

Chapter 1. Introduction

Animal breeders aim to increase the productivity of their animals through better management practices and genetic improvement. Genetic improvement has been historically based on selecting animals based on confirmation, visual assessment and objective measurements. Henderson (1950) introduced best linear unbiased prediction (BLUP) that uses pedigree and phenotypic measurements of animals and their relatives to estimate breeding values (EBVs) for given traits. This changed the landscape of breeding programs where animals could have EBVs estimated where environmental and management bias was accounted for. The methods were widely introduced in the 1980s and the implementation of EBVs has allowed breeders to select animals for future generations to continue increased productivity through genetic improvement. This genetic improvement, also known as genetic gain, can be manipulated with a number of tools at breeders' hands. Breeders can manipulate rates of genetic gain through changing selection intensity, selection accuracy and generation intervals of male and females.

Selection accuracy, also known as the accuracy of EBVs, can be altered by a number of factors. Accuracy depends on pedigree information, phenotypic measurements on individual and relatives, number of relatives and genomic information. For example the accuracy of a breeding value for an animal will be low if there are measurements on its parents only. Accuracy will begin to increase when phenotypic measurements are made on the individual and/or genomic testing is done. Accuracy will further increase if the individual has progeny with their own performance data. Optimization of phenotyping and/or genotyping has been developed and continues to be refined usually based on cost-benefit scenarios (i.e. what allocation for performance/genomic recording will return the highest benefits?). Recording measurements on individuals and performing genomic testing costs money, but are necessary to continue obtaining accuracies. Accuracy can now also be increased with genomic prediction, the big change being that it can be based on measuring other animals, and the information can be available at a young age.

Multiple ovulation and embryo transfer (MOET) is a female reproductive technology performed on sexually mature females that can increase the fecundity of female breeding stock. Selection of high ranking females can increase selection intensity and has the ability to increase rates of genetic gain. Juvenile *in vitro* embryo production and transfer (JIVET) is another technology that can yield many progeny per female per program. Being performed on juvenile females, not only can the selection intensity be high but generation intervals can also significantly decrease. However, selection accuracy can be low because phenotypic measurements are yet to be recorded on these young individuals. There may be little difference between rates of genetic gain achieved in JIVET and MOET programs as the lower generation intervals achieved in JIVET are often cancelled out by the reduced selection accuracy of such programs (Leitch *et al.* 1994). This was often the case until marker assisted selection (Meuwissen and Goddard 1996) was developed and selection accuracy on animals without phenotypic measurements increased. Genomic selection is now commonly practiced in many livestock industries (Meuwissen *et al.* 2013). Strong synergies have been shown to exist between genomic selection and reproductive technologies (Pedersen *et al.* 2005; Pryce *et al.* 2010) because of the ability to select young selection candidates without phenotypic records more accurately and increase the selection intensity. However, almost all studies have investigated the short-term genetic implications of breeding programs where blanket MOET or JIVET is performed. There have been very few studies that optimize combinations of technologies in stochastic simulations where there is a focus on maintaining long-term genetic merit with genetic diversity, and where those technologies are applied selectively to an optimal proportion of selected parents.

One problem associated with reproductive technologies being used in breeding programs is the ability to significantly accelerate the rates of inbreeding. This is caused by increasing selection intensity on elite families rather than maintaining a high selection differential across families, this as a result of using family information in Best Linear Unbiased Prediction (BLUP) of breeding value for traits not (yet) measured on the candidates themselves. High rates of inbreeding should be avoided due to decreased production, reduction in variance in future generations (Sorenson *et al.* 2008; Smith *et al.* 1998), a decline in fitness levels (van Raden *et al.* 2011) and

increased chances of inheriting homozygous lethal recessive genotypes (Shariflou *et al.* 2011). One method to decrease the rate of inbreeding when using truncation selection in breeding programs using MOET and JIVET is to slightly decrease the selection intensity on males (Brash *et al.* 1996; Kinghorn *et al.* 1991). Optimal contribution selection (Wray and Goddard 1994) is a useful method to not only optimally allocate number of matings (or progeny) to individual animals; it can also be used to control long-term inbreeding by placing a penalty on future co-ancestry. Optimal contribution selection (OCS) has been shown to maximise genetic gain while minimising rates of inbreeding so that long-term gains can be achieved in breeding programs. The benefit of using reproductive technologies can be assessed from modelling breeding programs. Deterministic models could be used, but it would be hard to simulate the consequences of OCS. Stochastic simulation could be used to explore the potential of using the effect of reproductive technologies, either without or combined with the use of genomic selection, under a scheme that uses OCS and optimizes the rate of inbreeding versus genetic merit. Such benefit will depend on the specific breeding program, its breeding objective, and how easily traits can be measured before selection.

Female reproductive technologies are expensive tools to use to produce progeny compared to natural mating or artificial insemination. Therefore the cost of reproductive technologies should be accounted for during selection. Cost could be accounted for in optimal contribution selection and they should be weighted with the benefits of accelerating genetic gain. These benefits are not necessarily all captured by the seed stock producer, who would be the one investing in the breeding technologies. Therefore a cost benefit analysis should account for the degree of economic remuneration to breeders investing in the acceleration of genetic gain.

The aim of this thesis was to examine the impact of optimizing breeding programs using various combinations of reproductive technologies and genomic selection. We use optimal contribution selection in stochastic simulation to focus on maximising genetic gain while keeping co-ancestry at sustainable levels. A cost-benefit analysis is

then performed in a deterministic model of a sheep breeding program. We then presented an optimal selection method that accounted for cost.

Chapter 2 is a review of literature that discusses how reproductive technologies and genomic selection can influence genetic gain in breeding programs. It discusses implications of the breeding programs using these technologies. Topics covered are accelerated genetic gain, accelerated inbreeding, genomic selection, methods to optimise allocation of technologies and a cost benefit analysis of investment in breeding programs. There is a review of studies on modelling breeding programs.

Chapter 3 explores the optimization of breeding programs using a combination of AI or natural mating, MOET and JIVET in sheep, beef and dairy breeding programs. We use optimal contribution selection with a range of penalties applied to future co-ancestry, thereby achieving optimal rates of genetic gain and inbreeding. Chapter 3 also examines the effects of using genomic selection in these breeding programs alongside reproductive technologies.

Methodologies in Chapter 4 expand from Chapter 3 to examine the impact of multiple trait selection. Two Australian sheep indexes are used to examine the impact of genomic selection and reproductive technologies in sheep breeding programs. We contrast a terminal index where all traits are measured within the first six months of life and a dual purpose Merino index where most traits are measured in the second year of life or lowly heritable. This chapter explores the impact of reproductive technologies and the influence genomic selection on genetic gains for individual traits of actual sheep breeding objectives in Australia.

Chapter 5 examines the economic impact of utilizing reproductive technologies and genomic selection in a 2-tier sheep breeding program. We use results from Chapter 4 on the proportion of matings allocated to the various reproductive technologies and perform a cost-benefit analysis in a deterministic model of a single operation where a breeder would breed rams in a closed nucleus to sire lambs for a commercial second tier. The gene flow method

is used to predict the flow of genetic superiority through the commercial tier and cumulative discounted expression of that merit in crossbred progeny of a terminal sire or in merino progeny in self-replacing merino flocks.

Chapter 6 includes the cost of reproductive technologies in the objective function during the optimal contribution selection for the same breeding program structure as used in Chapter 4. As the ability for the breeder to invest in breeding technologies depends largely on how much of the benefits of genetic gain they actually receive, we investigated use of premiums. These premiums were determined by a ram buyer's willingness to pay for improved EBV of a ram, and this was determined by the proportion of the benefit they received.

Chapter 7 is the general discussion that covers four main points as covered in the four research chapters of this thesis. These are: 1) Benefits of female reproductive technologies and genomic selection across species from a genetic merit and inbreeding point of view 2) The benefits in sheep breeding programs based on the actual selection indexes they use and the effect on the various traits within these indexes 3) Cost benefit in a two tier sheep breeding structure 4) True costs of reproductive technologies factored into selection and the need for commercial producers to contribute to the higher investments incurred by the breeders in their breeding programs, e.g. paying a premium based on sire's merit and not following market trends. I will end with a number of recommendations from this thesis.

Chapter 2. Review of Literature

2.1. Introduction

Breeding programs are ultimately designed to improve the overall phenotypic performance of livestock. This change in performance can be measured through response to selection. Response to selection can be predicted by what is known as “the breeders’ equation” (Rendel and Robertson 1950):

$$\Delta G = \frac{i \cdot r_{IA} \cdot \sigma_g}{L}$$

where i is selection intensity of candidates, r_{IA} is the correlation between true breeding value (A) and estimated breeding value (EBV, but often indicated with I for index), σ_g is the genetic standard deviation and L is the generation interval. The correlation r_{IA} is also known as the accuracy of selection. Breeders can increase the rate of genetic gain through 1) increasing selection intensity 2) increasing selection accuracy and 3) decreasing generation interval. Methods to increase selection intensity include the use of fewer females and males to produce the next generation. Reproductive technologies are important here as they can increase the number of progeny per selected parent and therefore have the potential to increase selection intensity. Artificial insemination (AI) allows semen from males to be potentially mated to hundreds or even thousands of females. Technologies to increase number of progeny from females include multiple ovulation and embryo transfer (MOET), mature *in vitro* embryo production and embryo transfer (MIVET) and juvenile *in vitro* embryo production and embryo transfer (JIVET). JIVET is also an effective way of reducing generation interval. Selection accuracy has been increased through measurement of traits, recording of pedigree and optimal use of all information through using the best linear unbiased prediction (BLUP) methods (Henderson 1950) for genetic evaluation. Marker assisted selection (Meuwissen and Goddard 1996) and more recently genomic selection (Meuwissen *et al.* 2001) was developed and has facilitated accuracy of EBVs to increase, particularly in younger stock who have not had any performance measurements yet, if the trait is sex-limited (i.e. milk production) or hard-to-measure (i.e. carcass traits), or has a low heritability (i.e. reproduction). Breeding programs have been developed to assess the implications of using reproductive technologies where traditional performance recording methods were in place. More recently there

have been some studies that assess some of the synergies that may exist between the use of reproductive technologies and genomic selection. This literature review will discuss how these technologies can be applied in sheep and cattle breeding programs, their implications for genetic gain and inbreeding, and identify areas where more research could be undertaken.

2.2. Reproductive Technologies

2.2.1. Multiple Ovulation and Embryo Transfer

MOET is the super-ovulation of sexually mature females where they are artificially inseminated (usually) and then 5-7 days later, embryos are retrieved and transferred into recipient females who have had their oestrus cycles synchronised with the donor female (Nicholas 1996). Donor females need their oestrus cycles manipulated for MOET programs due to producers usually performing MOET on more than one donor female at a time. The female donors' (and recipients') oestrus cycles are manipulated through a series of hormonal injections.

The success of MOET programs are determined by the number of live animals born or weaned. Success of programs can depend on a wide range of factors which include: age, genetics, breed, endocrine levels, health, nutrition, lactation status of donors and recipients, semen quality, climatic factors and skill of practitioners (Cognie 1999; Gonzalez-Bulnes *et al.* 2004). Live number of offspring can range from zero to 80 from a single MOET program in most domesticated ruminant species (Armstrong *et al.* 1999; Hasler 2001). However, past MOET studies have concluded that a “successful” MOET program results in an average of 2-8 live offspring per donor female (Armstrong *et al.* 1999; Hasler 2001; Nicholas 1996). MOET is an expensive reproductive technology especially when comparing the cost per animal born from AI or natural mating (Brash *et al.* 1996; Pryce *et al.* 2010). The cost can be up to 8 times more expensive on a cost per progeny scale. The benefits of MOET include increasing selection intensity of females, more offspring per straw of semen which may be expensive and/or rare, increasing fecundity of females that rear financially valuable offspring and dissemination of genetics domestically and potentially worldwide with the use of freezing and thawing embryos.

2.2.2. Mature *In Vitro* Embryo Production and Embryo Transfer

MIVET is the extraction of immature oocytes from ovaries of mature females. This can be achieved non-surgically in cattle, but needs to be extracted surgically in smaller ruminants such as sheep and goats (Fry and Dryancourt 1996). Once oocytes have been extracted they are matured and then fertilized *in vitro*. Suitable embryos are then transferred into recipients whose oestrus cycles have been synchronized to ovulate at the same time the oocytes were fertilized. While MIVET benefits are similar to described in MOET, success rates are typically 10-20% lower. This is caused by *in vitro* mediums not being able to exactly replicate the *in vivo* conditions of a live donor (Pomar *et al.* 2005; Ptak *et al.* 1999). Two major advantages of *in vitro* technologies is a straw of semen can be used across up to 20 donors and oocytes can be divided into smaller groups so multiple sires can be used for each individual donor (Amridis and Cseh 2012). Further advantages of MIVET include not having to super-ovulate or synchronise oestrus cycles of donors, oocyte extraction can be done while the donor is in early stages of pregnancy which does not disrupt annual breeding programs. However the overall cost is similar to that of MOET breeding programs (R Fry 2013, pers. comm., 24 July).

2.2.3. Juvenile *In Vitro* Embryo Production and Embryo Transfer

JIVET is similar to MIVET except oocytes are surgically extracted from juvenile female donors. The juvenile donors also need two injections of follicle stimulating hormone to mature follicles on their ovaries. Typically JIVET is performed on heifers aged 1-4 months of age and 3-10weeks age on juvenile ewes and does (Earl *et al.* 1994). JIVET embryo yields can often reach over 100 embryos (A Michael 2013, pers. comm., 21 March). However there are low pregnancy rates in JIVET at around 17-30% (Morton 2008). Several studies (Armstrong *et al.* 1999; Earl *et al.* 1994; Morton *et al.* 2005) and personal communication with breeders and *in vitro* companies suggest that JIVET can generate on average between 4-16 live offspring per donor. The overall cost per JIVET program is generally more expensive/per donor female compared to MOET or MIVET largely due to the cost of recipients that fail to hold pregnancy. However, the cost per progeny is usually 20-30% less per progeny born live compared to MOET and MIVET (Mapletoft and Hasler 2005; Morton 2008). JIVET shares all the benefits of MIVET that come with being an *in vitro* technology. However there is a slightly increased risk that the juvenile

donor may never breed naturally due to the early hormonal stimulation of the ovaries and the surgical procedures at such a young age (Earl *et al.* 1994). JIVET further increases selection intensity compared to MOET with the increased number of progeny per donor. JIVET also is a very effective method to reduce generation interval (Kinghorn *et al.* 1991).

2.3. Breeding Programs

Optimisation of breeding programs involves a series of complex decisions where breeders need to manipulate parameters of the breeders' equation to maximise genetic gain. The breeders' equation can be manipulated through using reproductive technologies described earlier. MOET and JIVET are capable of increasing female selection intensity, while JIVET is highly effective in decreasing generation interval. Breeding programs that utilise reproductive technologies has been studied since the 1970s and have ranged across dairy cattle, beef and sheep breeding programs.

The use of MOET in breeding programs was initially investigated in 1975 in beef where Land and Hill concluded MOET breeding programs could increase genetic gain by 100% when compared to conventional AI or natural breeding programs. However they also found that inbreeding increased by 110%. Gearheart *et al.* (1989) also concluded that MOET breeding programs increased genetic gain in beef by 67% with an increase of inbreeding of 86%. In dairy cattle breeding programs, Nicholas and Smith (1983) were able to increase genetic gain by up to 30% compared to traditional progeny proven breeding programs with the rate of inbreeding also increasing as the generation interval decreased. This was a landmark paper, mainly because it emphasized that selection in breeding programs could be based on less accurate selection with shorter generation intervals, rather than long generation intervals and accurate selection based on progeny, as commonly practiced in dairy. For many, this was somewhat revolutionary. They noted there was more inbreeding, but they still underestimated that amount as they didn't account for the Bulmer effect (1971). This makes the between-family variance smaller, and effectively leading to larger correlations among EBVs of related selection candidates when selected based on family information, as in BLUP. Leitch *et al.* (1994) further demonstrated the power of both increasing selection intensity and decreasing

generation interval in dairy cattle breeding programs by studying the effects of using MOET and then decreasing age of female selection candidates from two years of age to one year of age. They concluded that compared to traditional AI programs genetic gain would increase by 9% when selection candidates were two years old and by 93% when selection candidates were one year old. The use of MOET in simulated sheep breeding programs has had similar effects to beef and dairy. Horton (1996) estimated closed nucleus sheep breeding schemes that implemented MOET increased genetic gain by 32%, while inbreeding increased at 115%. Brash *et al.* (1996) stochastically simulated wool production would increase in a closed nucleus by 17% compared to traditional breeding programs without significantly increasing rates of inbreeding. A decade earlier, Smith (1986) using a deterministic model predicted the impact of using MOET in sheep breeding programs compared to conventional breeding programs where the single trait or index is measured in the first year of life or in the second. He found MOET to accelerate genetic gain by 74% and 28% and inbreeding to also increase by 54% and 114% for breeding scenarios where traits are measured early or late, respectively.

All of the studies mentioned so far investigated the genetic implications of MOET in breeding programs. JIVET was developed in the 1990s (Earl *et al.* 1994), but was quickly dismissed because selection accuracy of juvenile selection candidates was very low. A balance needs to be found between selection accuracy and generation interval. Selecting females for JIVET based on relative's information often saw the benefits of reduced generation interval cancelled out by low selection accuracy. Lohuis (1995) simulated that JIVET performed on 1-5 months old heifers could increase genetic gain by up to 20% compared to traditional dairy breeding programs. They also simulated that MOET breeding programs would deliver up to a 15% increase in genetic gain over traditional breeding programs, giving JIVET breeding programs a slight advantage in that particular scenario. There were very few studies investigating the long-term effects that JIVET had on breeding programs prior to the implementation of genomic selection (Meuwissen *et al.* 2001).

2.4. Genomic Selection

One of the earlier papers to systematically investigate the effect of marker assisted selection (MAS) on the rate of genetic gain was by Meuwissen and Goddard (1996). They considered one marker (or more) to track the inheritance of a quantitative trait locus (QTL) (or more) from individuals through to their descendants. The association between markers and QTL was assumed to be estimated in a previous generation and in following generations it would be possible to select individuals with desirable alleles. An important point made in this paper was that the benefit of marker assisted selection depended on 1) the amount of variation explained by the markers, 2) whether a trait could be measured before the moment of first selection and 3) the trait heritability. In essence, when a trait is difficult to improve by conventional selection, then the benefit of MAS will be relatively larger. Meuwissen *et al.* (2001) expanded on MAS by fitting many dense markers in the model such that at least one marker would be in linkage disequilibrium (LD) with QTL. The genome of animals can be divided into small segments with effects of these segments estimated in a reference population of which animals are genotyped and phenotyped (Goddard, 2009). Through Meuwissen *et al.*'s (2001) method, the effects of all loci that contribute to genetic variation can be captured by genetic markers, including the many loci with very small effects, i.e. those that would normally not be detected in the QTL detection methods proposed previously. Once a reference population is in place, subsequent generations can be genotyped to determine what chromosomal segments of their ancestors they carry (Goddard 2009). With this information the sum of all the effects can be added to give a genomic breeding value (GBV) or molecular breeding value (MBV). A genomic enhanced breeding value (GEBV) is calculated when genomic information is combined with information on phenotyped animals that are not genotypes but related through pedigree (Hayes *et al.* 2009). Accuracies of genomic prediction as high as 85% were simulated by Meuwissen *et al.* (2001) in dairy breeding schemes where abundant phenotypic information is available in progeny tested bulls and where the effective population size is small. However accuracies in beef and sheep are much lower due to relatively smaller reference populations, multi-breed facets and less performance recording overall (Daetwyler *et al.* 2010).

With added accuracies of EBVs facilitated through genomic testing, rates of genetic gain can be increased.. Similar to MAS, genomic selection benefits breeding programs most where traits in an index are sex-limited, hard-to-measure, measured late in life and/or have a low heritability. Genomic selection has been shown to increase genetic gain in dairy cattle by up to 33-108% (de Roos *et al.* 2011; Lillehammer *et al.* 2011; Schaeffer 2006). Van der Werf (2009) estimated GS to increase index response in terminal sheep breeding programs by 16-32%. However individual trait responses were significantly higher in the carcass traits (e.g. dressing %) than that compared to traits measured earlier in life (e.g. weaning weight). Similar trends were observed in Merino sheep breeding programs where lowly heritable traits such as number lambs weaned increased by 600% compared to clean fleece weight that increased by 100% (van der Werf 2009). In general GS will benefit breeding programs to different degrees and will depend largely on the accuracy increase of GEBVs versus EBV, the age at which animal can be measured for most of the traits and the difficulty (or cost) of measuring the traits. Potential benefits can be tested in modelling studies by assuming a range of accuracies for the GEBV.

Indexes are made from using a combination of traits, where estimated breeding values (EBVs) of various traits are weighted by the economic value of the trait. Genomic information, family information, economic weightings, correlations between traits, heritabilities of traits and whether the trait is measured will have an impact on the accuracy of the EBVs and therefore selection response (Hazel *et al.* 1994; van der Werf 2009). Many breeding programs that assess the impact of reproductive technologies measure a single trait with a single heritability and standard deviation (Mrode 2014). There are very few studies that assess the impact of reproductive technologies on individual traits within an index. These responses could differ between traits due to different times of trait measurement, heritability of trait and genomic accuracy of trait or whether the trait gets measured at all.

2.5. Breeding Programs using Genomic Selection and Reproductive Technologies

Studies discussed so far have focused on either reproductive technologies or GS and their implications to breeding programs as single treatments. However, there is scope to investigate both of these technologies combined and assess if any synergies existed between them. Van der Werf and Marshall (2005), Goddard and Hayes (2007) and

Kinghorn (2007) discuss the potential to rapidly accelerate rates of genetic gain using reproductive technologies with GS. This could be achieved by manipulating the breeders' equation with increased selection accuracy combining with decreased generation intervals. Pederson *et al.* (2012) concluded that when MOET was performed on half of a nucleus breeding dairy cows with GS, genetic gain was increased by 23%. Furthermore, Pryce *et al.* (2010) studied the impact of using JIVET compared to conventional breeding programs in dairy. Using deterministic simulation they found that JIVET breeding schemes could increase genetic gain by 98% while inbreeding increased at a rate of 65% annually. From these studies we can observe that GS allows us to increase selection accuracy of young female selection candidates and therefore it is easier to justify (i.e. more optimal) to choose young animals for breeding. This decreases generation interval and using fewer females also increased selection intensity selected, and as GS facilitates more accurate selection of candidates at younger ages which suggests higher rates of genetic gain could be achieved (Sorenson and Sorenson 2010). However the use of female reproductive technologies and genomic selection do have the ability to significantly increasing rates of inbreeding.

2.6. Inbreeding

Especially when used on young selection candidates, reproductive technologies have a strong tendency to accelerate rates of inbreeding through increasing selection emphasis on elite families rather than selection of the best members of families. The reason for this is that at a young age, EBVs are often largely affected by family information, such that relatives have high correlations among their EBVs and ranking based on EBV tends to favour co-selection of relatives (Belonsky and Kennedy 1988). With GS allowing more accurate selection decisions to be made on young selection candidates, generation interval is likely to decrease. Decreased generation intervals can further increase the rate of inbreeding (Daetwyler *et al.* 2007). However the use of genomic information also has the ability to decrease the rate of inbreeding as the genomic information can differentiate between siblings and other relatives and hence co-selection of siblings can be avoided (Daetwyler *et al.* 2007). High rates of inbreeding should be avoided due to declines in production due to reduction in variance in future generations (Sorenson *et al.* 2008; Smith *et al.* 1998), a reduction in fitness (van Raden *et al.* 2011) and an

increased likelihood of inheriting homozygous lethal recessive alleles (Shariflou *et al.* 2011). Several studies (van Arendonk and Bijma 2003; Brash *et al.*, 1996; Kinghorn *et al.* 1991; Lillehammer *et al.* 2011; Pryce *et al.* 2010) were able to maintain or decrease rates of inbreeding while using reproductive technologies through decreasing selection intensity of male selection candidates. This usually came at a slight decrease of genetic gain compared to programs with high male selection intensity.

Many breeding schemes aim to achieve a balance between genetic gain and inbreeding. Toro and Perez-Enciso (1990) selected parental pairs to maximise the parent average EBVs while restraining the average inbreeding coefficient using a linear model. De Boer and van Arendonk (1994) claimed this would be only a short-term fix to inbreeding and would have no impact on reducing the long-term inbreeding because the linear model only considered relationships between pairs rather than all the pairs in the mating population. Another method to optimize genetic gain with inbreeding was developed by Wray and Goddard (1994). They developed optimal contribution selection (OCS) where long-term genetic gain is balanced with long-term genetic diversity. This algorithm maximises selection response while constraining the level of inbreeding (Meuwissen 1997; Grundy *et al.* 1998) in the population by optimizing mating proportions of parents. Meuwissen (1997) concluded that OCS out-performed standard best linear unbiased prediction (BLUP) truncation selection for long-term response by 20-60% when a predefined rate of inbreeding was set. Optimal contribution selection has been used in practical breeding programs such as dairy (Kearney *et al.* 2004), sheep and beef (Avendano *et al.* 2003) and aquatic species such as salmon (Hinrichs and Wetten 2006). Further parameters and considerations can be added into the OCS procedure provided an efficient optimization procedure is used, as demonstrated by Kinghorn's (2011) Matesel program, which can account for cost, avoiding matings with undesirable specific alleles (such as developmental duplication in Angus cattle) or promote matings with desirable alleles (polled gene). Optimal contribution selection methods could be an effective tool to optimize allocations of reproductive technologies while maintaining sustainable and realistic inbreeding levels.

2.7. Modelling of breeding programs

A large amount of modelling occurs to test potential methods instead of undertaking costly and/or time consuming selection experiments. There are two types of modelling: 1) deterministic and 2) stochastic.

Deterministic models have low computational requirements, are flexible and usually quick to run. Therefore they are useful to perform multiple scenarios over short periods of time (Pryce and Daetwyler 2012). Stochastic models automatically account for individual variability, and the change of within family variation and between family variation due to selection, something that deterministic models cannot easily capture in complex population structures, e.g. with unequal family sizes and overlapping generations (Mullin and Park 1995). Moreover, it is not easy to predict with deterministic models the consequence of optimal contribution selection for rate of genetic gain and inbreeding. However, stochastic simulations are usually far more time-consuming than deterministic simulations. This could be important when modelling breeding programs that use reproductive technologies where inbreeding could increase very quickly and optimal contribution selection is paramount for achieving a sustainable long term gain.

Stochastic simulation is time consuming but it is easier to simulate realistic breeding programs with selection across age classes, and dynamic age structures. Stochastic simulation also automatically accounts for the Bulmer effect (1971). This is important when estimating gains in simulated breeding programs as the genetic variance of the population will decrease over time as a population becomes more related (van Grevenhof *et al.* 2012) and the effect is large when selection is based on family information, as would often be the case for MOET and especially JIVET. Furthermore, a stochastic simulation is required if optimising individual contributions of selection candidates to further generations and the inbreeding rate can be derived from the pedigree information that develops, rather than predicting it in advance. The OCS method is very effective in determining individual contributions within populations, but can be time consuming in stochastic simulations (Grundy *et al.* 1998; Kinghorn, 2011).

Another important aspect of modelling breeding programs is genomic selection. There are two types of stochastic models that can be used when simulating genomic selection in breeding programs. One method to simulate genomic breeding values is to generate them as a trait correlated to the true breeding value with a heritability of one and correlation equal to accuracy (Dekkers 2007). The second and more time consuming process is to simulate genomes and SNPs of individual animals (Pryce and Daetwyler 2012). Models that simulate SNPs can allow for more realistic accuracies of genomic selection as estimated from SNP effects, especially when the distance between selection candidates and reference population changes over generations (Lillehammer *et al.* 2011; McHugh *et al.* 2011). The accuracy of genomic prediction could then deteriorate due to a fading LD structure between markers and QTL. While simulating actual genomes with genotypes for markers and QTL could provide slightly more accurate predictions in breeding programs, it may not be practical and too time consuming in simulations that require many years of breeding with many replications.

2.8. Economics of using technologies in breeding programs

Genetic improvement programs that incorporate the use of genomic selection and/or reproductive technologies can increase the rate of genetic gain as discussed earlier. Accelerated rates of genetic gain will benefit nucleus breeders with improved performance. However these benefits may not be enough to offset the costs of reproductive technologies, particularly in sheep and beef where life-time margins of individual animals are small compared to dairy (van der Werf 2006; van Raden 2004). Most livestock populations are formed into tiers (Figure 2.1) where most genetic improvement is made in the top tier. This genetic improvement is multiplied over many animals in a population with the benefits accumulating over time, so at a population level, small improvements may quickly lead to large benefits (e.g. see Banks and van der Werf 2009). However, population-wide benefits rarely flow back to the breeder making the investment Banks *et al.* (2014), hence for a cost benefit analysis relevant to the breeders it becomes relevant what proportion of the benefit he or she actually receives via an increased price of the seedstock sold.

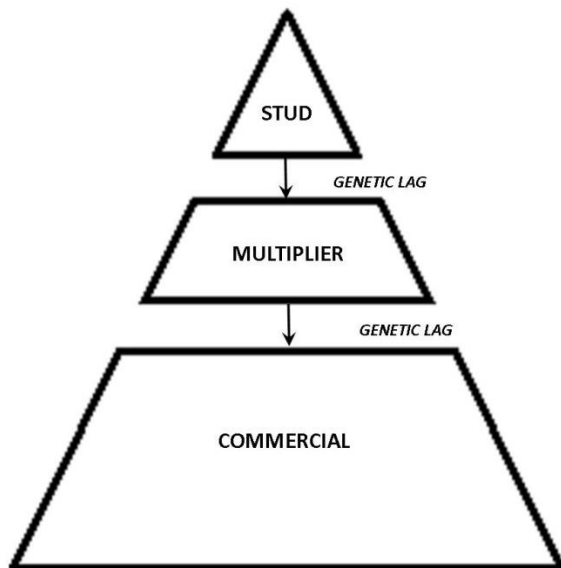


Figure 2.1- Traditional animal breeding pyramid structure

Performance recording of individuals is an important, yet costly exercise to help improve accuracies of EBVs so rates of genetic gain can improve. Furthermore implementation of reproductive technologies and/or genomic selection to further accelerate genetic gain bears even more of cost to production. The cost of reproductive technologies includes costs of semen, drugs, labour, professional services and recipient management. Often, cost of reproductive technologies need to be absorbed by the breeder who engages in these activities (Brash *et al.* 1996; Horton 1996; van Arendonk and Bijma 2003).

Structures of breeding programs could be purported in three ways. Firstly, selection decisions can be based on the three tiers (Figure 2.1) being a single entity as van der Werf *et al.* (2011) did where benefits of selection decisions were evaluated for made to benefit the entire industry. Horton (1996) investigated a similar scenario where he estimated the effects of genetic improvement programs in sheep over three tiers. Both studies suggest commercial breeders benefit more than the studs they buy from as they invest smaller amounts of resources into genetic improvement programs, yet yield most of the benefit. This is supported by Horton *et al.* (2014) suggested if commercial breeders retain up to 94% of benefit of genetic improvement, then there is still merit for nucleus breeders to invest in genomic selection. This is assuming there are clear price signals for genetic improvement.

The second structure is a two-tier breeding program where a nucleus supplies sires for a commercial flock (Figure 2.1). A typical example of this is where a producer has a nucleus that breeds sires for its self-replacing herd in the second tier.

Nitter *et al.* (1994) used Hill's (1974) gene flow method in a beef simulation where annually the rate of nucleus genetic gain increased year-on-year and was then disseminated through a lower tier. They concluded that for each dollar gained in the second (multiplier) tier per female's progeny, was minimalised when the benefit was spread over so many animals in the lower tier. Furthermore, Horton *et al.* (2014) discusses that cost of genetic improvement programs in nucleus is further diluted once those genetics reach the commercial population via the multiplier population. The gene flow method (Hill 1974) calculates a cumulative discounted expression (CDE) for genetic contributions into future generations of the various tiers and this depends on age class contributions (determining generation intervals and genetic lag between tiers) and whether contributions to lower tiers are terminal or continues via replacements. The initial gene flow and transmission of superiority is an important tool when investigating investment decisions made at a current point of time. Long-term gene flow predictions can also determine that each unit of superiority in the nucleus accumulates by a factor of $1/(\text{sum of generation intervals})$ each year, which is the equivalent to the breeder's equation (Rendel and Robertson 1950). The CDE factors in a discount rate to discount future benefits which gives economic predictions as a net present value (McClintock and Cunningham 1974). The net present value is an important tool to use in economic analysis of genetic improvement programs (Amer *et al.* 2007), as it accounts for pricing uncertainty in the future. Finally, selection decisions could be based on a closed nucleus or stud that uses reproductive technologies and/or GS to improve rates of genetic gain to improve performance within their own system.

If an animal is born to a reproductive technology, there would need to be financial incentive to make the initial investment. To justify the use of reproductive technologies in this case a premium needs to be paid for animals bred. Brash *et al.* (1996) discusses ram breeders need a \$300-\$400 premium paid for rams bred via MOET breeding schemes. This way both breeders and buyers can benefit from accelerating genetic gain. However, sheep

return small margins compared to dairy cattle that are capable of producing over \$15,000 (AUD) worth of milk over a lifetime (Macdonald *et al.* 2008). Using reproductive technologies within a dairy herd could be a very attractive option when breeding from top ranking females. Furthermore, with genetic standard deviations of the breeding objective up to \$80 (AUD) in dairy cattle (Pryce and Hayes 2011) and the cost of genomic testing currently at \$50, and becoming cheaper, it is now becoming standard practice in dairy systems to genotype potential female replacements. Furthermore, Schaeffer (2006) suggested that dairy bull studs could save up to 92% of costs by genomic selecting young bulls and abandoning traditional progeny test schemes.

2.8. Conclusion

Past studies have shown reproductive technologies to increase rates of genetic gain. Furthermore, genomic selection can help improve selection accuracy and decrease generation interval which accelerates rates of genetic gain. Together they possess strong synergies to further accelerate rates of genetic gain. However inbreeding levels should be kept to realistic and manageable levels which few studies address. Optimal contribution selection appears to be an effective method in optimising genetic contributions (and hence reproductive technologies) while controlling inbreeding levels in stochastic simulations with this type of study done relatively little. Research into optimising breeding programs using optimal contribution selection to selectively assign reproductive technologies and genomic testing in stochastic simulations should be investigated. Response to both single trait index selection and index selection that contains multiple traits should also be considered. With few methods existing that make selection decisions optimally while accounting for cost, a cost-benefit analysis should also be undertaken due to the expense of using reproductive technologies and genomic testing.

Chapter 3. Increased genetic gains in sheep, beef and dairy breeding programs from using female reproductive technologies combined with optimal contribution selection and genomic breeding values.

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Chapter 4. Increased genetic gains in multiple sheep traits using female reproductive technologies combined with optimal contributions selection and genomic breeding values

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Chapter 5. Cost-benefit analysis of MOET and JIVET in 2-Tier sheep breeding program

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Chapter 6. Optimised nucleus sheep breeding programs where cost of reproductive technologies are considered during selection.

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Chapter 7. General Discussion

This thesis optimised breeding programs in livestock populations using reproductive technologies and genomic selection. Optimal contribution selection (Wray and Goddard 1994) was used in Chapter 3 to optimally assign reproductive technologies to selection candidates maximise genetic gain while maintaining genetic diversity. Implications of these breeding programs were initially assessed over several species and time of trait measurement was varied. Initially a single trait was used and the main aim was to explore the efficacy of reproductive technologies in relation to genetic gain and inbreeding. Costs were not considered hence, these were scenarios that would reflect the maximum usage of the technologies. It was shown that even if costs are not considered, reproductive technologies are not always beneficial for breeding programs. The various scenarios demonstrated the most favourable scenarios across species, and it was shown that without genomic selection the addition of MOET accelerated rates of genetic gain in all breeding programs. However, the further addition of JIVET to breeding programs without genomic selection proved that there was little to no benefit when compared to breeding programs with AI/N + MOET. When genomic selection was used, scenarios to benefit most were those when traits were measured late in life or sex-limited. Furthermore, the added accuracy that genomic selection provided made breeding programs that contained JIVET the highest rates of genetic gain.

In Chapter 4 we used real indexes in sheep breeding programs and measured individual trait responses. The main purpose of this chapter was to show the potential gains for real selection indexes in sheep. The multiple trait examples also show that not only total gain might increase, but also the relative gain that is achieved for the different traits. In other words, the relative selection emphasis on the various traits might change. Use of genomic selection increased responses in individual traits most when individual traits within an index were heavily weighted and when combined with reproductive technologies i.e. number of lambs weaned. It also further accelerated responses to traits with lower

accuracies or hard to measure. Some further discussion on the benefit for real indexes, and the relative change of emphasis across traits will follow.

When we observed the potential gain from using reproductive technologies, a cost-benefit analysis was undertaken for a two-tier system where a nucleus bred rams for its commercial flock in Chapter 5. This was deterministically simulated with genetic improvement programs in tier one based from Chapter 4 results. We found reproductive technologies were economically viable in Merino breeding programs only when genomic selection was used as well. However the terminal sheep breeding programs yielded the highest economic returns when less money was invested into breeding programs apart from when JIVET was used with genomic selection.

The scenarios in Chapter 5 generally overused somewhat the reproductive technology, as the level of use was derived from Chapter 4 (where there was no cost factored into allocation of these technologies). Nevertheless, the chapter gives a clear insight in the elements that determine whether these technologies provide a good investment option. We observed that all nucleus breeding programs were profitable over 20 years. However some nucleus breeding programs were more profitable than others. In the terminal index the most profitable breeding program was AI/N+MOET+JIVET (using GS). We observed that AI/N+MOET breeding programs were less profitable than AI/N and the use of genomic selection in either of these scenarios reduced profitability. In the Merino index, it was observed that any use of reproductive technology was economically viable using without genomic selection. When genomic selection was used the most profitable breeding programs were those who had the highest genetic gain. These results were approximations as static scenarios were used, with a predetermined proportion of JIVET and MOET matings. A tactical approach that is more dynamic would be a more appropriate, assigning matings in relation to expected benefit and estimated cost and using the opportunity of prevailing candidates. However, the main advantage of a deterministic model is that it is relatively simple and transparent with no variation in outcome. It is also relatively easy to explore the effect of a number of parameters of the breeding program. One important aspect that affects the feasibility of using technologies is whether the breeder who is required to invest in them

receives a sufficient proportion of the benefits that the genetic improvement generates. This aspect will be further discussed in this chapter.

In the last experiment we revisited the optimal contribution selection algorithm this time also taking into account the cost of these technologies. When accounting for cost we should be more confident that the optimal selection strategy will assign the most optimal proportion of matings to reproductive technologies. In many cases this optimal level of use was quite low. It was observed breeders needed to recoup at least 6% of the benefit of genetic improvement before he has an incentive to use reproductive technologies in the Merino index and 32% is needed for the terminal index.

The general discussion will cover four main points from the thesis. These are: 1) The benefits of reproductive technologies and genomic selection across species; 2) How individual traits within an index are affected in similar sheep breeding programs; 3) How cost effective these sheep breeding programs are in a two tier breeding structure; and 4) Factoring cost into nucleus selection and the payment of premiums which is determined by who receives the benefits. A list of 5 recommendations will follow these discussion points, with conclusions completing the chapter.

7.1. Benefits of female reproductive technologies and genomic selection across species

In our results from Chapter 3 we observed in all breeding programs that the addition of reproductive technologies enhanced the rate of genetic gain compared to the control of AI/N mating programs. Without genomic selection there was little benefit of using JIVET in the early measured traits in sheep and beef and no benefit in the late measured traits of sheep and beef or the sex-limited dairy trait. When reproductive technologies were used, slightly higher benefits (proportionally) were observed (in genetic standard deviations) in traits that were measured early in life. When genomic selection was used in AI/N or AI/N+MOET breeding programs, we saw low-modest rates of genetic gain in early measured traits of sheep and beef and, moderate to high rates of genetic gain when genomic selection

was used with JIVET. Furthermore, in the late in life measured traits in beef and sheep and the sex-limited dairy trait, we observed genetic gain to increase by up to 143% with generation intervals reducing by up to 50%. This was expected with genomic selection previously shown to give the largest benefits to traits measured later in life, hard to measure, a low heritability or sex-limited (Dekkers 2007, van der Werf and Banks 2010, van der Werf *et al.* 2010). This further supported conclusions that strong synergies exist between genomic selection and reproductive technologies as reported by Dominik *et al.* (2009), Pryce *et al.* (2010), Pederson *et al.* (2012) and discussed by van der Werf and Marshall (2005).

A major difference in Chapter 3 with previous studies assessing the impact of reproductive technologies was that the technologies were used selectively and optimally, with optimal allocation of matings for each individual while achieving sustainable inbreeding levels i.e. 1.0% increase per generation (Bijma 2001, Buch *et al.* 2012). Optimal contribution selection was effective in optimally assigning individual selection candidates to respective technologies. Genetic diversity was maintained with high proportions of MOET and/or JIVET matings assigned. This was achieved through slightly decreasing selection intensity on males. Decreasing selection intensity on males was also used by Brash *et al.* (1996), Kinghorn *et al.* (1991) and Pryce *et al.* (2010) to help reduce inbreeding while still maintaining high levels of genetic gain.

Genetic gain and inbreeding levels each year were measured as the average true breeding value and average inbreeding of the entire drop, respectively. Rates of genetic gain and inbreeding were then measured as averaged over years. Breeding values were calculated via pedigree based BLUP (Henderson 1975) and inbreeding was also calculated based on pedigree (Meuwissen and Luo 1992). The optimal contribution also used the NRM in the objective function when penalizing co-ancestry of selected parents, which is a good predictor of inbreeding rate (Meuwissen 1997). Some authors have shown that using a genomic relationship matrix (GRM) has some advantages over a pedigree derived relationships matrix (NRM, A), allowing similar rates of genetic gain with slightly slower rates of inbreeding (Nielsen *et al.* 2011; Dagnachew and Meuwissen 2014). By using the GRM, we could

slightly decrease rates of inbreeding while still achieving the same amounts of genetic gain would be achieved using the NRM.

We assumed the genomic breeding value was available shortly after birth. It was assumed that the accuracy of the gene test did not change, and it was similar to being derived as an external reference population. Some studies have pointed out that the linkage disequilibrium (LD) pattern across generations might change (Farnir *et al.* 2000) such that prediction accuracies could deteriorate. Deterioration of predictive ability across generations was demonstrated by Wolc *et al.* (2011). On the other hand, families that increase in proportion of nucleus over generations through use of MOET and JIVET could slightly increase the accuracy of their GEBVs (Risch and Teng 1998) and provided the genotypes and phenotypes are captured in a database, this could increase the accuracies over time. A more exact long term prediction of response maybe difficult and requires simulation of the actual marker genotypes to capture the change of the LD structure over time due to selection (van Raden 2008).

7.2. Breeding programs using multiple trait indexes

Chapter 4 followed the same methodology as Chapter 3, but the aim was to assess individual responses of multiple traits from two sheep indexes currently used in Australia. The indexes used were the terminal *Lamb 2020* index and the Merino *MP+* index (<http://www.sheepgenetics.org.au/Getting-started/ASBVs-and-Indexes/LAMBPLAN-Terminal-Indexes>). The index responses were comparable to the ‘early’ and ‘late’ measured sheep trait scenarios from Chapter 3 with all traits measured within the first 6 months of life in Lamb 2020 and most traits measured after the first year of life in the *MP+* index. Another important difference between indexes is that the Lamb 2020 index reflects a much lower variation in profit, due to the lower value of the traits involved. In other words, the standard deviation of the Lamb 2020 breeding objective is much lower. This has an effect of the feasibility of investing in technologies in nucleus breeding programs.

Overall, very similar responses in total genetic merit were observed in Chapter 4 when compared with Chapter 3 where a single trait was simulated. More interestingly, genomic selection facilitated proportionally larger responses in some traits compared to others. In the Merino index, we observed an increase of up to 250% in number of lambs weaned (NLW) when genomic selection was used. NLW is a trait with a large economic value but with a low heritability. The large increase was achieved even with assuming a relatively low genomic accuracy of 0.2. The example shows that even small improvements in accuracy can have a large effect on the response of an individual trait, especially when they are weighted so heavily in an index.

The responses of individual traits differed when comparing the same breeding programs with and without genomic selection. This reflects a general principle in breeding programs that the relative gain for a trait is not only determined by its economic value, but also by the amount of information available to estimate the breeding value (Henderson 1975). Both factors determine the relative emphasis that is imposed on a trait. The genetic, and to a smaller extent the phenotypic correlation structure does play a large role in determining what changes are possible. But within certain boundaries, the response can be manipulated by economic weights as well as trait measurement. There are many examples in breeding programs that can be used to illustrate this point (Hazel *et al.* 1994; Shook 2006, Veerkamp *et al.* 2000). Genetic improvement for reproductive performance in sheep is possible by indirect selection, e.g. via body weight of mature sheep. However, selection on body weight might result in a response for reproductive rate, but a larger consequence is likely more increase in body weight. Only actual measurement of reproductive rate could result in increased reproductive performance, with the possibility of not increasing weight (Rosati *et al.* 2002). Genomic selection has a similar effect with the potential to select on 'hard to measure traits' without having to resort to indirect selection. An important prerequisite is that the traits are measured somewhere in a reference population, either in historically recorded animals, or in a specifically design resource flock when it involves measurement of new traits (e.g. carcass traits) (van der Werf *et al.* 2010).

7.3. Cost benefit in two tiers

Chapter 5 used a deterministic model to measure the cost benefit of a sheep producer who bred rams (tier 1) to sire lambs in their commercial flock (tier 2). The MP+ index breeding program demonstrated in this scenario that reproductive technologies were only an economically viable option if it was used in conjunction with genomic selection. Furthermore, in this breeding scenario use of genomic selection is essential as it facilitates higher genetic gain but relative to reproductive technologies the extra costs is not as high (if measured per commercial ewe). However, the terminal Lamb 2020 breeding programs demonstrated that the most profitable nucleus breeding program was where JIVET and genomic selection was used. Apart from when JIVET was used with genomic selection, the use of reproductive technologies was less profitable when selecting for Lamb 2020 breeding objective. The difference between the two indexes was caused by three factors. The first was the comparatively lower dollar value in the rate of genetic gain in the Lamb 2020 index which is caused by the lower standard deviation of the breeding objective and gives less variation in the economic value of the genetic merit. The second factor causing Lamb 2020 to be less profitable was that the gene flow was only facilitated through the rams as they are a terminal breed, whereas the second tier Merino breeding program was a self-replacing flock where nucleus rams contributed directly as well as indirectly through their progeny. Finally, the terminal index has all of its traits measured in the first five months of life with medium to high heritabilities, hence providing further evidence that there are only small benefits to be gained from genomic selection when selection occurs after measurement.

We simulated nucleus breeding programs and genetic gain based on Chapter 4. We then deterministically simulated the economic benefits over 20 years, again using the terminal Lamb 2020 index and the Merino MP+ index. Each year, income and costs were calculated in net present value. We felt it important to measure in cumulative net present value as it takes into account when the improved genetic value is actually expressed. There can be considerable differences in time of expression of increased benefits and this has a large effect on the moment when the breeding

programs can break even. We used the gene flow method (Hill 1974) where cumulative discounted gene expression are calculated, reflecting the total current value of the improvement. This was considered important because the genetic lag is better predicted compared to a simpler model. This again depends on important breeding program parameters such as time at first matings, reproductive rates and the general age structure of the population. The age structure in the nucleus has a large effect on the rate of genetic gain in the nucleus, and therefore, the rate in the larger population. The age structure in the commercial tier is more a determinant of the genetic lag between the nucleus and the commercial tier, and therefore affected the net present value of introducing new technology. It was assumed breeding programs to start a new strategy at year zero, with the additional cost of the new strategy commencing at once. Monetary benefits resulting from genomic selection will eventuate after an initial lag passes and initial costs are recouped. These costs can be considerable for the proposed new technologies, potentially quadrupling the cost of running the breeding program. These increased costs may turn many breeders from ever using these technologies despite the potential long-term benefits.

A clear issue from both sheep breeding programs demonstrated that programs that had large amounts of MOET assigned were less profitable due to the higher cost per lamb compared to AI or JIVET. Furthermore, when genomic selection was used, MOET dams often had progeny with lower EBVs than progeny from JIVET. It was clear that the cost of technologies needed to be factored in to nucleus breeding decisions. It was also clear that the extra genetic gain each year would not justify the cost of the reproductive technologies through the own performance of the nucleus ewes (i.e. higher weaning weight). Therefore if ram breeders were to use reproductive technologies, a premium would need to be paid per ram to justify the usage of reproductive technologies and genomic selection an economically viable decision.

7.4. True costs factored into selection

Chapter 6 used the same stochastic simulation as Chapter 4 with the terminal Lamb 2020 index and Merino MP+ index. However, in the objective function of optimal contribution selection, a true cost was placed on reproductive technologies. The main result demonstrated that the higher the proportion of merit that is captured by the breeder (and hence higher premium), the more reproductive technologies were used and genetic gain accelerated. Interesting observations included when proportion of the benefit paid was 0.06, very little reproductive technologies were used. When they were used, we suspect they would have been strategic matings that were outliers in the population that would have significantly contributed to future generations. These strategic matings had the ability to increase rates of genetic gain by 2-4% annually.

The premium we used reflects a proportion captured by the breeder of 6% is consistent with Horton *et al.* (2014) concluding that ram buyers can retain up to 94% of the benefits from genetic improvement programs, meaning they pay only a 6% premium to the ram breeder. Horton *et al.* (2014) only considered investment in genomic testing, hence optimal allocation of technologies as proposed in this thesis allows relatively more use of technology. Further to this Banks *et al.* (2014) concluded from an industry survey that Australian ram buyers, are only willing to pay 25-50% of the breeding program investment of ram breeders which did not include cost of reproductive technologies. This means that ram buyers may not be willing to pay as big a premium as they indicated in that survey if the costs for breeding programs are increasing drastically. However rams that have higher merit will contribute more as predicted by the long term genetic contribution theory (Wooliams *et al.* 1999), where future contributions are predicted from the superiority of the animal, and accordingly, it may be expected that ram buyers may pay a higher price the best rams (Banks *et al.* 2014). In practice there is a slight correlation between merit and ram price but the relationship may not reflect the true difference in genetic value (Banks *et al.* 2014) as it does more-so in beef (Amer *et al.* 2007).

The size of the premium could be argued to be higher for a ram breeder, who breeds rams for their own flock as in Chapter 5, to be closer to 100%. When we simulated higher premiums in Chapter 6 and costs of reproductive technologies applied we also observed a shift in allocations of types of matings. We observed less MOET matings proportionally to that of Chapter 4 and more of JIVET matings. As more reproductive technologies were assigned, the genetic gain accelerated. This demonstrated that if ram buyers want higher merit animals; they need to share the benefit with the stud breeder and hence increase the premium. The idea of a premium paid by ram buyers is not new and is in agreement to Brash *et al.* (1996) and Horton (1996) who discuss that premiums need to be paid to stud breeders who invest in reproductive technologies so that both parties can “enjoy” the benefits of accelerating rates of genetic gain.

The premiums paid to the ram breeders in Chapter 6 were based on proportion of the benefit captured by ram buyers. We used Hill’s (1974) gene flow method to determine the cumulative discount of expression of genetic contributions where we had to assume the age structure of the nucleus deterministically. While not exactly precise, it has small impact on the final CDE and hence the premiums we assigned should have been robust. Chapters 5 and 6 assume that a population structure of only 2-tiers. If there was a third tier as Horton (1996) simulates, we would observe further benefits from an industry perspective. The 2nd tier would pass on a higher premium to the 1st tier with better ram prices received due to the 3rd tier also paying some of the benefit they receive. Therefore from an industry point of view we could have been quite conservative in assessing the value of premiums. However, considering poor market signals where buyers find it hard to see clearly the value of a better ram in the short term, and the low proportion of value placed to the breeder (Banks *et al.* 2014), our study is likely to be realistic.

The future use of reproductive technologies in the Australian sheep industry may continue to sparsely use reproductive technologies. The advent of genomic selection has made the possibility of JIVET to potentially become the main reproductive technology used in sheep due to its lower cost per lamb and acceleration of genetic gain. However the use of reproductive technologies may continue to be

sporadic until ram buyers (who are often practitioners who operate on low cost) are willing to pay higher premiums for these genetically elite animals. Therefore we only expect breeders who are the nucleus of the population and the main breeders contributing to long term gains to be the only people who use reproductive technologies to accelerate rates of genetic gain.

7.5. Future research and extension

The study of benefits and implications of using reproductive technologies in breeding programs have been comprehensively covered over the last 40 years. This thesis adds to knowledge in the field by looking at strategies to optimize allocations of matings with inbreeding and genetic gain, implementing cost of reproductive technologies into selection and assessing how individual traits respond when using index selection. It is clear that reproductive technologies have more benefit in breeding programs where the dollar value of the breeding objective is large (e.g. dairy) is high. The use of genomic selection with reproductive technologies has clear financial benefits to lower tier populations where the benefit of genomic selection is greater than 20% (compared to breeding programs not using genomic selection). Following this thesis it would seem that research into benefits of reproductive technologies and genomic selection have again matured and refinement of selection tools to optimize reproductive such as MateSel (Kinghorn 2011). These selection tools that can optimize matings based on genetic merit and minimize inbreeding should be used more at nucleus level where human emotion can be, somewhat, taken away from selection decisions.

Further study could investigate selection decisions before exploiting genomic selection with reproductive technologies. Further investigation is needed for optimization of 2-stage selection which would help lower costs of genomic selection or phenotyping costs without sacrificing too much genetic gain. Further to this, phenotyping vs genotyping strategies should be investigated particularly in breeding programs that have low dollar value breeding objectives such as current Australian terminal sheep breeding indexes. However this should not stop the extension of conveying the benefits of reproductive technologies and genomic selection.

Currently the dairy industry worldwide has invested heavily into the extension of using reproductive technologies. To a lesser extent the beef industry has also with sheep somewhat lagging behind. However there are clear benefits (as demonstrated in Chapter 5) to use reproductive technologies and genomic selection at a nucleus level if the amount of genetic gain can reach at least \$3.50 a year. This is very achievable in beef and Merino sheep and will be possible in meat sheep when carcass trait breeding values can be predicted from genomic selection. Further extension into these breeding programs could help accelerate genetic gain within industries while being financially sustainable or even profitable. As the research into benefits of using reproductive technologies and genomic selection with optimal contribution selection has matured, a concerted effort should be made into conveying to industry the potential financial risks and rewards associated with using these technologies.

7.6. Recommendations

1. Optimal contribution selection should be used in breeding programs looking to optimize genetic gain and maintain genetic diversity.
2. Cost of reproductive technologies must be considered during selection, as must a form of premium to justify the expense of the breeding programs.
3. Further optimisation of selectively genotyping selection candidates should be investigated particularly on female selection candidates that are available for reproductive technologies to form a diversity of families. This should be more economical compared to genotyping all selection candidates as has been investigated in genotyping strategies in rams by Horton *et al.* (2014) and van der Werf *et al.* (2014).
4. Optimisation of phenotyping and/or genotyping methods should be developed particularly where economic margins and genetic gain in true dollars is low (e.g. using Lamb 2020 index).
5. The use of the reproductive technologies and/or genomic selection while using the Lamb 2020 index breeding objective does not look profitable and breeders wanting to accelerate

genetic gain using these technologies should use a terminal index with an index with a breeding objective that has a higher dollar value.

7.7. Conclusion

Optimal contribution selection is an effective tool to assign reproductive technologies to female selection candidates. It is also effective in maintaining sustainable rates of inbreeding which can be a problem when using reproductive technologies. The use of genomic selection and reproductive technologies appear to be synergistic with the highest benefits coming in traits or indexes that are measured later in life or sex-limited. Applying a cost to using reproductive technologies delivers more practical breeding programs when using optimal contribution selection where only a small proportion of females are assigned reproductive technologies where rams are sold to breeders who can afford to pay a premium for the rams sold.

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