexes were calculated, the cow and bull populations were updated so that selection could take place again.

3.7 Utilisation of a QTL in Breeding Scheme

Nine scenarios were simulated; three different size QTL, 0.1, 0.3 and 0.5 σ_G and three different starting QTL frequencies, 0.01, 0.1 and 0.35. The QTL sizes and starting frequencies were chosen to give a representation of small, medium and large size QTL at low, medium and high starting frequencies.

The study looked at four strategies of utilising the QTL in the breeding scheme (Appendix III):

- a) Continuing with the current scheme with no genotyping of animals (control).
- b) Continuing with the current scheme, but also genotyping the animals and using this information in conjunction with the EBV's.
- c) Genotyping animals to generate solely QQ bulls.
- d) Genotyping animals to generate QQ and Q+ bulls.

3.8 Economic Analysis

Economic analysis was undertaken by comparing the three strategies to the control for each of the QTL sizes and starting frequencies. The economic analysis was based on returns for the New Zealand dairy industry. The expenses for the strategies were the starting costs for identification of the markers for the QTL in addition to ongoing costs for genotyping of animals to utilise the QTL. The income from the strategies was from the extra milk production from the cows due to their higher genetic merit. The investment analysis was undertaken by calculating net present values (NPV) for three time horizons (20, 25 and 30 years) and for two discount rates (5% and 6.5%).

3.8.1 Expenses

The first year of the investment stream was the year when the marker for the QTL was identified. The capital cost of setting up the laboratory and the cost of identifying the markers was approximately four million dollars (\$NZ), (B. Wickham, pers com.). The ongoing cost of identifying the QQ and Q+ animals in each of the strategies was based on a costing of ten New Zealand dollars per genotype (B. Wickham, pers com.).

3.8.2 Income

The income stream was derived from the situation where the genetic merit was higher in the MAS strategies in comparison to the 'control'. Genetic merit was measured from the yearly female progeny means in units of genetic standard deviations. One genetic standard deviation was taken to be worth approximately \$160, for a cow over her lifetime from milk production (Appendix IV). Sensitivity analysis was undertaken on the monetary value of one genetic standard deviation. It was assumed that 250,000 heifers, resultant from Livestock Improvement Holstein-Friesian matings, would enter the national milking herd per year (Appendix V). The benefit of the genetic standard deviation had been discounted back to the year the cow was conceived and thus the benefits were calculated as being received then. If the female progeny means were less than the control, the same process was undertaken, but the decrease in milk production was viewed as an expense (figure 10).

3.8.3 Discount rate

The discount rates used in the analysis were five, and six and a half percent. They were calculated on the basis of the long term rate of return from investing in the bank. At the time of writing the interest rate for long term government bonds was 6.5 percent. Inflation was not included in the analysis and so inflation (2%) was deducted from this rate. A risk premium was added. Two risk premiums were used, one of 0.5 percent and the other, two percent. Taxation and debt repayment implications were ignored.

Figure 10: Economic analysis.

Year	
0	Identification of markers - genotyping cost.
1	Identification of QTL animals and utilisation in breeding scheme. First progeny conceived; discounted returns from milk production increases/decreases over a cow's lifetime.
...	
30	Final year of selection.

If the female progeny means never exceeded those of the control, no economic analysis was deemed necessary as it was assumed that the strategy was uneconomic in comparison to the control.

CHAPTER FOUR

MAIN FINDINGS

4.1 Current Breeding Scheme

The current breeding scheme was simulated for sixty years of selection to obtain a stable starting point for the QTL analysis. As an aside the asymptotic rate of genetic gain measured by Rendel and Robertson's (1950) method using current industry structure was $0.29 \sigma_G$ per year (Appendix I). The rate of genetic gain may be slightly over-estimated as the generation intervals' for the cow to bull and the cow to cow pathways were under-estimated. The generation intervals and genetic superiority for the stable situation are presented in table 2.

Table 2: Genetic superiority and generation intervals for the four selection pathways in the current breeding scheme.

Selection pathway	Genetic superiority (σ_G)	Generation interval (years)
Bull to bull	2.40	6.30
Bull to cow	2.07	6.55
Cow to bull	1.65	3.46
Cow to cow	0.00	4.83

The bull to bull pathway had the largest genetic superiority, even though the cow to bull pathway has the most selection pressure. This was due to the higher r_{gg} that the bulls have after being progeny tested on eighty five daughters, compared to a cow with her own lactation records.

The majority of animals were selected from the younger age groups which had superior EBV means in comparison to the older age groups (table 3). The extra lactation records only increased the r_{gg} of the cows slightly (Appendix I), and therefore the variance of

the EBV's was not increased enough to override the increase in genetic merit of younger cows, resulting from the annual rate of improvement.

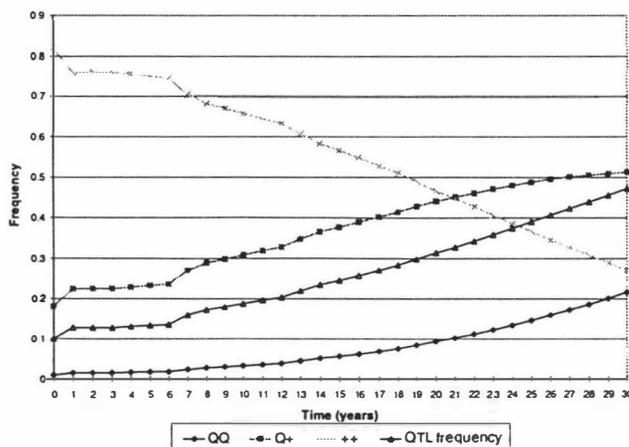
Table 3: Percentage of animals selected from each age group in the current breeding scheme (age at selection).

Pathway	Age at selection (years)					
	2	3	4	5	6	7
Cow to bull	65	27	7	1	0	0
Bull to bull	-	-	-	70	30	-
Bull to cow	-	-	-	58	29	13

4.2 Current Scheme with no Genotyping - 'Control'

The current scheme with a QTL added, was used as the control with which to compare three marker assisted selection (MAS) strategies. No selection information was known about the QTL, other than that expressed in the EBV's. Animals with the QTL were selected at a higher proportion than non QTL animals as the mean EBV's of the QQ and Q+ sub-populations were higher than the ++ sub-population. Therefore the proportion of QQ and Q+ female progeny increased over time (Figure 11).

Figure 11: Change in proportion of QQ, Q+ and ++ female progeny and QTL frequency, due to selection without any knowledge of a $0.5 \sigma_G$ QTL at a starting frequency of 0.1.



Selection on EBV's that included part of the QTL effect, resulted in an increase in the QTL frequency (frequency of Q allele), (figure 11). Therefore the presence of the QTL had an effect on the rate of genetic gain without animals being genotyped.

Excluding the QTL effects from ancestry EBV's favoured MAS. It was assumed that the QTL effect only influenced the EBV's from lactation or progeny test records. Therefore the QTL effect was under-estimated, more so in the younger animals who had less records. As a result of the under-estimated QTL effect, less QQ and Q+ animals were selected in the control than would be when the ancestral QTL effect was included. When the QTL cows were selected, the generation interval for that pathway was increased, as the QTL cows were selected at older ages when more of the QTL effect was expressed in their EBV's. Therefore the control was selecting less QQ and Q+ cows and when selected, they were older than they would be in practice. This had the effect of under-estimating the control's rate of genetic gain and thus over-estimating the MAS strategies.

4.3 Using Genotyping in the Current Scheme - 'Strategy one'

The first MAS strategy evaluated was the current breeding scheme but with genotyping of the active cow and bull populations. Once the marker had been identified all of the bulls in the progeny test system were genotyped. Each new crop of progeny test bulls was subsequently genotyped.

All of the active two year old cows in the first five years of selection were genotyped. From this time on, only some of the two year olds needed to be genotyped. The two year olds from QQ(sire)/QQ(dam), QQ/++ and ++/++ matings have known QTL genotypes (table 1) and therefore need not be assessed by genotyping. Two year olds from other matings were genotyped.

With the genotyping of the animals, the full QTL effect was known. The QTL class could be included in a genetic evaluation as a fixed effect, with the fixed effect solution

added to the additive genetic effect to assess the breeding value of each individual. Selection on EBV's was then undertaken across all sub-populations by truncation.

At the start of this strategy it was assumed that the full QTL effect in the active cow population was known for all age groups, even though only the two year olds were genotyped. This did not over-estimate the response for strategy one by a great deal, as approximately seventy percent of the animals selected for the cow to bull pathway were two year olds.

4.3.1 Genetic response

The rate of genetic gain, assessed by annual changes in the mean breeding value (BV) of the female progeny, was superior in strategy one in comparison to the control, for all QTL sizes and frequencies over the thirty year time horizon (Appendix VI). This was as expected, as the only variable altered from the control, was that the true genetic worth of the QTL was known from genotyping the animals. The genetic superiority from strategy one over the control was influenced by the difference in the QTL frequency between the strategy and the control, and the size of the QTL.

When the QTL size was small ($0.1 \sigma_G$), utilising the genetic marker in strategy one resulted in a minor improvement in the rate of increase in the QTL frequency and genetic merit, in comparison to the control. This was due to the QTL effect being small and the extra QTL effect being 'uncovered' by genotyping was minimal in terms of genetic standard deviations. Therefore the proportion of QQ and Q+ animals selected in strategy one was not much higher than in the control. At the end of thirty years the QTL frequency was 0.5, 4 and 7 percent higher in strategy one, compared to the control for the three starting QTL frequencies of 0.01, 0.1 and 0.35 respectively (table 4). With the small superiority in QTL frequency and the small QTL effect, the genetic superiority of the strategy one female progeny was minimal at the different time horizons, as shown in table 4.

Table 4: QTL frequencies at year thirty and the difference in the female progeny means over time between strategy one and the control, for the QTL size of $0.1 \sigma_G$ at the three starting QTL frequencies.

	QTL starting frequency		
	0.01	0.10	0.35
QTL frequency (control)	0.015	0.144	0.449
QTL frequency (strategy 1)	0.020	0.183	0.517
Strategy one's genetic superiority (σ_G)			
10 years	0.0001	0.0002	0.0004
20 years	0.0002	0.0006	0.0013
25 years	0.0002	0.0009	0.0016
30 years	0.0002	0.0012	0.0020

The larger differences in QTL frequency between strategy one and the control at the higher starting QTL frequency, in comparison to the lower starting frequencies, resulted in a larger difference in the genetic merit of the female progeny.

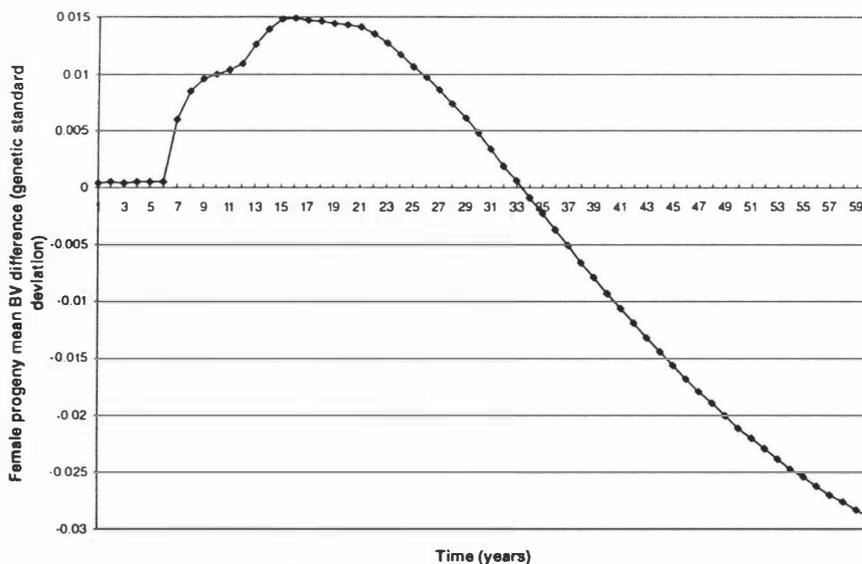
The extra milk revenue resultant from the genetic superiority was very small and less than ten percent of the initial cost of finding the genetic markers (\$4 million), let alone the cost of genotyping to identify the QTL animals (Appendix VI, table 16).

For the QTL size of $0.3 \sigma_G$, the difference in the mean EBV's between the QQ and ++ sub-populations was larger than that for the QTL size of $0.1 \sigma_G$. Therefore at this size QTL, proportionally more QQ and Q+ cows were selected compared to the smaller sized QTL. As a result the QTL frequency increased at a greater rate than it did for the QTL size of $0.1 \sigma_G$ and the QTL frequency difference between the control and strategy one was greater than it was for the smaller QTL. This had the effect of increasing the genetic superiority of strategy one over the control. However the strategy was unprofitable by approximately \$6 million for the different QTL starting frequencies and time horizons, in comparison to the control (Appendix VI, table 18). The economic

profitability for the strategy was insensitive to the QTL starting frequency, discount rate and time horizon.

At the largest sized QTL analysed ($0.5 \sigma_G$), and at the starting QTL frequency of 0.35, the genetic superiority of strategy one generated females over the control's peaked at year sixteen and decreased to be slightly superior in year thirty. The simulation for strategy one and the control was run for another thirty years. The female progeny means for strategy one become inferior to those of the control beyond year thirty four (figure 12).

Figure 12: Female progeny mean breeding value difference between the control and strategy one, at the QTL size of $0.5 \sigma_G$ and QTL starting frequency of 0.35.



Similar results were published by Saefuddin and Gibson (1991) and Gibson (1994), who stated that this is caused by the effective selection applied to the quantitative background, when selection is also applied to the single locus. The more accurate the single locus information (eg. strategy one), the less selection intensity applied to the quantitative background and thus loss in additive genetic gain.

The loss of additive genetic gain is demonstrated in the following example. A population was set up with 100,000 animals from which 100 were selected. The

100,000 animals were in the three sub-populations at the frequencies in table 5. The population had a QTL of size $0.5 \sigma_G$ identified. The population EBV means (before selection) were calculated for strategy one and the control (table 5).

Table 5: Example population (before selection) to demonstrate reduced selection differential for strategy one in comparison to the control.

Sub-population	Frequency	Strategy 1 mean EBV	Control mean EBV	r_{EG}
QQ	0.10	19.00	18.66	0.6
Q+	0.45	18.75	18.58	0.6
++	0.45	18.50	18.50	0.6

Truncation selection was undertaken across the three sub-populations for both strategy one and the control. The greater EBV superiority that the QQ sub-population had with genotyping, resulted in a higher proportion of QQ animals selected for strategy one in comparison to the control (table 6). Thus the selection differential within this sub-population was less for strategy one. The proportion selected and therefore the selection differential in the Q+ sub-population, was similar for strategy one and the control, whereas the selection differential within the ++ sub-population was higher for strategy one. Weighting the within sub-population selection differentials by the proportion selected, resulted in the selection differential for strategy one being $0.07 \sigma_G$ lower than the control (table 6).

Table 6: Within sub-population selection differentials and overall selection differential for strategy one and the control for the example population with a $0.5 \sigma_G$ QTL.

Sub-population	Frequency selected		Selection differential (σ_G)	
	Strategy 1	Control	Strategy 1	Control
QQ	0.40	0.17	1.78	1.93
Q+	0.49	0.50	2.01	2.00
++	0.11	0.32	2.24	2.07
Weighted selection differential (σ_G)			1.94	2.01

The QTL frequency for the selected animals in strategy one is 0.23 greater than that for the control. The genetic effect of the greater QTL frequency is approximately $0.11 \sigma_G$ (QTL size multiplied by QTL frequency difference). Therefore the overall genetic increase (selection differential) in the selected animals for strategy one is $0.04 \sigma_G$ greater than that for the control.

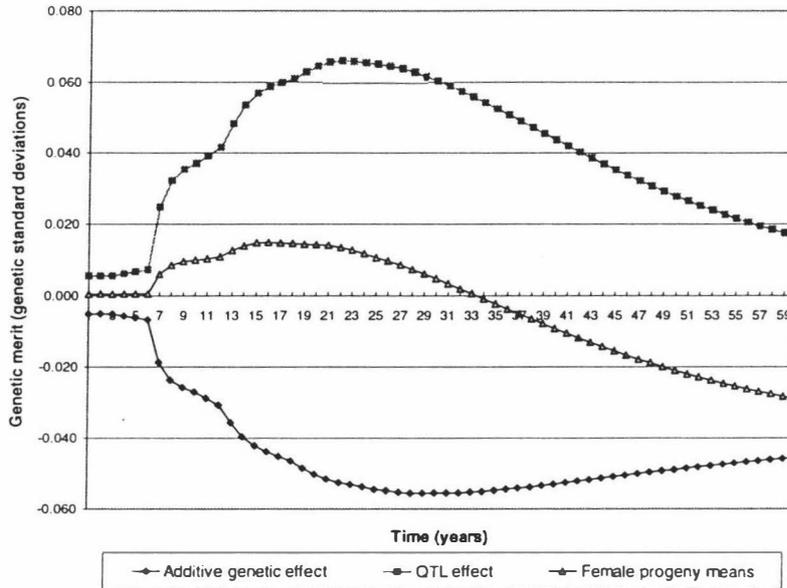
Loss of quantitative genetic response is thus the cost of single locus response which reduces the response of the single locus to less than the gene effect (QTL frequency difference multiplied by QTL size), (Gibson, 1994).

Meuwissen and Van Arendonk (1992), commented that both selection methods would fix the positive allele of the QTL and would achieve the maximum possible response for the QTL. But the conventional selection method (control) allocated less selection differential to the fixation of the major gene and thus more selection differential to QTL with small effect. Meuwissen and Van Arendonk (1992), concluded that conventional selection would be superior in the long term, when QTL with large effect are present. This was demonstrated in the current simulation for the QTL size of $0.5 \sigma_G$ at a starting QTL frequency of 0.35 (figure 12).

The difference in the female progeny means between the control and strategy one can be broken into two parts; additive genetic gain and QTL effect. Figure 13 outlines the

contribution of the two components to the female progeny mean BV difference between strategy one and the control for a $0.5 \sigma_G$ QTL at a starting frequency of 0.35.

Figure 13: Difference between strategy one and the control for additive genetic gain, QTL effect and female progeny breeding value means for the QTL size of $0.5 \sigma_G$ and at the QTL starting frequency of 0.35.



The QTL effect from strategy one's higher QTL frequency, is greater than the loss in additive genetic gain for the first thirty-four years. Therefore the progeny means were superior for strategy one over this period. As the QTL neared fixation in strategy one, the QTL effect superiority decreased. The loss in additive genetic gain for strategy one became more than the QTL effect and thus the female progeny means became inferior from year thirty-four.

The long term loss was not observed for the other starting QTL frequencies at this size QTL. Simulation for another thirty years for the 0.1 starting gene frequency resulted in strategy one still being slightly genetically superior at year sixty.

Strategy one, for the QTL size of $0.5 \sigma_G$, was profitable at the starting QTL frequency of 0.1, at the thirty year time horizon and five percent discount rate (table 7). At a discount rate of 6.5% the profitable scenario became unprofitable (Appendix VI, table 20).

Table 7: Economic return for selection strategy one at a $0.5 \sigma_G$ QTL at the three starting QTL frequencies and three time horizons and five percent discount rate (NPV \$).

Years	Starting QTL frequency		
	0.01	0.10	0.35
20	-4,960,698	-2,666,734	-4,711,190
25	-4,057,465	-608,617	-4,221,910
30	-2,685,409	1,290,003	-4,032,205

The selection strategy was sensitive to the monetary value of one genetic standard deviation. A decrease of fifteen percent in the value resulted in the strategy becoming uneconomic at all time horizons.

The cumulative discounted returns for the profitable scenario became positive in year twenty-seven. The method of discounting the returns of one genetic standard deviation for a cow, assumed that the income from the genetic superiority was received in the year the cow was conceived, not from the lactations which occur over the next seven years. Therefore, the break-even year is likely to be approximately four years later, year thirty-one.

4.4 Generation of QQ Bulls only - 'Strategy two'

The bulls were generated from matings between QQ or Q+ males with QQ or Q+ females. Once the marker had been identified all of the bulls in the progeny test system were genotyped. Therefore the selection of QQ or Q+ bulls to generate the next crop of QQ cows was known with certainty. The resulting male offspring from all but the QQ/QQ matings were genotyped to identify the QQ sons.

The cow population was not initially genotyped in entirety, so the cows were initially selected on EBV and then genotyped to identify which cows had the QTL. Selection

was continued until it was calculated that there were enough QQ/Q+ cows selected, to mate to the selected QQ/Q+ bulls, to generate 140 QQ bulls.

It was assumed that cows selected as three year olds or older for the cow to bull pathway had already been selected as two year olds, ie. a cow that was to the left of the truncation line in one age group did not move to the right of it in later years. This assumption had the implication that the older cows selected, after the first round of selection, had been genotyped. Therefore only the two year olds selected had to be genotyped. In addition, two year olds from QQ/QQ, QQ/++ and ++/++ matings were not genotyped as there was no doubt about their genotype with respect to the QTL locus (table 1).

4.4.1 Genetic response

The selection intensity for strategy two on the cow to bull and bull to bull pathway's was usually dramatically reduced in the first five years. Instead of selecting from the three sub-populations, selection only took place from the QQ and Q+ sub-populations for the fore-mentioned pathways. Thus the effective active cow and bull populations were decreased in size (table 8).

Table 8: Active cow and bull populations for the cow to bull and bull to bull pathways for the control and strategy two at the three QTL starting frequencies.

QTL frequency	Cow to bull pathway		Bull to bull pathway	
	Control	Strategy 2	Control	Strategy 2
0.01	169,000	3,363	280	5.5
0.10	169,000	32,110	280	53.2
0.35	169,000	97,600	280	161.7

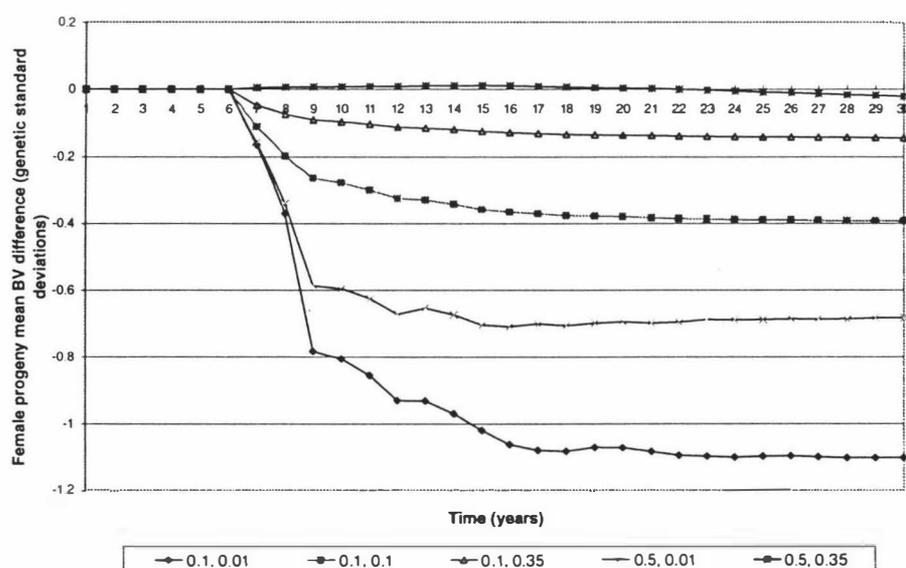
The control had the active cow population of 169,000 for all three starting QTL frequencies, as the cows in the control were selected from all three sub-populations. For the bull to bull pathway, selection was from five and six year old bulls. Therefore 280 bulls were eligible for selection in the control. The effective active cow and bull populations for strategy two were only two percent of the control's at the QTL

frequency of 0.01, and nineteen and fifty-eight percent for the starting frequencies of 0.1 and 0.35 respectively.

The cow to bull selection differential was further reduced as more cows were needed for strategy two for the cow to bull pathway, in comparison to the 455 cows that were required for the control. This was due to three quarters of the Q+/Q+ matings and half of the QQ/Q+ matings producing offspring that were not QQ. The decrease in the selection differential in the two pathways resulted in the mean breeding values of the progeny test bulls being less than the control.

The lower mean BV for the progeny test bulls generated from the first year of selection did not affect the female progeny BV's until the seventh year of selection (figure 14). This was the year that the progeny test bulls had progeny as proven sires.

Figure 14: Difference in genetic merit of female progeny, between selection strategy two and the control for QTL sizes of 0.1 and 0.5 σ_G at starting QTL frequencies of 0.01, 0.1 and 0.35.



The starting QTL frequency had a major effect on the genetic response for strategy two. At the higher starting QTL frequencies the effective cow population were larger (table 8). Thus the selection differentials on the cow to bull and bull to bull pathways were not reduced to the same extent as they were for the 0.01 starting frequency and therefore the

progeny test bulls were less inferior to the control than they were at the small QTL frequency. This had the effect that the female progeny BV's did not drop behind the control to the same extent as it did with the lower starting frequency (figure 14).

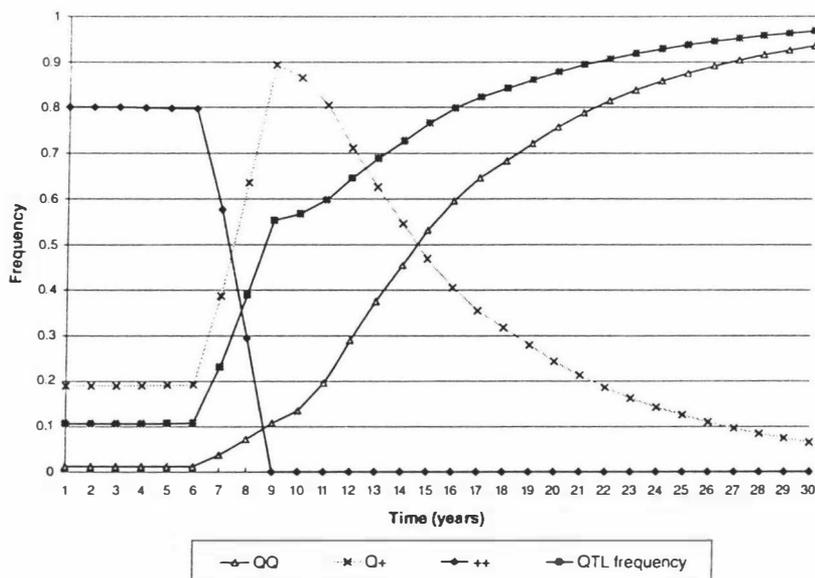
The QTL size also had an effect on the genetic response of strategy two. Figure 14, shows the difference between the control and strategy two female progeny BV means for the QTL frequency of 0.01 at two QTL sizes, 0.1 and 0.5 σ_G . The decrease in selection intensity was the same for both QTL sizes, but the extra QTL effect of the larger QTL decreased the inferiority of strategy two.

The QTL size of 0.5 σ_G and frequency of 0.35 was the only scenario for which the response from the QTL effect was superior to the reduction in selection differential (Appendix VII, table 23). The superiority was small as the line on figure 14 is just above the x-axis in the early years. The superiority was also short-lived as the female progeny means become inferior to the control in year twenty-two (figure 14). This illustrates that the quantitative background was not as intensely selected in strategy two, in comparison to the control. The strategy is unprofitable by approximately \$2 million for the 0.5 σ_G QTL and 0.35 frequency (Appendix VII, table 24).

4.4.2 QTL frequency

The general trend for the number of female progeny in each of the three sub-populations for strategy two is demonstrated in figure 15 for the QTL size of 0.1 σ_G and starting frequency of 0.1.

Figure 15: Proportion of female progeny in the three sub-populations for QTL size 0.1 σ_G and QTL starting frequency of 0.1.



The QTL frequency increased quickly from year six when the first QQ proven bulls were used. This corresponded with the increase in the Q+ sub-population. At year nine the rate of increase slowed as the sub-population of ++ female progeny became non-existent. Thus any increase in QTL frequency from this year on was from Q+ to QQ.

4.5 Generation of QQ and Q+ Bulls only - 'Strategy three'

The bulls were generated from matings between males and females selected from all three sub-populations. Sires that were ++ for the QTL genotype were not mated to ++ cows.

Sires to breed sons were selected and the number of bulls from each sub-population was calculated. The cows were selected on EBV's and then genotyped. Knowing the number of bulls and cows from each sub-population enabled the calculation of the expected number of QQ and Q+ bulls that would be generated from the matings. If the expected number of bulls was less than 140, more cows would be selected until the expected number of QQ and Q+ bulls reached the target number.

All male progeny were genotyped, except those from QQ/QQ matings, to identify the QQ and Q+ bulls. As with strategy two, it was assumed that the older cows selected, after the first round of selection, had been previously genotyped. Two year olds from QQ/QQ, QQ/++ and ++/++ matings were not genotyped as there was no doubt about their genotype with respect to the QTL locus (table 1).

4.5.1 Genetic response

Despite the fact that selection of cows to generate the next crop of progeny test bulls was from all three sub-populations, the selection intensity on this pathway was reduced in comparison to the control. The control required 455 cows for this pathway, whereas strategy three required more, as not all of the Q+/Q+ and Q+/++ matings resulted in QQ or Q+ bulls.

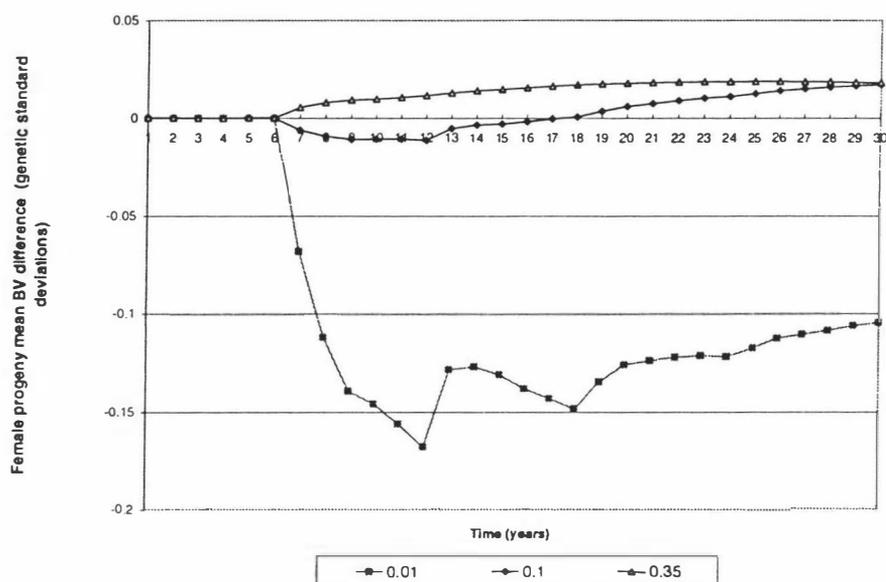
The gene frequency influenced the amount of selection intensity lost in the cow to bull pathway. With a lower QTL frequency, less QQ and Q+ sires were selected for the bull to bull pathway in comparison to higher QTL frequencies. Therefore more cows for the cow to bull pathway were required to generate the 140 QQ and Q+ bulls and thus the selection intensity decreased.

A smaller QTL size decreased the selection intensity in the cow to bull pathway as less QQ and Q+ cows were selected on EBV's, as the small QTL size did not make them greatly superior to the ++ cows. Therefore selection on the cow population, with a small QTL size, resulted in the majority of the selected cows being ++. The mating of ++ cows to the selected bulls resulted in no QQ and less Q+ bulls than would be generated from QQ and Q+ cows. Therefore a small QTL size resulted in more cows being selected to generate the required number of bulls.

The decrease in selection intensity for the QTL size of $0.1 \sigma_G$ at all starting frequencies was not offset by the gain generated from the increased QTL frequency over time (Appendix VIII, table 25). The QTL starting frequency had a large influence on the genetic merit of the female progeny at the QTL size of $0.3 \sigma_G$. At the QTL starting frequency of 0.01, strategy three was genetically inferior for the thirty year horizon. The

higher starting frequency of 0.1 resulted in genetically superior females being generated from year eighteen and superior progeny for the full thirty years at the starting frequency of 0.35 (figure 16), (Appendix VIII, table 26).

Figure 16: Difference in genetic merit of female progeny, between selection strategy three and the control at QTL size of $0.3 \sigma_G$ for all starting frequencies.



There was no initial decrease in the female progeny genetic means, for the $0.3 \sigma_G$ QTL and starting frequency of 0.35, as seen for the previous QTL frequencies and QTL sizes for this strategy. This was due to the combination of high QTL frequency and the QTL size and thus the selection intensity on the cow to bull pathway was not reduced to any great extent compared to the control. However, it took twelve years before the progeny means of the bulls exceeded those of the control. The female progeny means exceeded the control in the early years, due to the proven bull EBV means being higher. This was due to the bulls being genotyped and thus more QQ and Q+ bulls being selected than in the control. Therefore the QTL frequency increased more quickly in the early years and the QTL effect was greater than that caused by the reduction in selection intensity.

The economic profitability of the strategy for the $0.3 \sigma_G$ QTL was sensitive to starting frequency. At the starting frequency of 0.10 the strategy was very unprofitable. At the higher starting frequency, the profitability of the scenario was sensitive to time horizon and discount rate (table 9). It was more profitable for the longer time horizons and

lower discount rate as the benefits from strategy three were mostly received in the later years, whereas the major expenses were in the early years (figure 16).

Table 9: Economic return for selection strategy three for QTL size of $0.3 \sigma_G$ and starting frequencies of 0.10 and 0.35, at two discount rates and three time horizons (NPV \$).

	0.1		0.35	
	5%	6.5%	5%	6.5%
20 years	-5,672,738	-5,468,196	-424,958	-1,062,322
25 years	-5,026,400	-5,002,706	781,338	-190,640
30 years	-4,230,906	-4,467,875	1,725,252	445,045

At the shorter time horizons for the 0.35 starting frequency the strategy would be profitable if the \$4 million cost of finding and identifying the QTL was ignored.

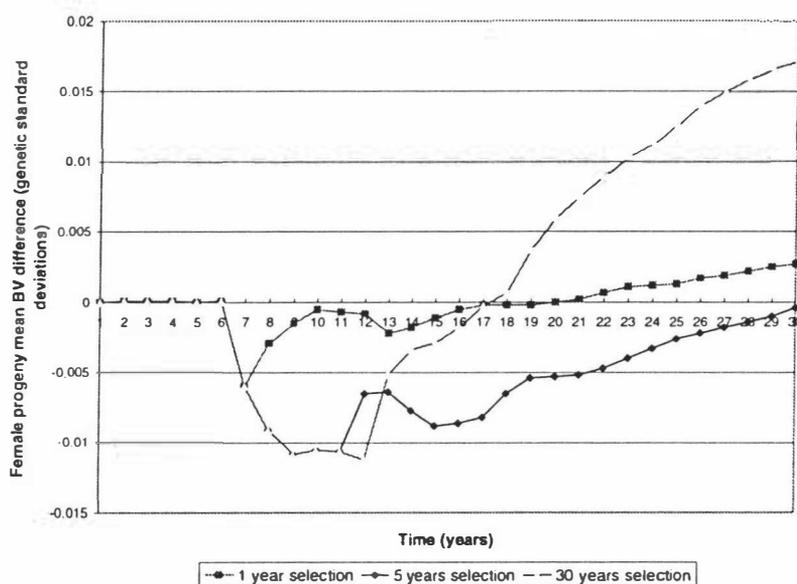
The cumulative discounted returns became positive at year twenty-two and year twenty-seven for the discount rate of 5 and 6.5% respectively. In reality it is more likely to be several years later, as the returns from milk production in this analysis were assumed to be received in the year the cow was conceived.

The profitability of strategy three was sensitive to the monetary value of one genetic standard deviation. A decrease in the value of σ_G by thirty percent, made the strategy uneconomic for all time horizons and discount rates. Without the research costs, the value of one genetic standard deviation would have to be less than \$2 before the strategy was unprofitable.

Operating the MAS strategy for thirty years may be less profitable than a shorter operation as there will be less genotyping costs. Operating strategy three for one and five years instead of thirty years, was investigated at a $0.3 \sigma_G$ QTL. The one year operation resulted in the female progeny means not dropping behind the control's to the extent that they did when the strategy operated for 30 years (figure 17). This is due to

having only one year where the selection intensity in the cow to bull pathway was reduced, in comparison to the control. Utilising strategy three for one year, resulted in superior female progeny means to the control from year twenty onwards, but inferior to the thirty year operation from year eighteen.

Figure 17: Difference in genetic merit of female progeny, between selection strategy three being undertaken for 1,5 and 30 years and the control for a QTL size of 0.30 and starting frequency of 0.10.



The first six years of strategy three was the period when the selection intensity on the cow to bull pathway was reduced the most. By utilising the strategy for five years, the progeny means dropped behind the control to the same extent as using the strategy for thirty years. However, the genetic benefits of the strategy were reduced, over the later years when strategy three was stopped at year six, as the QTL frequency increased at a slower rate in comparison to the thirty year operation.

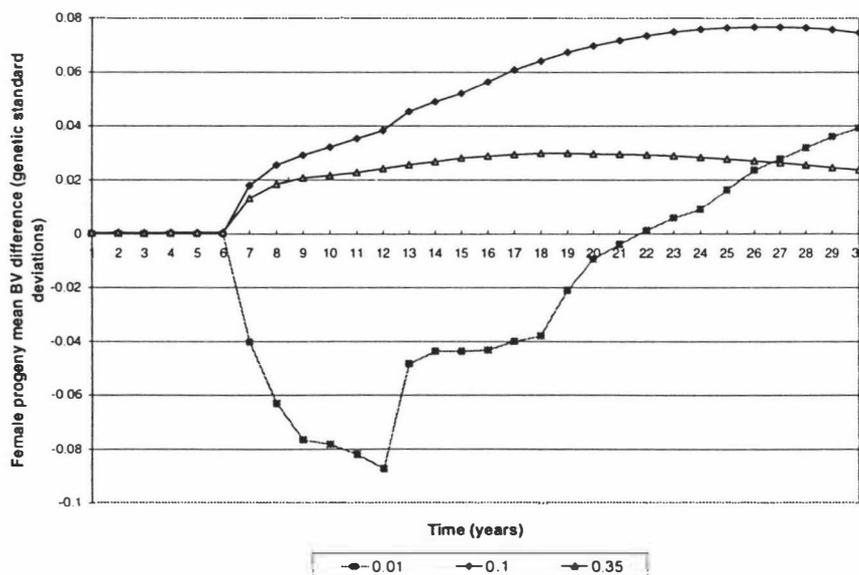
Undertaking the same variations at the 0.35 QTL frequency resulted in inferior rates of genetic gain for the one and five year operations in comparison to the thirty year operation (Appendix VII, figure 21).

The economic return from operating strategy three for one year was superior to the thirty year operation, at the QTL starting frequency of 0.1, for all scenarios except one (30 years, 5% discount rate), (Appendix VIII, table 30). The extra return for the one year operation over the thirty year procedure, was from two sources; less genotyping of animals and a smaller decrease in milk production in the early years, as the genetic merit did not fall behind the control as much as the thirty year scenario (figure 17).

The saving on genotyping was approximately \$90,000 for the three time horizons. Therefore, most of the extra return was from the smaller depression in milk production, in years seven to seventeen. Despite the superiority of the one year operation over the thirty year procedure, it was not superior to the control. The five year operation was economically inferior to the thirty year procedure (Appendix VIII, table 30).

For the QTL size of $0.5 \sigma_G$ the female progeny means were superior at year thirty for all of the QTL frequencies. The QTL starting frequency of 0.01 had inferior progeny BV means until year twenty-two, whereas at the two higher starting frequencies, the female BV means were superior for the entire thirty year time horizon (figure 18).

Figure 18: Difference in genetic merit of female progeny, between selection strategy three and the control at QTL size of $0.5 \sigma_G$ for all starting frequencies.



The greater superiority of the 0.1 starting frequency made it the most profitable scenario for this size QTL (table 10).

Table 10: Economic return for selection strategy three for $0.5 \sigma_G$ QTL at the three starting QTL frequencies, two discount rates and three time horizons.

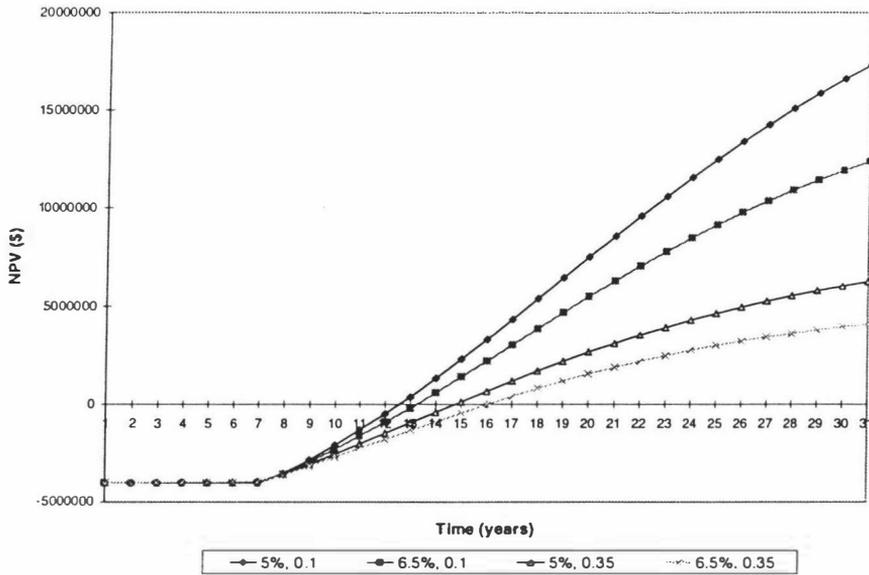
	0.01		0.1		0.35	
	5%	6.5%	5%	6.5%	5%	6.5%
20 years	-20,470,136	-18,022,565	8,565,636	6,284,550	3,097,527	1,875,067
25 years	-20,136,444	-17,787,807	13,413,455	9,786,802	4,966,015	3,226,145
30 years	-18,543,534	-16,719,181	17,299,560	12,433,749	6,261,379	4,099,098

Starting at a QTL frequency of 0.01 instead of 0.1 or 0.35 made a large difference in the profitability, as strategy three was highly uneconomic at the 0.01 starting QTL frequency, but very profitable at the other two starting QTL frequencies.

The monetary value of a genetic standard deviation would have to decrease by eighty and sixty percent for strategy three to be unprofitable for a $0.5 \sigma_G$ QTL at the starting frequencies of 0.1 and 0.35 respectively.

The cumulative discounted returns at the 0.1 starting frequency, became positive in years 12 and 13, for the discount rates of 5 and 6.5 percent respectively. For the 0.35 QTL starting frequency the strategy became profitable at years 15 and 16 for the discount rates of 5 and 6.5% respectively (figure 19).

Figure 19: Cumulative discounted returns from selection strategy three, at a $0.5 \sigma_G$ QTL and starting frequencies of 0.10 and 0.35, at discount rates of 5 and 6.5%.

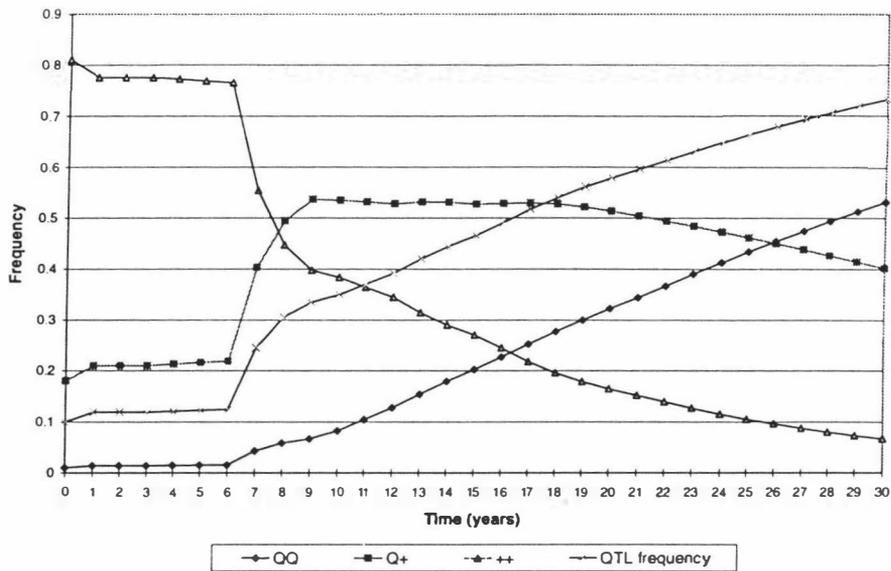


4.5.2 QTL frequency

The general trend for the number of female progeny in each of the three sub-populations for strategy three is demonstrated for the QTL size of $0.3 \sigma_G$ and starting frequency of 0.1 in figure 20.

There was very little change to the proportion of animals in each sub-population until year seven, when the progeny of the proven QQ/Q+ bulls were born. The increase in QQ female progeny is approximately linear from year six. For the Q+ sub-population there was a large increase in years 7, 8 and 9 with the use of the proven QQ/Q+ bulls. The increase in the Q+ sub-population saw a corresponding decrease in the ++ sub-population. The percentage of heterozygotes reaches fifty percent by year ten and then stabilised near that level until year twenty when it started to decrease.

Figure 20: Proportion of female progeny in the three sub-populations, and QTL frequency for QTL size $0.30 \sigma_G$ and QTL starting frequency of 0.10.



The QTL frequency had a sharp increase between years seven and ten which corresponded to the increase in the Q+ sub-population. From year ten the increase was slower and approximately linear until year twenty. This increase in QTL frequency corresponded with the linear increase in the QQ sub-population and the stable nature of the Q+ sub-population. From year twenty the rate of increase slows as the Q+ sub-population becomes smaller.

CHAPTER FIVE

CONCLUSIONS

The assumption that the genetic marker was the QTL meant that there was no recombination between the genetic marker and QTL and the degree of association between the QTL and marker was the same for all sire-families. This assumption had the effect of over-estimating the genetic and economic response for the MAS strategies.

The economic analysis had the research costs of identifying the QTL linked markers pooled into one year, whereas they were incurred over several. If the research costs were allocated to the years that they were incurred, the returns in the later years of analysis would have been discounted more heavily. This had the effect of favouring the MAS strategies. The research costs also ignored those incurred before Livestock Improvement became involved in identifying QTL linked genetic markers.

The decision on how to utilise the QTL may occur after the research to identify the genetic marker and the QTL frequency has been undertaken and thus the \$4 million has already been spent. The investment decision on how to utilise the QTL therefore may ignore the research cost and be based on future expenses and returns. The selection strategy chosen may only return \$2 million on income less future expenses and thus the overall project has cost \$2 million. This would be preferable to ignoring the QTL and having the project losing \$4 million.

The size of the QTL had a major effect on the economic viability of the MAS strategies. The analysis for the small QTL ($0.1 \sigma_G$) showed that only strategy one was genetically superior to the control. However, the genetic superiority of strategy one was minor due to the small QTL effect and thus unprofitable. Therefore if an additive QTL of size $0.1 \sigma_G$ was discovered, the best strategy to utilise the QTL would be to ignore it and continue with the current breeding scheme.

At the medium sized QTL ($0.3 \sigma_G$), there were more situations where the MAS strategies were genetically superior to the control. Strategy one was superior at all QTL starting frequencies and strategy three at the two higher frequencies. However, economically strategy one was unprofitable at all starting QTL frequencies. Excluding the \$4 million research cost still resulted in a loss in excess of \$1 million. Strategy three was profitable at the starting QTL frequency of 0.35, but not at the starting frequency of 0.1, even when excluding the \$4 million research expense. Therefore if a single additive QTL of size $0.3 \sigma_G$ was identified it would have to be at a frequency of about 0.35, for MAS strategy three to utilise the QTL more profitably than the current breeding scheme.

At the large QTL ($0.5 \sigma_G$), undertaking strategies one or three resulted in genetically superior progeny at all three starting frequencies and strategy two produced genetically superior progeny at the 0.35 starting frequency. The QTL starting frequency influenced the profitability of strategy one. The starting frequency of 0.1 was the only starting frequency that had a profitable return for strategy one, but this was sensitive to time horizon, discount rate and monetary value of a genetic standard deviation. The economic returns at the longer time horizons for the starting frequency of 0.01 and all time horizons for starting frequency of 0.10 were profitable for strategy one when the \$4 million research cost was ignored, as was strategy two for the starting frequency of 0.35. Strategy three was profitable at the 0.10 and 0.35 starting frequencies for all time horizons and profitable at the low QTL frequency when the research cost was removed. If a single additive $0.5 \sigma_G$ sized QTL is identified, utilising the QTL in strategy three is the most profitable for the range of QTL frequencies evaluated.

Strategy one, where the QTL genotype of all active animals was known, resulted in superior rates of gain at all QTL sizes and starting frequencies. Selecting on the full knowledge of the QTL effect resulted in less selection intensity being applied to the quantitative background (smaller QTL) in comparison to selecting on the QTL effect expressed in the EBV's (control). This resulted in short-term genetic gain but long-term loss when genotyping for QTL with large effects. The long-term loss was not observed

for the smaller sized QTL, but the additional genetic gain from selecting on the small genotyped QTL was minimal.

Strategy two, where QQ bulls were generated only, was not economically viable for any of the QTL sizes and frequencies. This was due to selection of bulls and cows for the generation of progeny test bulls being only from the QQ and Q+ sub-populations. The effective active populations, in the first three years of selection, were only two, nineteen and fifty-eight percent of the control's active population, at the QTL starting frequencies of 0.01, 0.1 and 0.35 respectively. The loss in selection intensity on the bull to bull and cow to bull pathways in the early years was too large for the QTL effect to overcome in later years. Strategy two may be a more profitable selection strategy if the QTL was dominant as the frequency of Q+ animals increases rapidly and by year nine the full QTL effect will be expressed, which is approximately ten to fifteen years earlier than it is with the additive QTL.

Strategy three was the most promising of the three MAS strategies. The strategy had reduced selection intensity on the cow to bull pathway in the generation of QQ and Q+ bulls. At the higher QTL frequencies and larger QTL sizes, the loss in selection intensity was overcome by the utilisation of the QTL. The majority of the decrease in selection intensity occurred in the first five years. Operating the strategy for one year reduced the decrease in selection intensity and for one situation evaluated, was more profitable than the thirty year option. Undertaking the strategy for five years, received the full effect of the decrease in selection intensity but only a small benefit on the utilisation of the QTL and therefore was inferior to the thirty year option. The optimum length of the selection programme therefore may be less than thirty years. This would have to be ascertained for all of the selection strategies at the differing QTL sizes and frequencies.

The economically profitable MAS strategies were sensitive to time horizon and the monetary value of a genetic standard deviation. The $0.5 \sigma_G$ QTL at the two higher QTL starting frequencies for strategy three was the exception to this sensitivity. Discount rate did not have a major influence on profitability.

Fixation of the QTL does not occur in the short-term. Selection for the QTL for the progeny test bulls does not affect the QTL frequency in the female progeny until seven years later. Strategy two at the large QTL size took approximately twenty years from the initial selection, before the QTL frequency in the female progeny reached ninety percent. The only method to increase this rate of fixation would be to actively select for the QTL on the cow to cow pathway, which is likely to be genetically disadvantageous.

For the profitable situations, the effective (adjusted) break-even point was year sixteen at the earliest. The time lag between selection and break-even date was caused by the largest expense, identifying the QTL (\$4 million), occurring in year one and the earliest returns from extra milk production, from selection decisions on bulls entering the progeny test system, being received eight years later. The increase in the QTL frequency was not immediate and thus the benefits of the increased QTL frequency were received in the later years of the analysis. Therefore MAS is a long-term selection strategy.

Once a QTL is identified it is very important to identify its size and frequency in the active cow and bull populations. Once this has been ascertained a decision can be made on how to utilise the QTL with respect to MAS strategy and the optimum operation period for the strategy.

The use of MAS in the present New Zealand breeding scheme may be profitable for a single additive QTL of size $0.5 \sigma_G$, with the degree of profitability being influenced by the starting QTL frequency.

5.1 Areas of future research

The study only looked at the effect of an additive QTL and therefore the results may not be transferable to the situation of a dominant QTL. Both strategy two and three increased the number of female progeny in the Q+ sub-population rapidly and therefore the benefit of the QTL may be received a lot earlier and in greater amounts for the selection strategies for a dominant QTL.

The use of multiple ovulation and embryo transfer (MOET) may be beneficial in the generation of multiple sons per mating. This will decrease the selection differential loss in strategies two and three, especially when the QTL is at a low starting frequency. Genotyping the offspring will enable the full-sibs to be differentiated on a genetic basis and the bull with the most favourable QTL progeny tested.

The study looked at the identification and utilisation of only one QTL. If there were more than one QTL of varying effects, the response to MAS may be different. The response may be influenced by the degree of linkage between the QTL.

Recombination rate was ignored in this study, which favoured the profitability of MAS. Further work may be needed to establish what is the real effect of recombination rates with the use of single genetic markers and/or haplotypes.

The QTL frequency was assumed to be the same in both cow and bull populations. This may not be the case and thus the degree of response to MAS should be investigated at different starting frequencies in the two populations.

The New Zealand breeding scheme is based on progeny testing bulls to identify the sires that should be used to breed cows and the next crop of bulls. The study only looked at this situation. MAS may be profitable in variations on the progeny test eg. using unproven bulls to breed cows and/or bulls, or in MOET nucleus herds.

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APPENDICES

Appendix I: Cow and Bull population starting parameters for the QTL analysis

Table 11: Cow population age structure starting mean EBV's and r_{gg} 's for the QTL analysis.

Age (years)	Number	Mean EBV's (σ_G)	r_{gg}
Calf	42,000	17.52	0.18
1	40,000	17.23	0.18
2	38,000	16.94	0.55
3	35,500	16.65	0.60
4	31,000	16.36	0.62
5	25,500	16.07	0.63
6	21,000	15.78	0.64
7	18,000	15.49	0.64

Table 12: Bull population age structure starting mean EBV's and r_{gg} 's for the QTL analysis.

Age (years)	Mean EBV's (σ_G)	r_{gg}
Calf	18.74	0.05
1	18.45	0.05
2	18.16	0.05
3	17.87	0.05
4	17.58	0.05
5	17.29	0.92
6	17.00	0.92
7	16.71	0.92

Appendix II: Number of cows needed to generate a progeny test bull

From one cow selected as bull dam.

10 percent rejected based on conformation.	0.90 of a cow
80 percent get in calf to contract sire.	0.72 of a cow
50 percent have bull calves	0.36 of a cow
95 percent calf survival	0.34 of a cow
10 percent of bulls rejected on conformation or semen quality.	0.31 of a cow

The inverse of 0.31 is 3.23. Therefore approximately 3.25 cows are required to generate one bull to be progeny tested.

Appendix III: Brief outline of the three marker assisted selection strategies

Strategy one: Using genotyping in the current scheme

The current breeding scheme but with genotyping of the active cow and bull populations. With the genotyping of the animals, the full QTL effect was known. The QTL class could be included in a genetic evaluation as a fixed effect, with the fixed effect solution added to the additive genetic effect to assess the breeding value of each individual. Selection on EBV's was then undertaken across all sub-populations by truncation.

Strategy two: Generating homozygote QTL (QQ) bulls only

The bulls were generated from matings between QQ or Q+ males with QQ or Q+ females. Once the marker had been identified all of the bulls in the progeny test system were genotyped. Therefore the selection of QQ or Q+ bulls to generate the next crop of QQ cows was known with certainty. The cow population was not initially genotyped in entirety, so the cows were initially selected on EBV and then genotyped to identify which cows had the QTL. Selection was continued until it was calculated that there were enough QQ/Q+ cows selected, to mate to the selected QQ/Q+ bulls, to generate 140 QQ bulls.

Strategy three: Generating homozygote and heterozygote QTL (QQ and Q+) bulls only

The bulls were generated from matings between males and females selected from all three sub-populations. Sires to breed sons were selected and the number of bulls from each sub-population was calculated. The cows were selected on EBV's and then genotyped. Knowing the number of bulls and cows from each sub-population enabled the calculation of the expected number of QQ and Q+ bulls that would be generated from the matings. If the expected number of bulls was less than 140, more cows would be selected until the expected number of QQ and Q+ bulls reached the target number.

Appendix IV: Calculation of the worth of one genetic standard deviation

Until recent times, returns to the farmer for the main milk components (milkfat, protein and milk volume) have been reported in terms of per kilogram milkfat. The milkfat payment structure is used to estimate the worth of improvement by one genetic standard deviation of an index of the three main milk components.

Livestock Improvement assume 900 kg^2 as the phenotypic variance for milkfat (J Rendel, pers com). The genetic variance is 225 giving a heritability of 0.25 and genetic standard deviation of 15 kilograms.

The average production for a cow in New Zealand based on mature equivalents is 180 kg (J. Rendel, pers com). The percentage of production on mature equivalent basis are presented in table 13 (New Zealand Dairy Board, 1981).

Table 13: Percentage of mature equivalent production by lactation.

Lactation	Percent mature equivalent
1	0.73
2	0.84
3	0.91
4	0.96
5	1

The average production for a cow over a life of 4.5 lactations is 159.6 kg milkfat based on the figures in table 13 and 180 kg milkfat average mature equivalent production. It is assumed that phenotypic improvement is equal to the genetic improvement (15 kg) and thus the average 'genetically improved' mature equivalent is 195 kg milkfat. The lifetime average for the genetically superior cow is therefore 171.2 kg milkfat or an additional .11.6 kg actual milkfat.

The value of the three milk components on a kilogram milkfat basis is estimated to \$5.50 and thus the extra genetic standard deviation is worth \$82.50 ($\$5.50 \times 15 \text{ kg}$

milkfat) per mature equivalent lactation. This monetary value is the benefit only when feed is unlimited. This is seldom the case and thus feed requirements must be considered. It is assumed that there was no extra feed available for the extra production, so less cows have to be farmed.

The average milkfat production as calculated above is 159.6 kg per year, the average herd size 187 and the average farm size 77 hectare (Livestock Improvement 1994). It was assumed that it takes 24 kilograms of dry matter (kgDM) to produce a kilogram of milkfat. Included in this 24 kilograms are maintenance, pregnancy and lactation feed requirements. Thus it takes 3,830 kgDM to produce 159.6 kg milkfat. At a stocking rate of 2.43 cows per hectare (187 cows/77 hectares) this is a feed requirement of 9302 kgDM per hectare and the total annual feed requirement for the farm being 716,285 kgDM.

Each extra kilogram of milkfat is assumed to require 11 kgDM above maintenance. If the genetically superior herd replaced the average herd the feed requirements for the herd would be the current requirements plus the extra average production of 11.6 kg milkfat multiplied by 187 cows multiplied by 11 kgDM per kg milkfat. The extra feed requirement is 23,861, which at 3,958 kgDM per cow producing 171.2 kg milkfat is equivalent to 6 cows. The cost of lost production in reducing the herd size by 6 cows at 171.2 kg milkfat and \$5.50 per kg milkfat is \$5,677. This cost is borne by the 181 genetically superior cows milked and is \$31.37 per cow. The monetary value of one genetic standard deviation is \$82.50 less \$31.37 which is \$51.13 per mature equivalent lactation .

The returns from the four and a half lactations are discounted at 5% back to the year the animal was conceived (table 14).

Table 14: Returns per cow per genetic standard deviation increase in milkfat.

Year	Percent of Mature equivalents	Nominal return per cow per year	Discounted returns
0	0	0	0
1	0	0	0
2	0	0	0
3	0.73	37.33	32.24
4	0.84	42.95	35.34
5	0.91	46.53	36.46
6	0.95	49.09	36.63
7	1	25.57	18.17
			158.84

The monetary value of one genetic standard deviation increase for an index of the three main milk components based on a milkfat payment system is approximately \$160 per cow.

Appendix V: Number of heifers entering the national dairy herd per year

Livestock Improvement has approximately 70 percent share of the artificial breeding market. Two million two hundred thousand cows were inseminated in the 1993/94 season (Livestock Improvement, 1994). Approximately 70 percent of the inseminations were Holstein-Friesian. Therefore approximately 1.1 million cows were inseminated with Livestock Improvement Holstein-Friesian semen. Assuming a replacement rate of 22.5 percent per year, approximately 250,000 replacements will be generated from these matings.

Appendix VI: Genetic and economic responses for Strategy one

Table 15: Female progeny mean breeding value differences between selection strategy one and the control, for a QTL of 0.1 σ_G at the three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	0.0001	0.0002	0.0004
15	0.0001	0.0004	0.0008
20	0.0002	0.0006	0.0013
25	0.0002	0.0009	0.0016
30	0.0002	0.0012	0.0020

Table 16: Economic return of extra milk revenue from strategy one for QTL size of 0.1 σ_G at the three starting QTL frequencies, and a discount rate of five percent for three time horizons (NPV \$).

	0.01	0.1	0.35
20 years	10,057	74,938	168,053
25 years	15,217	112,312	237,396
30 years	20,331	149,938	301,135

Table 17: Female progeny mean breeding value differences between selection strategy one and the control, for a QTL of $0.3 \sigma_G$ at three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	0.0005	0.003	0.004
15	0.0009	0.006	0.008
20	0.0019	0.010	0.010
25	0.0034	0.015	0.011
30	0.0056	0.020	0.011

Table 18: Economic return for selection strategy one for a $0.3 \sigma_G$ QTL at the three starting QTL frequencies, two discount rates and three time horizons (NPV \$).

Years	0.01		0.1		0.35	
	5%	6.5%	5%	6.5%	5%	6.5%
20	-5,772,871	-5,702,892	-5,958,402	-5,888,605	-6,470,037	-6,331,937
25	-5,699,558	-5,650,172	-5,556,410	-5,599,222	-6,233,196	-6,181,216
30	-5,574,729	-5,566,423	-5,004,272	-5,228,403	-5,980,768	-5,991,418

Table 19: Female progeny mean breeding value differences between selection strategy one and the control, for a QTL of $0.5 \sigma_G$ at three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	0.002	0.011	0.010
15	0.005	0.022	0.015
20	0.012	0.034	0.014
25	0.026	0.042	0.011
30	0.040	0.045	0.005

Table 20: Economic return for selection strategy one for a $0.5 \sigma_G$ QTL at the three starting QTL frequencies, two discount rates and three time horizons (NPV \$).

Years	0.01		0.1		0.35	
	5%	6.5%	5%	6.5%	5%	6.5%
20	-4,960,698	-5,053,891	-2,666,734	-3,214,129	-4,711,190	-4,873,132
25	-4,057,465	-4,403,845	-608,617	-1,728,801	-4,221,910	-4,518,707
30	-2,685,409	-3,483,131	1,290,003	-451,001	-4,032,205	-4,390,037

Appendix VII: Genetic and economic responses for Strategy two

Table 21: Female progeny mean breeding value differences between selection strategy two and the control, for a QTL of 0.1 σ_G at the three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	-0.805	-0.279	-0.091
15	-1.020	-0.358	-0.124
20	-1.071	-0.380	-0.136
25	-1.097	-0.390	-0.141
30	-1.102	-0.393	-0.144

No economic analysis undertaken for a 0.1 σ_G QTL as strategy two female progeny were genetically inferior over the thirty year time horizon.

Table 22: Female progeny mean breeding value differences between selection strategy two and the control, for a QTL of 0.3 σ_G at the three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	-0.700	-0.196	-0.036
15	-0.861	-0.225	-0.043
20	-0.880	-0.229	-0.048
25	-0.887	-0.233	-0.054
30	-0.885	-0.237	-0.061

No economic analysis undertaken for a $0.3 \sigma_G$ QTL as strategy two female progeny were genetically inferior over the thirty year time horizon.

Table 23: Female progeny mean breeding value differences between selection strategy two and the control, for a QTL of $0.5 \sigma_G$ at the three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	-0.595	-0.102	0.008
15	-0.704	-0.110	0.012
20	-0.694	-0.109	0.004
25	-0.687	-0.119	-0.007
30	-0.683	-0.136	-0.020

No economic analysis undertaken for a $0.5 \sigma_G$ QTL at the 0.01 and 0.1 QTL starting frequencies as strategy two female progeny were genetically inferior over the thirty year time horizon.

Table 24: Economic return for selection strategy two for a $0.5 \sigma_G$ QTL at the 0.35 starting frequency, at two discount rates and three time horizons (NPV \$).

	5%	6.5%
20 years	-1,627,435	-2,020,499
25 years	-1,748,053	-2,104,283
30 years	-2,497,564	-2,606,343

Appendix VIII: Genetic and economic responses for Strategy three

Table 25: Female progeny mean breeding value differences between selection strategy three and the control, for a QTL of $0.1 \sigma_G$ at the three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	-0.214	-0.062	-0.012
15	-0.220	-0.072	-0.017
20	-0.244	-0.082	-0.019
25	-0.254	-0.086	-0.022
30	-0.255	-0.086	-0.023

No economic analysis undertaken for a $0.1 \sigma_G$ QTL as strategy three female progeny were genetically inferior over the thirty year time horizon.

Table 26: Female progeny mean breeding value differences between selection strategy three and the control, for a QTL of $0.3 \sigma_G$ at the three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	-0.147	-0.011	0.004
15	-0.131	-0.004	0.008
20	-0.124	0.006	0.010
25	-0.118	0.013	0.011
30	-0.105	0.017	0.011

No economic analysis undertaken for a $0.3 \sigma_G$ QTL at the 0.01 QTL starting frequency as strategy three female progeny were genetically inferior over the thirty year time horizon.

Table 27: Economic return for selection strategy three for a $0.3 \sigma_G$ QTL at the 0.1 and 0.35 starting frequencies, at two discount rates and three time horizons (NPV \$).

	0.1		0.35	
	5%	6.5%	5%	6.5%
20 years	-5,672,738	-5,468,196	-4,249,58	-1,062,322
25 years	-5,026,400	-5,002,706	781,338	-190,640
30 years	-4,230,906	-4,467,875	1,725,252	445,045

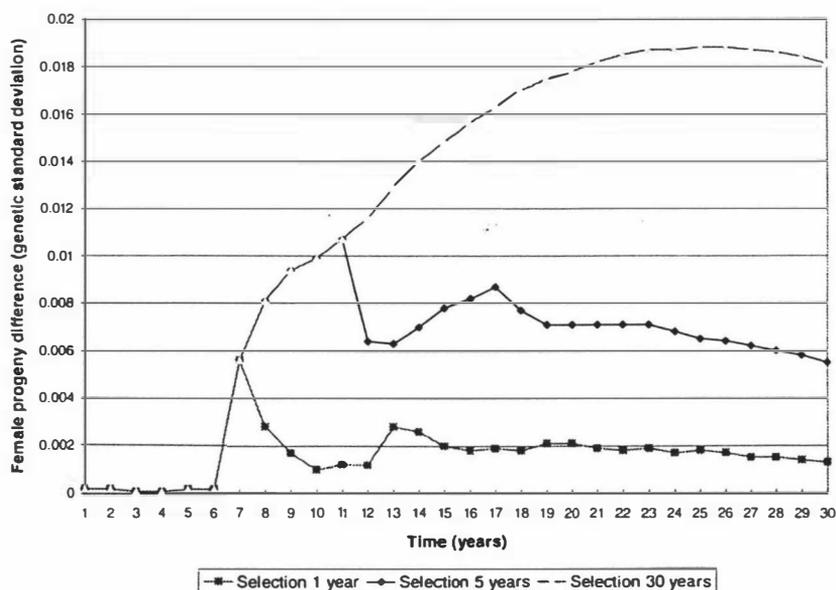
Table 28: Female progeny mean breeding value differences between selection strategy three and the control, for a QTL of $0.5 \sigma_G$ at the three different starting QTL frequencies (σ_G).

Years	QTL starting frequency		
	0.01	0.1	0.35
5	0	0	0
10	-0.078	0.032	0.021
15	-0.044	0.052	0.028
20	-0.009	0.070	0.030
25	0.016	0.077	0.028
30	0.039	0.075	0.024

Table 29: Economic return for selection strategy three for a $0.5 \sigma_G$ QTL at the three starting QTL frequencies, two discount rates and three time horizons (NPV \$).

	0.01		0.1		0.35	
	5%	6.5%	5%	6.5%	5%	6.5%
20 years	-20,470,136	-18,022,565	8,565,636	6,284,550	3,097,527	1,875,067
25 years	-20,136,444	-17,787,807	13,413,455	9,786,802	4,966,015	3,226,145
30 years	-18,543,534	-16,719,181	17,299,560	12,433,749	6,261,379	4,099,098

Figure 21: Difference in genetic merit of female progeny, between selection strategy three being undertaken for 1,5 and 30 years and the control for a QTL size of 0.30 and starting frequency of 0.35.



le 30: Extra economic returns of the one and five year operation of strategy three over the thirty year operation at a $0.3 \sigma_G$ QTL and 0.1 and 0.35 QTL starting frequencies at two discount rates and three time horizons (NPV \$).

	0.1 QTL frequency				0.35 QTL frequency			
	1 year		5 years		1 year		5 years	
	6.5 %	5 %	6.5 %		5 %	6.5 %	5 %	6.5 %
6.5 %	36,082	1,041,785	-787,406	-608,776	-2,901,854	-2,366,813	-1,259,092	-999,901
5 %	4,468	615,479	-1,698,688	-1,266,636	-3,991,452	-3,154,109	-2,015,068	-1,545,913
6.5 %	1,604	149,805	-2,567,712	-1,851,399	-4,861,018	-3,739,649	-2,653,859	-1,975,950