

final report

Project Code:

B.BSC.0094

Prepared by:

Julius van der Werf University New England

Date published: April 2010

PUBLISHED BY Meat and Livestock Australia Limited Locked Bag 991 NORTH SYDNEY NSW 2059

Value of alternative methods to determine parentage

Meat & Livestock Australia acknowledges the matching funds provided by the Australian Government to support the research and development detailed in this publication.

This publication is published by Meat & Livestock Australia Limited ABN 39 081 678 364 (MLA). Care is taken to ensure the accuracy of the information contained in this publication. However MLA cannot accept responsibility for the accuracy or completeness of the information or opinions contained in the publication. You should make your own enquiries before making decisions concerning your interests. Reproduction in whole or in part of this publication is prohibited without prior written consent of MLA.

Executive Summary

The paper presents an assessment of the value of DNA parentage testing. Most of the perceived benefit is from increasing selection accuracy, which is about 20%, and a handle to manage inbreeding. The increased selection accuracy is relatively easy to predict, although it does assume that breeders select objectives that are similar to those used by Sheep Genetics. The value of inbreeding management is more difficult to quantify. Inbreeding may not be a huge concern for an individual breeder, unless he does not open his flock to any outside material.

A cost benefit analysis at the population level shows that investment in parentage testing is beneficial but DNA testing is less cost effective than conventional mothering up. The reason is a very small difference in benefit in terms of selection accuracy and a higher cost. To be cost effective, DNA testing cost should not exceed those of mothering up. The Pedigree Match Maker, however, seems more cost effective than the other two methods for parentage recording.

The cost benefit evaluation at a flock level appeared not beneficial for DNA parentage testing. The model assumed that costs of obtaining parentage were fully passed on through ram sales, and the benefit was evaluated only for a flock buying these rams. All parentage test methods took at least 5 years before they have a higher return than a no pedigree method. The pedigree Match maker seems most cost effective, but this technology has not been used widely so far. In the flock model, conventional mothering up showed lower return than PMM but higher returns than DNA parentage tests and a strategy of no pedigree recording. At flock level the cost benefit is less favourable than at population level because of the lower multiplier effect between stud breeder and client. The flow-on benefit from improved offspring of the client to lower tier levels was not taken into account. This is not reasonable from a sector approach, but maybe realistic for a flock approach as it could be more difficult to recoup invested cost through ram sales.

Overall, the results show that DNA parentage methods are unlikely to be more beneficial than other methods. The Pedigree Match Maker seems more profitable. These comparisons are mostly determined by the cost of each method, as the assumed benefit is very similar. The PMM method assumes an initial investment and no subsequent running cost, but the method might need more practical evaluation.

There are a number of practical aspects associated with the various parentage testing methods and those have not all been covered in this paper. However, there is no doubt that these more practical considerations maybe ultimately more important in determining the commercial value of parentage testing.

Introduction

Technology is available to test parentage in sheep via DNA testing. The merits of such a test will depend on both cost and benefit of parentage testing. The purpose of this document is to present the benefits of parentage testing, and where possible, quantity these benefits.

B.BSC.0094 - Value of alternative methods to determine parentage

For an appropriate assessment of investment in DNA parentage testing, these benefits need to be weighted again the cost of parentage testing, i.e. DNA sampling, and genotyping costs. These cost and benefits also need to be assessed relative to alternative ways to obtain pedigree information. Some of the benefits could be costs of alternative methods that maybe avoided. For example, DNA testing could alleviate the need for single sire paddocks, which is an alternative method to obtain parentage information, and removing the need for this saves costs of fencing and might have other management benefits such as increased lambing rates. Therefore, this document will attempt to balance the cost and benefits of alternative methods for obtaining parentage information, including the strategy of not obtaining it at all, but it will not give an exhaustive overview of all management benefits of the various options.

The benefits of having parentage information are twofold: 1) obtain more accurate genetic evaluation and higher selection accuracy 2) to manage inbreeding. In the next section, these benefits will be articulated and its value will be quantified where possible. Subsequently, a flock model will be presented that could serve as a framework to balance costs and benefits of alternative strategies.

Benefits of parentage information

Use of relatives information

In the absence of parentage information, the assessment of an animals breeding value can only be based on an own performance record. The accuracy of an EBV based on an own performance record is equal to the square root of the heritability. Own performance information can be reasonably accurate for highly heritable traits, such as fleece weight and fibre diameter. The accuracy of EBVs is important as it affects proportionally the rate of genetic change that can be obtained.

More accurate estimated breeding values can be obtained when information on relatives is used. This can be information on parents, sibs and progeny. We can compare accuracy of estimating EBV based on relatives' information with EBV accuracy without using pedigree. In the latter case, selection can be based only on own performance. When the sire is known we can use records on sire as well as on paternal half sibs. When in addition the dam pedigree is known we can use a record on dam performance. Progeny information can be used for older animals, giving EBVs with potentially very high accuracies. The benefit of using relatives' information depends on heritability, i.e. more benefit for lowly heritable traits.

In a typical breeding program we try to select animals at a relatively young age. However, more information is known for older animals (notably progeny information) and in an optimal breeding program, there will be an optimal use of both young and older sires (and dams). The comparison of accuracy of different scenarios should be based on a mix of age classes, i.e. an age structure that is optimal in a breeding program. In the absence of pedigree information, there is no increase in accuracy of breeding value over time, and optimal generation intervals will be lower.

Results of comparing accuracy of EBV with and without relatives' information are summarized in Table 1 for single trait selection. The loss in genetic progress from not using relatives' information varies from 42% for lowly heritable traits ($h^2 = 0.05$) to 9% for traits with a high heritability ($h^2 = 0.50$). The loss due to not using information through the dam pedigree is much lower; around 5%. The relatives information assumed known here is a performance record on sire, dam and paternal 39 half sibs. With no progeny information assumed known, these comparisons mimic selection of young animals after their own performance is recorded, and the trait can be measured on both sexes. For sex limited traits, the difference would be larger, especially for traits such as reproduction that can be recorded only on females and later in life (after an animal is selected as a parent).

Table 1: Accuracy and relative loss in accuracy when not including dam pedigree and sire and dam pedigree for single trait selection with varying heritability.

	Accuracy	Accuracy		Accuracy with no	
	full pedigree; all	sire pedigree	% loss relative to	pedigree; own	% loss relative to
Selection Objective	relatives' info	only, no dam	full pedigree	performance alone	full pedigree
Single trait heritab. = 0.05	0.38	0.36	-5.3%	0.22	-42.1%
Single trait heritab. = 0.25	0.63	0.60	-4.8%	0.50	-20.6%
Single trait heritab. = 0.35	0.70	0.67	-4.3%	0.59	-15.7%
Single trait heritab. = 0.5	0.78	0.75	-3.8%	0.71	-9.0%

Table 2 shows a loss of accuracy for multiple trait selection, based on some total merit indexes relevant to the industry. For the wool sheep example, we used a 7% micron premium index for merinos selected for wool, meat traits (live measured) and reproduction. For meat sheep we used the current 'Carcase Plus" index, where objective traits are weight and live animal scan traits and a Sheep Object –derived index for meat sheep based on actual carcass traits. For all three index scenarios the generation interval was optimized and some of the selected sires (dams) would have had some progeny information included (as opposed to the single trait scenarios).

The loss in genetic gain due to not using relatives' information is lower in wool sheep (17%) than in meat sheep (28%). This is mainly because fleece weight and fibre diameter are important traits in the

breeding objective and they have a high heritability. It should be noted that the effect on overall merit can be quite different than the effect on individual traits. Without pedigree information it is very difficult to select on a lowly heritable trait. For example, in the absence of pedigree information, it is expected that number of lambs weaned would decline by 0.2% whereas with pedigree information it would increase by 0.3%. It should also be noted that the loss in genetic gain is slightly smaller than the loss in accuracy, as optimal generation intervals are slightly lower in a scenario without relatives' information. Loss in genetic gain is 27% for the Terminal Sire indices and 16% for the wool index. Note that a loss of x% due to not pedigree-ing is equivalent to a gain of x/(1-x) when using pedigree (versus no pedigree). Hence, the additional gains due to increased accuracy from obtaining full pedigree information are 19% for wool sheep and 38% for meat sheep.

An evaluation of the implications of these results will be presented in the section on cost-benefit.

Table 2: Accuracy and relative loss in accuracy when not including dam pedigree and sire and dam pedigree for multiple trait breeding objectives in the Australian sheep industry.

	Accuracy	Accuracy		Accuracy with no	
	full pedigree; all	sire pedigree	% loss relative to	pedigree; own	% loss relative to
Selection Objective	relatives' info	only, no dam	full pedigree	performance alone	full pedigree
Termal Sire Index; Sh. Obj.	0.58	0.57	-2.1%	0.42	-27.7%
Carcass Plus Index	0.71	0.69	-2.4%	0.51	-27.9%
Wool Index 7% Sh. Obj.	0.52	0.50	-2.9%	0.43	-17.1%

Other benefits from knowing parentage

Across flock evaluation

Besides an increase in accuracy of estimated breeding values, knowledge of parentage has a number of additional benefits. At a population level, identification of sire allows linking of information across herds and across years, allowing estimation of breeding values across flock and across year, the latter leading to an estimate of genetic trend. Family information (mainly via sire) is also required to estimate genetic parameters. All of these factors are critical in an effective genetic evaluation system. The ability to compare sires across flock, and the ability to estimate genetic trend lead theoretically to an increase in genetic gain, as the selection differential is maximized across flocks and across age classes. This is difficult to quantify exactly, but could be in the order of 10-20%. However, the practical impact maybe much larger, as the ability to select sires optimally across flocks and across age classes leads to a natural

evolution of breeding program structure (into nucleus and multiplier breeding flocks) and additionally creates some unbiased comparisons and a fairer competition between flocks.

Increased accuracy due to less parentage errors

0.48

0.50

0.52

0.48

0.50

0.51

0.6

0.8

1

DNA parentage testing is the most reliable method to determine pedigree. The usual method to determine pedigree, based on single sire paddocks and mothering up, has a certain error rate. Ballpark estimates for errors in conventional determination of sire and dam pedigree are 5% and 20% respectively. The first figure is confirmed by recent genotyping results in the sheep CRC, where 4.6% of 3450 genotyped animals had an erroneous mismatch between recorded sire and sire genotype. The figure varied considerably between sites: from 1.1 to 8.8%. The error rate in dam pedigree is based on an estimate by (Purvis). The loss of accuracy due to pedigree error is more or less proportional to the error rate (e.g. Gelderman, 1986). Assuming that the accuracy drops linearly with error rate as well as with the proportion of pedigree recorded, and using the wool index example where the maximum accuracy (full pedigree) is 0.53 and the no-pedigree error, and pedigree recording. Note that this is assuming random missing pedigree, whereas in reality one would choose to selectively record the best animals - effectively the nucleus - which would be closer to 100% recording. The point to make is that a more accurate method to determine pedigree, i.e. DNA testing versus the conventional method, will deliver 1-2% extra accuracy of selection, and therefore increase the rate of gain relatively by 1-2%.

of pedigree error.								
	Error rate							
% pedigee rec	0	0.05	0.1	0.2	0.5	1		
0	0.43	0.43	0.43	0.43	0.43	0.43		
0.2	0.45	0.45	0.45	0.44	0.44	0.43		
0.4	0.47	0.46	0.46	0.45	0.44	0.43		

0.48

0.49

0.51

0.47

0.48

0.49

0.45

0.45

0.46

0.43

0.43

0.43

Table 3. Accuracy of a wool index in flocks with varying degrees of pedigree recording and varying rates of pedigree error.

Ability to account for maternal effects

Without a dam identification associated with an animals' record, it is not possible to account for the maternal effect when assessing the breeding value of an individual. Especially for traits measured up to weaning, the maternal effects can be substantial, often of the same order of magnitude as direct additive genetic effects, and not accounting for maternal effects could lead to unbiased and less accurate estimated breeding values. Asadi-Fozi *et al.* (2005) have looked at maternal effects on wool production traits (fleece weight), and after estimating maternal effects, they looked at the loss in rate of

Table 4. Optimum, actual and expected response to selection on a wool index and proportional loss due to ignoring maternal effects in genetic evaluation for varying micron premium indexes.

Responses	Micron premium						
	3%	6%	12%	20%	30%		
Optimum	0.16	0.22	0.4	0.72	1.08		
Actual	0.14	0.21	0.39	0.71	1.08		
Expected	0.19	0.25	0.42	0.74	1.11		
Loss due to ignoring							
maternal effects	14.3%	4.8%	2.6%	1.4%	0.0%		

genetic gain if maternal effects were ignored in genetic evaluation. The loss could be up to 14% and the loss was greater for low micron premium production environments, as the relative value of greasy fleece weight is highest in this index. Note also that the actual response is substantially lower than the predicted response.

Another consequence of missing dam information is the inability to account for the pre-weaning environment in the broader sense. Mothering up usually provides information about birth weight and birth type (singles vs twins). Note that this information would also not be collected in case of DNA parentage testing. However, Atkins and Ramsey (2001) suggested by that a simple and adequate solution to adjust for this missing data is to consider weaning weight as a proxy for more detailed pre-weaning environmental effects. However, this maybe a practical problem is the data is missing on only a proportion of individuals. It would not be appropriate to make a weaning weight correction only for those with missing birth data as adjustment for weaning weight would also adjust for a proportion of growth potential, and basically changes the biological interpretation of the trait that was adjusted.

Managing Inbreeding

Pedigree information is important to avoid both short and long term inbreeding. Short term inbreeding refers to the mating of related individuals, and leads to an inbred individual. Long term inbreeding refers to the average rate of inbreeding of the population, which is mainly dependent on the effective population size. In smaller populations it is unavoidable to mate related individuals; hence the rate of inbreeding will increase population wide.

Both short and long term inbreeding can be managed by using pedigree information. This is obvious for short term inbreeding. Long term inbreeding has long been managed by simply keeping a large enough effective population size, which practically translated to recruiting a sufficient number of new rams each year. Using more sires typically leads to lower selection intensities and reduced selection differentials. However, Meuwissen (1997) has shown that selection response can be optimized for a given inbreeding constraint. This can lead to substantial increases (up to 60%) in selection differential at the same level of inbreeding, where the contribution of each sire to the next generation is optimized. Hence, optimal selection balances rates of genetic improvement and rates of inbreeding, and this optimization is dependent on knowledge of additive genetic relationships among individuals. Hence, pedigree information is needed for management of both short and long term inbreeding.

The cost of not managing inbreeding is hard to determine. A ball park figure for a responsible rate of inbreeding in a closed population is to keep it below 1% per generation. Highly inbred populations suffer from increased frequencies of genetic defects, often leading to culls or death, and subsequently development of DNA testing against the cases that are economically most damaging. Examples of increase of inherited disorders and development of DNA tests are mainly seen in Holstein cattle. It should be noted that intentional inbreeding to 'purge a population from deleterious alleles' is not a healthy strategy as it leads to unnecessary animal suffering and culling, and it is ineffective as each individual has many more genetic defects in its genome than the number that is expressed in a homozygous recessive form.

A second consequence of high inbreeding levels is a reduced phenotypic performance of the population, especially for fitness traits. This loss is termed 'inbreeding depression" and it is usually higher for fitness traits, that generally have lower heritability and more non-additive genetic variation.

Finally, inbred populations have less genetic variance, the loss being proportional to the inbreeding level, and the rate of improvement is proportional to the square root of genetic variance.

B.BSC.0094 - Value of alternative methods to determine parentage

The reason why it is difficult to quantify the effect of inbreeding management is that it is difficult to predict rates of inbreeding if it is not managed. Also, inbreeding can be high for an individual breeder, but the problem is immediately resolved if another breeder can provide competitive genetic resources that are relatively unrelated. This is less likely if the breeder constitutes a fair proportion of the actual breeding nucleus. Furthermore, managing inbreeding problem in the merino population is not a problem at the population level, as there is sufficient diversity in breeding between the various flocks. It might be a problem at an individual flock level, but this could quickly be resolved by an influx of genes from other flocks.

Other management benefits of DNA parentage testing

DNA parentage testing can alleviate management constraints such as single sire lambing paddocks and per-parturient identification and tagging, possibly leading to higher conception. There are some reports that the number of lambs weaned in such a system could be up to 10% higher (Fowler, 1975). However, it is unclear whether this results from mixed sire mating paddocks or mixed sire lambing paddocks. It is more likely to result from the former, but one should assume that breeders want to control matings and still use single sire mating paddocks, if not AI.

Summary of the benefits of parentage

Parentage information allows the use of relatives' information in breeding programs, which gives around 20% more accuracy of estimated breeding value for wool sheep and a similar increase in overall selection response. The increase for meat sheep would be a bit more, around 35%. The difference between sire only and full pedigree is about 5%. The effect on selection response is largest for low heritable traits, such as reproductive rate. The ability to account for maternal effects has an additional 5-10% effect on genetic improvement. Pedigree allows also managing inbreeding. The benefit of this is hard to quantify, but in the merino breed the problem is likely small at a population level, although it may be larger at flock level. The additional benefit of DNA parentage testing is a near removal of pedigree error, leading to another about 5% improvement in the rate of genetic gain compared to conventional mothering up. The overall effect of DNA parentage testing over no pedigree is about 25% additional genetic gain and the advantage over conventional parentage testing is around 5% more accurate pedigree (depending on pedigree error rates), which would translate into 1.25% more gain.

Cost-benefit of parentage testing

Evaluation perspective

One could evaluate the cost benefit of parentage testing. Basically, the benefits can be quantified as a net additional gain of around 20%, assuming some losses, and not including any benefits for managing inbreeding. The cost is that of genotyping, with a cost per lamb born, as well as some initial starting up costs. A cost benefit analysis can be done both at an industry level, and at a flock level. In each case we have a number of animals expressing the increased genetic value over time (commercial sheep), and a number of animals that is invested in to achieve that gain (nucleus sheep). At a population level, we assume 10 million commercial sheep and 200,000 nucleus sheep (progeny born). At a flock level we can assume a stud flock investing in e.g. 1000 ewes, and selling annually 20 stud rams to a client with 2000 ewes. The additional cost of parentage testing is fully passed on the price of stud rams. We can subsequently assume a client flock buying these rams, and evaluate their additional genetic gain versus their additional cost of buying these rams. In principle, the evaluation at population level is not different from an evaluation at flock level. However, a critical difference is that we assume a lower ratio of the number of nucleus animals to the number of commercial animals. At a population level we can assume a multi layered structure where relative to the total number of animals in the population, the percentage in the nucleus is small. In the flock model, the ratio of stud versus client animals is much higher as basically this is only a two-tier structure. The additional benefit of the client flock to sell on animals of genetically higher value is not accounted for. This represents a situation where the investment is not fully passed on through the population breeding structure, and only direct clients of stud breeders (who in many cases can be a part of the stud breeder operation) will benefit from the investment.

Modelling parameters

The assumed rate of genetic improvement is \$2 for a no-pedigree scenario, \$2.38 for a conventional pedigree scenario and \$2.40 for a DNA pedigree scenario. This is a 20% increase of selection response due to using pedigree information, and assuming that DNA testing provides a 100% accuracy whereas the conventional method produces a 95% pedigree accuracy. Potential rates of genetic gain estimated by Swan et al (2009) were around \$2/head/year for meat sheep and \$3/head/year for wool sheep and the realized rates were around \$2 and \$1 respectively. This gain is cumulative over years for the number of commercial sheep considered. We calculate the net present value (NPV) by multiplying benefit minus cost on an annual basis with the appropriate discount rate, assuming a discount rate of 5% (this is

basically market interest rates minus inflation). The assumed cost of phenotypic measurement of nucleus progeny is \$2.50 per head, the cost of the conventional parentage method of mothering up is assumed to be \$8 per nucleus lamb weaned and the cost of DNA testing is \$20 per nucleus lamb weaned. Mothering up requires an initial investment in infrastructure, assumed to be \$5k per 1000 stud ewes. DNA testing requires an initial investment of testing stud ewes and rams. In subsequent year, only stud progeny need to be tested.

Population level

The benefit at population level is the additional cumulative genetic gain over time in 10 million commercial sheep at an additional measurement cost in 200,000 nucleus progeny. We assume a 3 year delay before initial benefits flow through due the multi-layered character of the population structure.

The parameters for the model are summarized in Table 5.

Table 5: Input parameters for the population model

	NoPed	Conv	DNA
interest rate	0.05		
commercial sheep (M)	10		
nucleus prog/yr (M)	0.2		
cost of phenotyping (M)	0.5		
gain/yr	2	2.38	2.4
cost per sample	0	8	20
cost per annum (M)	0.5	2.1	6.5
initial cost	0.5	1	6.5



Figure 1 Gain (\$M Net Present Value per annum) over a 20 year period after introducing methods to obtain parentage in a population of 10 million ewes with 200,000 ewes in the breeding nucleus



Figure 2: Gain (\$M Net Present Value per annum) relative to a nopedigree strategy over a 20 year period after introducing methods to obtain parentage in population of 10 million ewes with 200,000 ewes in the breeding nucleus

Table6. Cumulative Net Present Value (million \$) after 5, 10 and 20 years of 3 parentage methods in a10 million ewe flock

	No					
	Pedigree	Conv	DNAtest			
5 years	48	50	35			
10 years	395	458	438			
20 years	1597	1881	1861			

There is an obvious benefit of recording pedigree, and the additional value of this increases each year. At an industry level, the investment is small relative to the benefit. There is only a small difference between DNA pedigree and conventional pedigree method, which is not surprising as the benefits are nearly identical (the differences in genetic gain are 5% of 20% is only 0.5%). There is a substantial difference is assumed cost, but because the cost is only a small fraction of the benefit, this becomes negligible. In fact, the annual cost is less than 20% of the annual *increase* in benefit each year and after 10 years the annual cost is only 2.6 % of the benefit. Therefore a cost benefit analysis at industry level is not every sensitive to assumptions about costing of parentage testing. The cumulative NPV over various time periods shows that is takes more than 5 years before the DNA testing method 'pays off'. IN fact, it is after year 7 that the cumulative NPV of DNA testing becomes higher than a no pedigree strategy. The cumulative NPV of the DNA method never really catches up with the conventional mothering up method as it provides only a very small additional benefit.

Individual flock level

We can do a cost benefit at flock level, again comparing the investment in obtaining parentage information with the benefit. The principle is similar than at population level but the main difference is the multiplication factor from nucleus to commercial. We will see that this causes the cost to be a much greater proportion of the benefit and this makes the outcomes more sensitive to assumed costs of the various methods. The flock model will also be more sensitive to assumed reproductive rates and the proportion of nucleus (stud) born males that can be sold as breeding rams.

On one hand it is relevant to do such sums at flock level, as after all, that is the unit level at which investment decisions are being made. So it is important to work out the cost and benefit for a stud breeder as well as for a commercial flock. However, on the other hand, an assessment at flock level brings with it some difficulties, as it is more difficult to translate more genetic improvement into tangible benefit. One would have to assume some relationship between breeding value of rams and sale price. More importantly, not keeping pace with the genetic gains made by competitive studs would in the longer terms mean a loss of market share in the ram sale market. Translating competitive advantage in terms of average genetic merit of the flock into financial benefit through increase ram sales is difficult. In the model proposed here, we assume that the additional cost of obtaining parent information is directly passed on in the ram sale price. Hence, the value proposition should be immediately clear for the ram buyer. This is realistic and in many cases, there is also a direct benefit to the stud breeder if he owns a significant number of sheep that benefit directly from genetic improvement (i.e. (s)he has a very large flock and uses only a part of his flock as nucleus). This approach has also been used by Russel et al (2006).

The following strategies are used to determine parentage, and these are compared with a no pedigree strategy.

DNA parentage method: Initially, all breeding animals (rams and ewes) in the stud have to be genotyped as well as their progeny. In subsequent years only progeny need to be genotyped. The cost of genotyping involves a labour cost for DNA sampling and a cost per sample for the service provider. I assume as a base value a sample cost of \$20, which includes sample collection, DNA extraction and genotyping. Currently, it would be difficult to achieve the service at this price, but it will be a starting point. I assume a 100% accuracy of parentage and a 20% increase in rate of genetic improvement compared to having no pedigree (\$2.20 per progeny per year)

Mothering up method: Russel et al. (2006) estimated this cost to be \$10 per lamb born, including cost of labour, and infrastructure (single sire paddocks). I assume a 95% accuracy in parentage and a 20% increase in rate of genetic improvement compared to having no pedigree (5% less than DNA parentage). This results in \$2.38 per progeny per year. The initial cost of setting up infrastructure for single sire lambing paddocks is estimated at \$5,000 (per 100 ewes). This number could be variable, especially as one could assume that this infrastructure is needed in any case to control mating at the stud level.

Pedigree matchmaker: Russel et al. (2006) estimate an initial cost for a 1000 ewe flock to be 20,000 with negligible costs in later years. I assume a 95% accuracy in parentage and a 20% increase in rate of genetic improvement compared to having no pedigree (\$2.38 per progeny per year)

Further variables are related to flock structure (ewes/ram, weaning rate, number of ewes). I will calculate cost and benefit for a 200 ewe ram buying client, and work back how many stud animals need to be measured to provide this flock with 20 new rams per year. The start up costs are calculated on a per nucleus sire bases (and multiplied by the number of nucleus sires needed to produce the 20 rams far the commercial stud). The annual costs as divided by the number of rams that is required each year (20 in the example of the 200 ewe flock)

Interest rate	0.05	blue cells to enter va	riables	
Nr Sheep Commercial Flock	2,000	marone cells are calc	ulate variables	
Dams/sire	40			
Sire replacement rate	0.4			
Weaning rate	0.75			
Nr new rams needed for comm				
flock/yr	20			
Prop. Nucl.Males sold as breeding				
ram	0.33333			
Nr. Nucleus born progeny tested/yr	120.00			
Nr. of Nucleus sires needed/yr	3.00			
Cost of phenotyping in				
\$/Nucl.progeny	2.5			
	NoPed	Conv	DNA	PMM
Rate of genetic gain/yr	2	2.38	2.4	2.38
Startup costs per nucleus sire	0	250	820	800
cost per sample	0	8	20	0
cost per annum	300.00	1260.01	2700.03	300.00
ongoing cost per breeding ram	15	63	135	15
cost per breeding ram first year	15	101	258	135

Table 7. Summary of base variables used in the flock model.

The additional cost per breeding ram depends heavily on the efficiency of the stud breeding scheme, and in particular on the proportion of males born in the stud that can be sold as a breeding ram. These variables determine the multiplication between nucleus and commercial sector. Table 8 compares the additional cost on a per ram sold basis.

We can calculate the cost and returns per year for a commercial enterprise that purchases rams at a higher price, the price increase fully covering the additional cost per ram sold. We can consider the NPV of the annual return and its cumulative value after a certain number of years (Figure 3). Figure 4 shows these annual NPV values for the three parentage methods relative to not recording pedigree.



	NoPed	Conv	DNA	PMM
Prop. Nucl.Males sold as breeding ram	0.33	0.33	0.33	0.33
ongoing cost per breeding ram	15	63	135	15
cost per breeding ram first year	15	101	258	135
Prop. Nucl.Males sold as breeding ram	0.5	0.5	0.5	0.5
ongoing cost per breeding ram	10	42	90	10
cost per breeding ram first year	10	67	172	90



Figure 3: \$Net Present Value of benefit per annum over a 20 year period after introducing methods to obtain parentage in a 2000 ewe commercial flock, paying full cost of testing to breeder through ram price (assuming stud breeder sells 33% of his males as breeding rams).

Again, all parentage methods are clearly more profitable than collecting no pedigree. And again, there is little difference between the parentage methods. The PPM method is most profitable as it provides accurate parentage information for less cost than DNA testing. The annual returns of DNA testing are never exceeding those of the conventional mothering up method as the higher cost is not offset by the very slight increase in annual genetic improvement. The cost of DNA testing is 50% of the annual increase in benefit, and after 20 years, the annual cost is about 4% of the annual benefit in the case of 33% of males sold as rams. All methods require some initial loss due to start up costs, and these are relatively lowest for PMM. Obviously, these start-up costs are strongly depending on purchase costs of the PMM equipment, and somewhat on the assumption that there are no ongoing running costs. Also, in reality, a stud breeder will not pass on his investment fully in the first year, but spread it over several years.



Figure 4: Relative gain (\$Net Present Value) over a 20 year period after introducing methods to obtain parentage in a 2000 ewe commercial flock, paying full cost of testing to breeder through ram price (assuming stud breeder sells 33% of his males as breeding rams).

Table 9 give the cumulative NPV over 5, 10 and 20 years for each of the parentage methods. It shows that after several years all of the parentage testing methods are more profitable than a no-pedigree strategy, with the return to investment reached in about 5 years, and earlier if the efficiency of breeding stud rams is higher. After 5 years, most methods are more profitable, with the conventional method still being more profitable than the DNA method. When only 33% of stud males are sold as rams after 20 years the DNA method still provides less cumulative profit compared to not pedigreeing at all.

Table 9. Cumulative Net Present Value after 10 years and 25 years of 4 parentage methods in a 2000 ewe commercial flock, paying full cost of testing to breeder through ram price for 2 levels of stud males sold as breeding ram.

33%	of	males					
sold				NoPed	Conv	DNAtest	PMM
			5 years	24583	24398	16401	27112
			10 years	97272	107682	95294	113815
			20 years	306313	351946	334496	362858
50%	of	males					
sold				NoPed	Conv	DNAtest	PMM
			5 years	25037	26557	21313	28367
			10 years	98082	111337	103411	115426
			20 years	307621	357692	347093	364967

Obviously, the cost benefit calculations are quite sensitive to assumptions about cost. Especially the ranking among the various methods is directly a function of costs as the differences in benefit are only minimal. Varying thee costs will give limited insight, as the y will mainly influence the distance between the curves in Figure 4. For example, DNA testing will never be as cost effective as conventional mothering up, unless the sample cost comes close to the cost of mothering up. Whether the cost of mothering up is really as low as \$8 might need some further evaluation, but even if it was \$20, it is unlikely to become higher than DNA testing, and therefore DNA testing is unlikely to become more cost effective. This comparison is not much affected by the multiplication factor between nucleus and commercial (and therefore by flock structure) unless the benefit of conventional pedigreeing is significantly lower than those of the conventional method. Overall, the PMM method seems most cost effective.

Discussion

The paper has presented prediction of the value of DNA parentage testing. Most of the perceived benefit is from increasing selection accuracy, which is about 20%, and a handle to manage inbreeding. The increased selection accuracy is relatively easy to predict, although it does assume that breeders select on objectives that are similar to those used by Sheep Genetics. The value of inbreeding management is more difficult to quantify. Inbreeding may not be a huge concern for an individual breeder, unless he does not open his flock to any outside material. At the population level, inbreeding

management is very important, but generally there is sufficient pedigree recording at the nucleus level, and for the section of the industry that does not record pedigree, there is unlikely to be a long term problem as these operators have limited common use of the same genetic material.

At the population level, investment in accurate parentage testing is beneficial and but DNA testing does not give more benefit than conventional mothering up. The reason is that there is very little difference between these methods in selection accuracy, but some difference in cost. These evaluations can be compared with Banks and van der Werf (2009) who looked at the cost-benefit of genomic selection. They also noted a net benefit (in spite of higher costs per sample) but noted that the risk maybe high. Such a risk is not high for parentage testing as the technology is likely to give a very high accuracy of parentage. The cost benefit at a flock level appeared not beneficial for DNA parentage testing. The flock model is more affected by the testing costs as effectively population level assessment uses a larger multiplier effect between nucleus and commercial, or, alternatively, between investment and benefit. At the population level we assumed an investment in 200,000 ewes to improve 10 million sheep. In the flock model, we tested annually 120 or 80 offspring (for 33% and 50% males sold as a ram) to sell 20 rams to a client with 2000 sheep. The flow-on benefit from improved offspring of the client to lower tier levels was not taken into account. This is not reasonable from a sector approach, but maybe realistic for a flock approach as it could be more difficult to recoup invested cost through ram sales.

A cost benefit analysis showed that DNA parentage methods are unlikely more beneficial than other methods. The Pedigree Match Maker seems more profitable. These comparisons are only sensitive to relative cost of each method, as the assumed benefit is very similar. The PMM method assumes an initial investment (assumed 20k per 100 ewes) and no subsequent running cost. However this method has rarely been used in commercial situations and more use of the technology will reveal whether these assumptions about cost and accuracy are correct, and whether there are no practical disadvantages of using it. The assumption of conventional mothering up costing \$8 per lamb is perhaps low, but the method is competitive with DNA testing as long as this cost per lamb is less than that of DNA testing.

There are a number of practical aspects associated with the various parentage testing methods and those have not all been covered in this paper. However, there is no doubt that these more practical considerations maybe ultimately more important in determining the commercial value of parentage testing. Dodds et al (2005) discussed a number of aspects associated with parentage testing in more extensive herds, and he proposed methods to accommodate uncertainty about pedigree information in genetic evaluation systems. There maybe some ways to reduce genotyping costs and only obtain

18

pedigree information about a subset of a breeding operation. It is also quite likely that costs of parentage are shared with the cost of more routine genotyping for predicting merit. Otherwise, it seems unlikely that the cost of DNA parentage testing is low enough to justify replacing conventional methods for obtaining parentage.

References

Banks and van der Werf. 2009. AAABG

- Dodds, K.G., J.A. Sise and M.L. Tate. 2005. Practical aspects of a genetic evaluation system using parentage assigned from genetic markers. Austral. J. Exp. Agric. 45:935-940.
- Gelderman, H. U. Pieper and W.E. Weber. 1986. Effect of misidentification on the estimation of the breeding value and heritability in cattle. J. Anim. Sci. 63:1759-1768.
- Russel, A., S. Mortimer, B. Murray, K. Atkins and P. Taylor. 2006. The cost and benefit of improving selection accuracy in Merino studs. Technical Note. Trangie QPLU\$ Open Day.

Swan et al. 2009. AAABG.