final report

Project code: B.SGN.0133

Prepared by: Sonja Dominik
CSIRO Livestock Industries

Date published: January 2012

ISBN: 9781741917680

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

Modelling the economic benefit of utilising genomic information to the wool and meat sheep industries

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

Abstract

The aim of the project was to evaluate the economic benefit of using genomic information in individual sheep breeding operations across the sheep industries. A frame work was developed to evaluate the break-even point, highlighting how much a sheep breeder can afford to spend on a DNA test, and also the genetic gain per year (per commercial ewe joined) that can be achieved with and without the use of genomic technologies. Twenty one case studies of Merino, terminal and maternal sire studs contributed to the results and were subsequently presented in two workshops. The case studies showed that the highest benefit can be achieved in the Merino sector compared to the maternal and terminal sector, but all sectors benefited to some extent. The factors that influenced the benefit were the increase of accuracy that could be achieved through the addition of genomic information and also for the Merino sector the opportunity to select rams at 8 months of age for breeding based on genomic information. The factors that influence the economic benefit that can be gained from the use of genomic information are complex and issues on the actual implementation of genomic technology on farm need to be explored further.

Executive Summary

In 2011, the first genomic research breeding values have been released. To further adoption of such new technology for genetic improvement, it is important to provide breeders with an understanding of the benefits they can gain and how that relates to the cost of this particular technology.

This study evaluated 21 case studies across Merino, maternal and terminal sire sector for the economic benefits that can be gained from using genomic information of varying accuracy and how much they can afford to pay for the technology.

All sheep breeding sectors benefited from the inclusion of genomic information. The main influencing factor on the benefit was the increase in accuracy that can be achieved by adding genomic information. Therefore, the benefit was the highest for the Merino sector, because maternal and terminal breeding operations generally have high index accuracy. Merino indexes however include life time production traits, like adult fleece characteristics, that are not actually measured, which reduces index accuracy. Such indexes benefit greatly from the inclusion of genomic information. In addition, Merino breeders can consider early ram selection at 8 months of age, because genomic information on rams own performance is available as soon as birth. This decreases the accuracy compared to later selection, but is overall beneficial due to the reduced generation interval.

Further research is needed to ensure successful implementation of genomic technology on-farm.

The results of this study have been presented to the participating breeders in a workshop setting.

Table of contents

Background

In the face of rapidly changing selection technologies, the challenge is to integrate new technologies into breeding programs. To successfully do this the main questions of relevance to the industry need to be addressed "What benefit do I gain from the new technology?" and "How much can I afford to spend on it?"

Genomic information has been successfully been incorporated in dairy breeding programs and research into the technology is underway in other species, including sheep. The Australian SheepInformation Nucleus released in December 2011 for the first time accuracies of genomic research breeding values for sheep. At this stage it is unclear, what these accuracies mean for sheep breeding operations and what benefits they can gain. Some analyses for beef cattle (Van Eenennaam et al. 2010) and meat sheep (Banks and van der Werf, 2009) have demonstrated the value of molecular information to livestock industries.

The aim of this study is to evaluate a number of case studies across the Merino, maternal and terminal sire breeding program for the benefit that can be gained from using genomic selection and how much the breeder can afford to spend on this new technology.

Project Objectives

1) To evaluate the economic benefit of utilising genomic information to seed stock and producers from the maternal, terminal and Merino sheep sector using different scenarios as compared with traditional selection techniques.
2) Determine patterns for the benefit cost of genomic information across scenarios that affect the benefit of using genomic information.

Materials and Methods

Case studies

As part of the project 22 breeders across the terminal, maternal and Merino sheep industry sectors were invited to participate in case studies. 17 breeders responded and provided data on their breeding operation. Some breeders provided information on two studs (e.g. maternal and terminal). In total 21 case studies were conducted; 5 maternal, 10 terminal 6 Merino and 1 Dohne case study (note that the Dohne case study was included in the Merino group). The participating stud breeders are listed in Appendix 1.

A form was sent to each breeder to facilitate the collection of the information on the structure of their stud. The requested information included parameters on numbers of ewes and rams, reproduction rate and mortality, mating ratio and numbers rams sold and used in the stud (Table 1).

Table 1 Parameters requested from participating stud breeders

	Stud
Breeding objective	
Number of rams used	
Number of dams used	
Lambing %	
Mortality % birth to weaning	
Mortality % weaning to adult	
Number of age classes female (breeding seasons)	
Number of age classes male (breeding seasons)	
Numbers of rams sold for breeding per year (%)	
Numers of rams sold for breeding per year	
Number of rams selected within stud for breeding %	
Number of rams selected within stud for breeding	
Mating ratio % (Rams per 100 ewes)	
List of traits measured at what age for selection	
Recording cost per ram	

Calculations

Stud parameters of each breeding operation were entered into excel spreadsheets (developed by Julius van der Werf). Individual breeding programs of the participants were simulated using phenotypes in addition to use of genomic information and just by itself (later termed with and without genomic selection). Two parameters provided criteria to assess the benefit gained from using genomic information in breeding programs: the break-even point and the genetic gain per year per ewe joined. In the scenarios that included genomic information, it was assumed that all male lambs born in the stud were genotyped and no females.

Break-even point

Firstly, the cumulative discounted expression (CDE) for the stud and the commercial operation were calculated using geneflow (Hill, 1974). The CDE is the discounted sum of the expression of sires' genes across years and generations. The younger sires are at mating the higher the CDE. CDE are higher in stud rams than commercial rams, because the stud rams genes are also expressed at a commercial level. The actual age structure of each of the breeding operations was entered into the gene flow calculations.

Breeding programs were simulated with and without the genomic information using selection index methodology (Lande and Thompson, 1990). Genomic information was used in addition to phenotypes in males, ewes were selected on the basis of phenotypic information. Stud parameters, SheepGenetics Index and selection criteria, as indicated by the breeders, were entered. The selection index calculations per round of selection require information on selection criteria and the age of measurement. Genomic information could be of high and low accuracy. The accuracy is depended on the heritability of the trait. In practical terms, the high accuracy is what can be achieved from the Sheep Information Nucleus in 2013. Low accuracy is a bit lower of what can currently be achieved. The accuracy of genomic information depends on the number of animals in the reference population.
Accuracies of selection were calculated with and without genomic information, per year and per round of selection.

Two parameters were evaluated to assess the economic benefit breeders can gain from the use of genomic technologies. One is the break-even point that highlights how much a breeder can afford to spend on a DNA test. The second parameter is genetic gain per year calculated with and without the use of genomic information.

The break-even point was calculated for the stud and commercial level. In this report only the sum of both (total break-even point) is outlined. For the calculations of the break-even point for the stud level, individual stud breeders' flock profiles were used. For the break even-point at the commercial level, a standard commercial client profile was assumed for each of the sheep industries sectors, maternal, terminal and Merino. At the commercial level, each ram is mated to 50 females over 2 years, yielding 100 progeny per commercial ram. The selection intensity for the commercial level was derived from the proportion of commercial rams sold of all the male lambs born in the stud level. There were three steps to calculate the break-even point (commercial or stud). In the first step, the value of a superior ram (in $) was calculated using the standard deviation of the breeding objective, the selection intensity (stud or commercial), the selection accuracy, the number of commercial offspring and the cumulative discounted expression (stud or commercial)

Value of a superior ram (in $) = ($SD_{obj}$ x i x r) x no of progeny x CDE (1)

with SDobj =standard deviation of the breeding objective
i = selection intensity (stud or commercial)
r = accuracy of the index (per round of selection) with and without genomic selection
No of progeny = number of commercial progeny per ram
CDE = cumulative discounted expression (stud or commercial)

The value per superior ram (1) was calculated with and without the use of genomic selection. The difference between the value of a superior ram with and without the use of genomic selection in the breeding program was called the additional $ value per ram (Add $ value per ram).

Add $ Value per ram = Value of superior ram $_{GS}$ – Value of superior ram $_{noGS}$ (2)

with Value of superior ram $_{GS}$ = Value of superior ram from breeding program with genomic selection
Value of superior ram $_{noGS}$ = Value of superior ram from breeding program without genomic selection

The last step is the calculation of the break-even point. For this purpose, the additional $ value per ram (2) was divided by the number of test per ram used within stud or by the number tests used per ram sold. The second term is used to calculate the break-even point for the commercial level.

Break-even point = Add $ Value per ram / no. of test per ram sold (selected within stud) (3)

Variations of the breeding programs were simulated using genomic information of high (r^2_{high}=h^2) and low accuracy (r^2_{low}=0.25* h^2). The accuracy of the genomic information (r^2) reflects the proportion of genetic variance explained by genomic information for each individual trait and is dependent on the number of individuals with both genotypic and phenotypic records (Goddard, 2009). The actual age structure of the studs was used in all case studies (conventional selection). In addition, early selection was simulated for Merino breeders, assuming that rams can be selected and used at 8 months of age. All of these variations affect the accuracy of the index, which subsequently affects the break-even point.

Genetic gain per year per commercial ewe joined

The comparison of genetic gain per year per commercial ewe joined with and without the use of genomic information is another indicator of the benefit breeders can expect from the application of genomic technologies. The calculations in this study were only undertaken for conventional selection and with genomic information of high accuracy.

The same selection index spreadsheet as in the previous paragraphs was used to predict index accuracies, but the figures were calculated per year, not per round of selection as in the previous section. The only additional information required compared to the calculations per round of selection was the entry of sources of phenotype information (e.g. traits recorded on 25 half-sibs, dam and sire). There were two steps to the calculations of the genetic gain per year per commercial ewe joined. Firstly, the superiority of males and females is calculated from the standard deviation of the breeding objective, the male / female selection intensity and the accuracy of the index. The accuracy of the index was obtained from the spreadsheet with and without using genomic selection and the superiority was calculated for females only without the use of genomic information and for males with and without the use of genomic information.

$$\text{Superiority} = SD_{obj} * i * r \qquad (4)$$

with SDobj =standard deviation of the breeding objective
i = selection intensity (male or female)
r = accuracy of the index (per year) with and without genomic selection

In the second step, the genetic gain per year is calculated by summing the male and female superiority and dividing it by the sum of the male and female generation interval. This was with and without the use of genomic information in the selection of the rams.

$$\text{Genetic gain / year} = (\text{superiority}_m + \text{superiority}_f) / (Lm + Lf) \qquad (5)$$

with superiority = male or female superiority of selected individuals (equation 4)
L = male / female generation interval

Results

Stud parameters

Summaries of the information on the participating stud parameters are provided in Table 2 - 4. Detailed tables can be found in the appendix 2 - 4.

Table 2 Summary of parameters for terminal sire studs.

	Terminal sire studs		
	Mean	Minimum	Maximum
No of rams	14	5	31
No of ewes	564	150	1000
Lambing %	136	110	175
Mortality % birth to weaning	9	5	18
Mortality % weaning to adult	4	1	8
Number of rams sold	236	75	450
Mating ratio % (Rams per 100 ewes)	3	1	7
Stud CDE	1.81	1.26	2.63
Commercial CDE	0.65	0.65	0.65
GenInt Male	2.38	1.41	3.54
GenInt Female	2.91	2.16	3.3
Selection intensity stud	2.24	1.76	2.7
Selection intensity comm	0.51	0.23	0.64
Selection intensity male	2.18	1.76	2.66
Selection intensity female	1.11	0.98	1.25

Table 3 Summary of parameters for maternal sire studs.

	Maternal sire studs		
	Mean	Minimum	Maximum
No of rams	17.00	5	34
No of ewes	1116.00	180	2400
Lambing %	147.00	125	160
Mortality % birth to weaning	13	7	30
Mortality % weaning to adult	4	2	6
Number of rams sold	467	65	1000
Mating ratio % (Rams per 100 ewes)	2	1	3
Stud CDE	1.71	1.26	1.90
Commercial CDE	0.66	0.65	0.69
GenInt Male	2.32	1.87	3.32
GenInt Female	2.94	2.30	3.32
Selection intensity stud	2.26	2.07	2.51
Selection intensity comm	0.65	0.43	0.80
Selection intensity male	2.26	2.07	2.51
Selection intensity female	0.98	0.43	1.23

Table 4 Summary of parameters for Merino sire studs.

	Merino studs		
	Mean	Minimum	Maximum
No of rams	21	10	30
No of ewes	1257	600	2400
Lambing %	109	74	140
Mortality % birth to weaning	11	1.5	25
Mortality % weaning to adult	3	2	4
No of rams sold per year	266	68	550
Mating ratio % (Rams per 100 ewes)	2.3	1.0	2.5
Stud CDE	1.41	1.00	1.74
Stud CDE (early selection)	1.76	1.20	2.26
Commercial CDE	0.68	0.68	0.68
GenInt Male early	2.22	1.42	3.21
GenInt Male	3.22	2.42	4.21
GenInt Female	3.16	2.09	3.72
Selection intensity Stud	2.24	1.94	2.82
Selection intensity comm	0.87	0.50	1.00
Selection intensity male	2.17	1.94	2.37
Selection intensity female	0.90	0.66	1.08

The summaries showed that on average terminal sire studs that participated in the case studies were smallest as judged by the number of ewes compared to Merino and maternal sire studs. They also used fewer rams. As can be expected, lambing percentage was highest in the maternal sire studs and lowest in the Merino studs. However, the maternal sire studs had on average also the highest mortality rate from birth to weaning, whereas the Merino studs had on average the lowest mortality of the three groups. Mortality from weaning to adult was very similar for all three groups. The summaries also showed that on average the maternal sire studs sold nearly twice as many rams as the terminal sire and Merino studs. The CDE was the highest for terminal sire studs, followed by the maternal sire studs and it was the lowest for Merino studs. However, when rams in the Merino stud were selected at 8 months of age, the CDE were nearly as high as for the terminal sire studs. Generation intervals were similar for maternal sire and terminal sire studs. For Merino studs, on average, both, male and female generation intervals were higher. Selection intensities did not vary greatly between the three groups.

Accuracies and break-even point per round of selection

Summaries of the accuracies (r) (Table 5 – 7) and break even points (Table 8 – 10) are shown below. Detailed information on the accuracies is outlined in appendices 5 - 7. Individual final and intermediate results for each breeder are presented in appendices 8 - 11. The individual break-even points for terminal, maternal and Merino are shown in appendices 12 - 14.

The comparison of accuracies from selection index calculations with and without genomic information for conventional selection across maternal sire, terminal sire and Merino studs highlights, that the initial index accuracies without genomic information is higher for the terminal sire studs (r mean = 0.71) than the maternal sire studs (r mean = 0.60). The accuracy was the lowest for Merino studs (r mean = 0.47). Across all three groups the index accuracy increased with the inclusion of genomic information and also with increasing accuracy of the genomic information. The increase in index accuracy between noGS and GS high_acc was higher for Merino studs (32%) compared to maternal sire studs (17%) and terminal sire studs (11%).

With the use of genomic technologies, Merino studs can potentially select their rams at 8 months of age. The comparison of the accuracies (Table 7 – Conventional vs early selection) show that the accuracies were slightly lower for early selection when genomic information was used, compared to conventional selection with genomic information. The reason was that we used a combination of phenotypic and genomic information in the selection index. If rams are selected early, less phenotypic information is available. This was also reflected in a lower accuracy without genomic selection.

Table 5 Summary of the accuracies without genomic information (no GS) and with genomic information of high and low accuracies (GS hig_acc and GS low_acc) for terminal sire stud operations

	Accuracies – Terminal sire studs		
	Mean	Minimum	Maximum
No GS	0.71	0.69	0.73
GS low_acc	0.73	0.71	0.75
GS high_acc	0.79	0.78	0.80

Table 6 Summary of the accuracies without genomic information (no GS) and with genomic information of high and low accuracies (GS hig_acc and GS low_acc) for maternal sire stud operations

	Accuracies – Maternal sire studs		
	Mean	Minimum	Maximum
No GS	0.60	0.60	0.60
GS low_acc	0.62	0.62	0.62
GS high_acc	0.70	0.70	0.70

Table 7 Summary of the accuracies without genomic information (no GS) and with genomic information of high and low accuracies (GS hig_acc and GS low_acc) for Merino sire stud operations. Accuracies shown for conventional and early selection.

	Accuracies - Merino studs					
	Conventional selection			Early selection		
	Mean	Minimum	Maximum	Mean	Minimum	Maximum
No GS	0.47	0.31	0.56	0.42	0.29	0.55
GS low_acc	0.51	0.36	0.60	0.48	0.35	0.59
GS high_acc	0.62	0.49	0.71	0.60	0.48	0.70

A comparison of the break-even point for conventional selection (Table 8 and 9) shows that it is around four times higher for Merino studs compared to terminal sire studs and around 1.5-fold higher for Merino studs compared to maternal sire studs. When genomic information of high accuracy was used, the mean break-even point for terminal sire studs was $64, $155 for maternal sire studs and $252 for Merino studs. When genomic information of low accuracy was used, the break-even point did not reach $100 for any of the three groups.

When early selection was applied in the Merino studs (Table 10), the mean break-even point was at $135 if genomic information was of low accuracy and $381 if it was of high accuracy.

Table 8 Summary of the break-even point (in $) for the use of genomic information of high and low accuracy in terminal sire stud operations.

Break-even point – terminal sire studs			
	Mean	Minimum	Maximum
GS acc_low	18	10	33
GS acc_high	64	39	116

Table 9 Summary of the break-even point (in $) for the use of genomic information of high and low accuracy in maternal sire stud operations.

Break-even point – maternal sire studs			
	Mean	Min	Max
GS acc_low	37	30	44
GS acc_high	155	108	215

Table 10 Summary of the break-even point (in $) for the use of genomic information of high and low accuracy in Merino sire stud operations.

	Break-even point – Merino studs					
	Conventional selection			Early selection		
	Mean	Minimum	Maximum	Mean	Minimum	Maximum
GS acc_low	72	32	102	134	36	255
GS acc_high	252	120	370	381	138	536

Figure 1 outlines the relationship between the difference in accuracy (no genomic information vs genomic information of high accuracy) and the break-even point. Twenty one case studies are not a large data sample, but clear trends can be observed between terminal sire, maternal sire, Merino conventional selection and Merino early selection. Overall, there is a linear relationship between the increase in accuracy when genomic information is used and the break-even point. The terminal sire studs all cluster at a low increase in accuracy and consequently low break-even point. Merino studs vary wider because the variation in the initial selection index variance without genomic information was much larger.

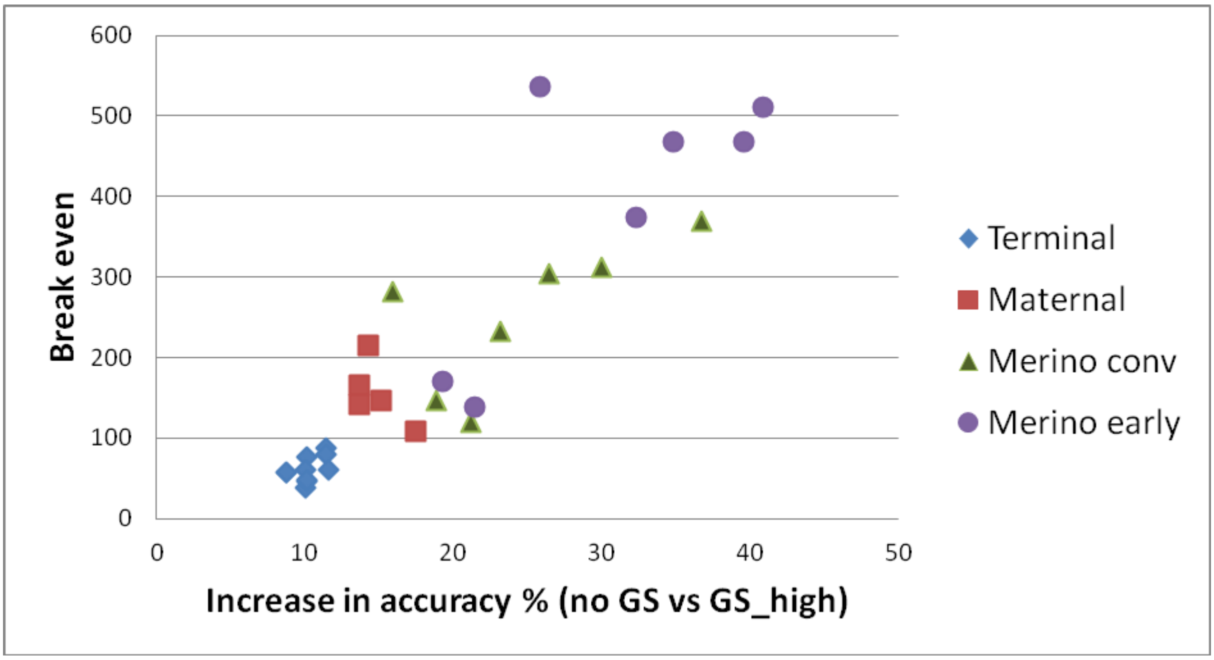

Figure 1 Relationship between difference in accuracy between noGS and GS_high.

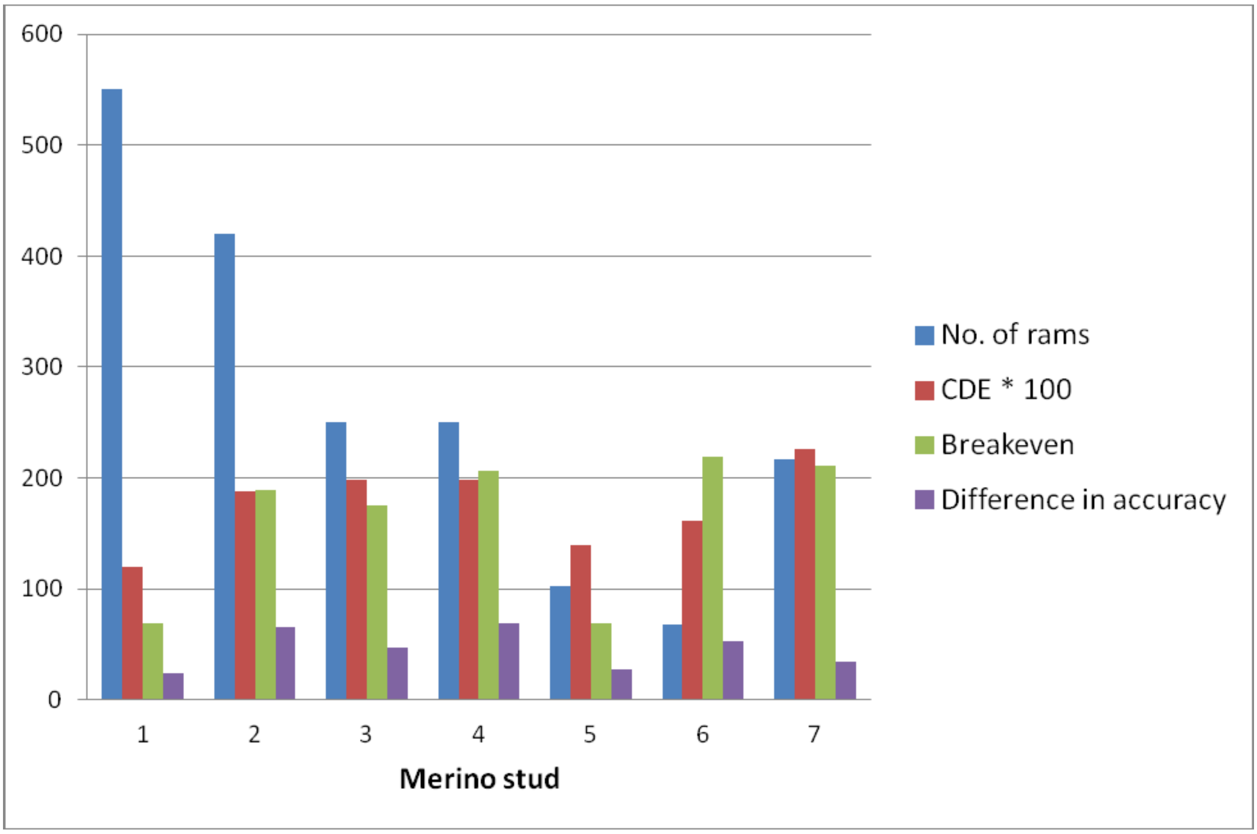

Figure 2 Effect of number of rams sold, difference in accuracy (between noGS and GS_high) and CDE on break-even point for Merino studs (early selection).

Figure 2 shows the effect of the number of rams sold, the CDE and the difference in accuracy on the break-even point in the Merino studs. It shows that neither the number of rams or CDE were the solely influential factor on the break-even point. For example stud 1, sold the largest number of rams compared to the other studs, but has the lowest break-even point. Similarly, the difference in accuracy is low for stud 7, but the break-even point is second highest. No clear trends can be observed in the comparison of the combination of the various on-farm variables.

Genetic gains per year

A summary of the genetic gains per year per commercial ewe joined are shown in tables 11 – 13. Individual results are shown in appendices 15 – 17

Breeding programs without genomic information had on average the highest male and female index accuracies in terminal sire studs, followed by maternal sire studs and the lowest accuracies for Merino studs. With the inclusion of genomic information in the selection index, male index accuracy increased on average for terminal sire studs by 10%, by 16% for maternal sire studs and by 24% for Merino studs. As a consequence, genetic gain per year increased with the inclusion of genomic information in the selection index on average by 4% for terminal sire studs, 12% for maternal sire studs and 23% for Merino studs. The actual genetic gain per year per commercial ewe joined is lower for the terminal sire studs, compared to the maternal sire and Merino studs because the standard deviation of the breeding objective is lower.

Table 11 Summary of mean index accuracies (male and female) and genetic gain per year per commercial ewe joined for terminal sire stud operations.

	Terminal sire studs		
	Accuracy male	Accuracy female	Genetic gain per year ($)
no GS	0.68	0.68	1.08
GS	0.75	0.68	1.12

Table 12 Summary of mean index accuracies (male and female) and genetic gain per year per commercial ewe joined for maternal sire stud operations.

	Maternal sire studs		
	Accuracy male	Accuracy female	Genetic gain per year ($)
no GS	0.54	0.54	2.23
GS	0.63	0.54	2.50

Table 13 Summary of mean index accuracies (male and female) and genetic gain per year per commercial ewe joined for Merino sire stud operations.

	Merino studs		
	Accuracy male	Accuracy female	Genetic gain per year ($)
no GS	0.46	0.46	2.17
GS	0.57	0.46	2.67

Discussion

In this study, we investigated the benefit of including genomic information in Merino, terminal sire and maternal sire breeding programs. Two studies in Australian sheep (van der Werf, 2009; Dominik et al. 2011) have reported increased accuracies and resulting genetic gain of around 30% for terminal sire breeding programs and 40% for Merino studs.

Our study explored gains resulting from the application of genomic information in the selection index for 21 studs across the terminal, maternal and Merino industries and agreed with the previous studies. Index accuracies and genetic gains increased when genomic information was used in selection decisions. Accuracies and gains were highest for Merino studs, then maternal sire studs and lowest for terminal sire studs. In this study the average increase in index accuracies and resulting genetic gains was lower for terminal sire studs (11%) than predicted by van der Werf (2009), with 30%. Genetic gains with and without genomic information are most likely overestimated, because selection intensities are often lower on farm due to consideration in selection decisions that are not captured in the selection index. However, this affects gains with and without genomic information equally and does not impact on the relative increase that can be achieved with the inclusion of genomic information.

The increase in index accuracy that can be achieved through the inclusion of genomic information is dependent on the initial accuracy gained with selection without genomic information and also the actual selection index used. Terminal sire studs had high initial accuracy of the selection index, because live weights and scan carcase traits are well correlated with the traits in the terminal sire indexes and selection candidates have records of own performance at time of selection. That also meant that a genomic test could not add a lot more information to the selection index. Terminal sire breeders will benefit substantially more when genomic information becomes available for actual carcase traits like lean meat yield. In contrast, the SheepGenetics Merino index had lower initial index accuracies without inclusion of genomic information, compared to the terminal sire indexes. This was due to trait, like e.g. adult fleece traits in the selection index, which are not actually measured. However, this is where genomic information can contribute, which is reflected in the higher increase in selection index accuracy after inclusion of genomic information, compared to the terminal sire indexes.

Another opportunity for Merino breeding operations in using genomic information is to shorten the generation interval on the male side. It provides the opportunity to select rams when they first become sexually mature based on genomic information only. Some selection index accuracy is compromised, compared to selection on phenotype and genomic information after first shearing, but the shortened generation interval has increased the genetic gains significantly. Single sire mating of young rams carries the potential risk that the ram is not sexually mature. Such risk can be reduced through syndicate mating and verification of pedigree following the birth of lambs. Obviously this would carry an additional cost, which has not been considered in evaluating the benefit of using genomic information to mate rams early in this study. Terminal sire and maternal sire breeders already select the majority of their young rams at 8 months of age, based on post-weaning carcase scan traits and live weights. Therefore, this aspect of the use of genomic technologies does not provide an opportunity to maternal sire and terminal sire stud breeders.

The increased accuracies that could be achieved in the Merino operations led to a higher break-even point that allows Merino breeders to spend currently more on DNA testing compared to terminal sire or maternal sire breeders. However, a combination of on-farm variables (e.g. number of rams sold, cumulative discounted expression) influence the break-even point, as was outlined in Figure 2. Even though the break-even point provides a good indicator to get a general understanding of the benefits of genomic technologies to an industry sector, the variability between different studs within a sector is high, more so when potential benefits are high. Once more information on the actual accuracies of genomic information of selection index traits becomes available, an optimisation tool, that balances various on-farm logistical factors and also the numbers and animals to genotype and phenotype could facilitate successful implementation of genomic technologies on farm.

Conclusion

It can be concluded that with the current level of genomic information available to sheep industries, the largest benefits can be achieved by the Merino industry, due to more accurate and earlier selection of rams. This study provided a good benchmark for the level of anticipated benefits for the terminal, maternal and Merino sector, however, a range of on-farm factors influence individual benefits for studs. Optimisation tools that can help breeders determine how to balance such factors would facilitate the successful implementation of genomic technologies on farm. The results of this study were presented in two workshops. A summary of the workshops is presented in Appendix 22. The comments from breeders collected during the workshop support the conclusions drawn from the results of the case studies.

Appendices

Appendix 1

List of case study and workshop participants

Name	Sector	Workshop
David Kain	Dohne	1 & 2
Kelly Pearce	Maternal	
Lynton Arney	Maternal	1 & 2
Don Pegler & John Keiller	Maternal/Terminal	2
Tom Bull	Maternal/Terminal	1
Mark Mortimer	Merino	1
Matthew Coddington	Merino	1
Tom Silcock	Merino	1 & 2
Warren Russell	Merino	2
Andrew Michael	Merino/Terminal	1
Dale Price	Terminal	1 & 2
Dawson Bradford	Terminal	2
George Carter	Terminal/Maternal	1 & 2
Murray Long	Terminal	1 & 2
Rodney Watt	Terminal	1
Steve Milne	Terminal	1
Troy Fischer	Terminal	1

Appendix 2 Detailed stud parameters of participating terminal sire breeders.

	Bradford	Bull	Carter	Fischer	Keiller	Long	Michael	Milne	Price	Watt
No of rams	31	10	11	10	5	18	9	5	23	20
No of ewes	966	1000	275	370	350	780	600	150	348	800
Lambing %	117	110	143	130	115	140	135	175	145	150
Mortality % birth to weaning	5	7	18	5	7	9	6	16	7	12
Mortality % weaning to adult	6	3	2	5	2	4	1	1	8	3
Number of rams sold	320	450	133	170	120	370	220	75	172	325
Mating ratio %	3.20	1.00	2.50	2.70	1.50	2.50	1.50	3.00	6.60	3.00
Stud CDE	2.63	1.48	2.02	2.09	1.86	1.55	1.26	1.74	1.89	1.61
Commercial CDE	0.65	0.65	0.65	0.65	0.65	0.64	0.65	0.65	0.65	0.65
GenInt Male	1.41	2.75	2.06	2.46	1.99	2.50	3.54	2.10	2.33	2.65
GenInt Female	2.16	2.76	3.11	2.72	2.92	3.11	3.30	3.09	3.02	2.90
Selection intensity stud	2.00	2.42	1.92	2.11	2.31	2.66	2.36	2.10	1.76	2.18
Selection intensity comm	0.64	0.23	0.35	0.45	0.60	0.45	0.62	0.50	0.64	0.64
Selection intensity male	2.00	2.42	1.92	2.11	2.31	2.66	2.36	2.10	1.76	2.18
Selection intensity female	1.03	0.98	1.07	1.11	1.01	1.12	1.12	1.22	1.25	1.15
SheepGenetics Index	LAMB 2020	LAMB 2020	LAMB 2020	LAMB 2020	LAMB 2020	LAMB 2020	LAMB 2020	LAMB 2020	LAMB 2020	LAMB 2020
SD BO	2.51	2.51	2.51	2.51	2.51	2.51	2.51	2.51	2.51	2.51

Appendix 3 Detailed stud parameters of participating maternal sire breeders.

	Arney	Bull	Carter	Keiller	Pearce
No of rams	18	20	5	34	8
No of ewes	700	2000	180	2400	300
Lambing %	150	140	160	125	160
Mortality % birth to weaning	12	7	30	7	7
Mortality % weaning to adult	5	3	3.5	2	6
No of rams sold per year	350	1000	65	800	120
Mating ratio %	2.50	1.00	2.50	1.40	2.70
Stud CDE	1.86	1.77	1.90	1.77	1.26
Commercial CDE	0.65	0.65	0.69	0.65	0.65
GenInt Male	1.93	2.51	1.87	1.99	3.32
GenInt Female	2.86	2.30	3.30	2.92	3.32
Selection intensity Stud	2.16	2.51	2.07	2.35	2.20
Selection intensity comm	0.43	0.80	0.65	0.60	0.75
Selection intensity male	2.16	2.51	2.07	2.35	2.20
Selection intensity female	0.43	1.14	1.04	1.07	1.23
SheepGenetics Index	Maternal $	Maternal $	Maternal $	Maternal $	Maternal $
SD BO	5.63	5.63	5.63	5.63	5.63

Appendix 4 Detailed stud parameters of participating Merino sire breeders.

	Coddington	Michael	Mortimer SS10	Mortimer DP10	Russell	Silcock	Kain (Dohne)
No of rams	30	22	25	25	18	10	16
No of ewes	2400	1800	1250	1250	796	700	600
Lambing %	112	115	113	113	74	93	140
Mortality % birth to weaning	10	5	25	25	8	2.5	1.5
Mortality % weaning to adult	4	2	4	4	2	3	2
No of age classes female	6	6	5	5	6	5	8
No of age classes male	7	4	3	3	6	2	3
Rams sold per year (%)	52	69	39	39	37		85
No of rams sold per year	550	420	250	250	103	68	217
Rams selected within stud (%)	2	1.5	1.8	1.8	1	1.5	1.5
No of rams selected within stud	10	6	23	23	3	4	4
Mating ratio %	1.25	1.70	2.00	2.00	2.30	1.50	2.70
Stud CDE	1.00	1.52	1.56	1.56	1.15	1.31	1.74
Stud CDE (early selection)	1.20	1.88	1.98	1.98	1.39	1.62	2.26
Commercial CDE	0.68	0.68	0.68	0.68	0.68	0.68	0.68
GenInt Male early	3.21	2.54	1.42	1.42	2.78	2.02	2.16
GenInt Male	4.21	3.54	2.42	2.42	3.76	3.02	3.16
GenInt Female	3.72	3.30	3.52	3.52	2.92	3.08	2.09
Selection intensity Stud	2.34	2.38	2.08	2.08	1.94	2.24	2.16
Selection intensity comm	0.80	0.97	1.00	1.00	1.00	0.50	0.80
Selection intensity male	2.34	2.38	2.08	2.08	1.94	2.24	2.16
Selection intensity female	0.97	1.04	0.84	0.84	0.66	0.89	1.08
SheepGenetics Index	DP7%	DP7%	Fine10%+SS	DP7%	Fine10%	Fine10%+SS	DP14%
SD BO	4.53	4.53	3.67	4.53	3.56	3.42	4.92

Appendix 5 Selection accuracies and standard deviation of the selection index (SD Index) with and without genomic selection of the terminal sire stud participants. Genomic information had high (acc_high) and low (acc_low) accuracies.

	Bradford	Bull Term	Carter	Fischer	Keiller	Long	Michael	Milne	Price	Watt
no genomic selection										
Accuracy	0.70	0.73	0.71	0.70	0.72	0.73	0.72	0.69	0.71	0.71
SD Index	1.76	1.82	1.79	1.75	1.82	1.82	1.81	1.73	1.78	1.78
genomic selection										
Accuracy (h2)	0.79	0.80	0.79	0.79	0.80	0.80	0.80	0.78	0.79	0.79
SD Index (h2)	1.98	2.01	1.98	1.98	2.01	2.01	2.01	1.95	1.98	1.98
Accuracy (0.25h2)	0.72	0.75	0.73	0.73	0.74	0.74	0.74	0.71	0.73	0.73
SD Index (0.25h2)	1.81	1.87	1.82	1.82	1.86	1.87	1.86	1.79	1.83	1.83

Appendix 6 Selection accuracies and standard deviation of the selection index (SD Index) with and without genomic selection of the maternal sire stud participants. Genomic information had high (acc_high) and low (acc_low) accuracies.

	Arney	Bull	Carter	Keiller	Pearce
no genomic selection					
Accuracy	0.57	0.60	0.57	0.56	0.52
SD Index	3.20	3.37	3.20	3.15	2.90
genomic selection					
Accuracy (h2)	0.66	0.70	0.66	0.66	0.63
SD Index (h2)	3.73	3.92	3.73	3.71	3.56
Accuracy (0.25h2)	0.59	0.62	0.59	0.59	0.55
SD Index (0.25h2)	3.32	3.51	3.32	3.3	3.08

Appendix 7 Selection accuracies and standard deviation of the selection index (SD Index) with and without genomic selection of the Merino sire stud participants. Genomic information had high (acc_high) and low (acc_low) accuracies. Selection was modelled with current age structure (conventional selection) and with using sires at 8 months of age (early selection).

	Coddington	Michael	Mortimer SS10	Mortimer DP10	Russell	Silcock	Kain (Dohne)
no genomic selection							
Accuracy	0.43	0.31	0.53	0.35	0.56	0.50	0.53
SD Index	1.96	1.41	1.96	1.56	1.99	1.71	2.62
no genomic selection (early)							
Accuracy	0.42	0.29	0.44	0.29	0.55	0.43	0.43
SD Index	1.91	1.31	1.62	1.31	1.98	1.47	2.13
genomic selection							
Accuracy (h2)	0.53	0.49	0.69	0.50	0.71	0.68	0.63
SD Index (h2)	2.41	2.22	2.52	2.25	2.53	2.33	3.11
Accuracy (0.25h2)	0.46	0.36	0.58	0.39	0.60	0.55	0.56
SD Index (0.25h2)	2.08	1.65	2.12	1.76	2.14	1.88	2.75
early genomic selection							
Accuracy (h2)	0.52	0.48	0.65	0.49	0.70	0.66	0.58
SD Index (h2)	2.35	2.17	2.38	2.21	2.49	2.25	2.85
Accuracy (0.25h2)	0.45	0.35	0.50	0.37	0.59	0.51	0.48
SD Index (0.25h2)	2.03	1.59	1.84	1.68	2.10	1.74	2.36

Appendix 8 Intermediate and final results for terminal studs and their commercial clients that lead to the break-even point

	Stud									
	Superiority			Value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Bradford	3.52	3.62	3.97	9549	9822	10776	273	1228	16	71
Bull	4.45	4.57	4.88	59289	60913	64974	1624	5685	32	111
Carter	3.39	3.54	3.83	8280	8635	9344	355	1065	24	73
Fischer	3.72	3.88	4.2	13220	13787	14920	567	1700	25	74
Keiller	4.17	4.3	4.64	18657	19175	20730	518	2073	14	55
Long	3.96	4.07	4.35	12633	12984	13861	351	1228	13	44
Michael	4.26	4.38	4.74	13130	13494	14589	365	1459	9	34
Milne	3.64	3.75	4.11	9507	9782	10747	276	1240	12	56
Price	3.2	3.3	3.57	4530	4657	5040	128	510	12	47
Watt	3.88	3.99	4.31	10147	10432	11290	286	1143	11	43
	Commercial									
	Superiority			Value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Bradford	1.12	1.16	1.27	73	75	82	2	9	4	16
Bull	0.42	0.43	0.46	55	56	60	2	5	1	5
Carter	0.61	0.64	0.69	40	42	45	2	5	1	4
Fischer	0.79	0.82	0.89	51	54	58	2	7	2	5
Keiller	1.8	1.11	1.2	70	72	78	2	8	1	5
Long	0.81	0.84	0.89	53	54	58	1	5	1	4
Michael	1.12	1.15	1.24	73	75	81	2	8	1	5
Milne	0.87	0.89	0.98	56	58	64	2	7	1	5
Price	1.14	1.17	1.27	74	76	82	2	8	1	6
Watt	1.14	1.17	1.27	74	76	82	2	8	1	5

Appendix 9 Intermediate and final results for maternal studs and their commercial clients that lead to the break-even point

	Stud									
	Superiority			Value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Arney	6.95	7.19	8.04	25127	26009	29094	882	3967	34	155
Bull	8.5	8.78	9.92	75224	77732	87761	2507	12537	39	193
Carter	6.63	6.86	7.68	16376	16951	18962	575	2586	29	128
Keiller	7.4	7.78	8.72	30822	32474	36326	1651	5504	40	134
Pearce	6.44	6.81	7.8	12163	12865	14737	702	2573	25	92
	Commercial									
	Superiority			Value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Arney	1.38	1.43	1.6	90	93	104	3	14	2	11
Bull	2.7	2.79	3.15	176	182	205	6	29	4	22
Carter	2.09	2.16	2.41	136	140	157	5	21	3	14
Keiller	1.89	1.99	2.23	123	130	145	7	22	4	13
Pearce	2.2	2.32	2.66	143	151	173	8	30	4	16

Appendix 10 Intermediate and final results for Merino studs and their commercial clients that lead to the break-even point with conventional selection

	Stud									
	Superiority			Value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Coddington	11.31	12.08	13.94	20742	22189	25565	1445.84	4821.12	34.72	119.04
Michael	8.28	9.62	13.09	24059	27939	38028	3878.72	13962.4	86.8	312.48
Mortimer SS10	8.69	9.50	11.30	12629	13821	16442	1277.58	4089.54	59.92	192.6
Mortimer DP7	8.21	9.13	11.73	8340	9293	11914	1463.2	5485.76	69.44	257.92
Russell	7.74	8.30	9.82	5115	5480	6485	364	1364	24	90
Silcock	8.24	9.05	11.19	23938	26332	32556	2392.52	8615.64	74.9	271.78
Kain	14.35	15.16	17.07	33839	35755	40224	1917.7	6393.18	73.66	246.38
	Commercial									
	Superiority			value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Coddington	3.844	3.8688	4.7616	263	281	324	17.36	62	7.44	27.28
Michael	3.3728	3.9184	5.332	230	267	363	37.2	133.92	14.88	57.04
Mortimer SS10	4.173	4.5582	5.4356	264	289	344	27.82	85.6	12.84	40.66
Mortimer DP7	3.9432	4.3896	5.6296	175	195	249	29.76	114.08	14.88	54.56
Russell	4.22	4.52	5.34	288	309	365	20	76	8	30
Silcock	1.8404	2.0116	2.4824	124	137	169	12.84	44.94	8.56	32.1
Kain	5.2832	5.588	6.2992	360	380	428	20.32	68.58	10.16	35.56

Appendix 11 Intermediate and final results for Merino studs and their commercial clients that lead to the break-even point with early selection

	Stud									
	Superiority			Value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Coddington	11.04	11.83	13.66	24311	26048	30099	1736	5785.84	42.16	143.84
Michael	7.74	9.35	12.82	27837	33596	46075	5756.08	18228	128.96	406.72
Mortimer SS10	7.21	8.20	10.66	13307	15122	19659	1947.4	6813.76	92.02	321
Mortimer DP7	6.80	9.13	11.48	13468	18112	22756	4642.56	9282.64	218.24	438.96
Russell	7.60	8.16	9.68	6072	6513	7728	440	1648	30	110
Silcock	7.08	8.39	10.85	25459	30195	39076	4735.82	13614.68	149.8	428
Kain	11.63	13.00	15.70	35659	39806	48098	4152.9	12456.16	160.02	482.6
	Commercial									
	Superiority			Value			Difference		Value per test	
	no GS	GS_low	GS_high	no GS	GS_low	GS_high	GS_low	GS_high	GS_low	GS_high
Coddington	3.7696	4.0424	4.6624	257	275	318	17.36	62	7.44	27.28
Michael	3.1496	3.8192	5.2328	215	259	356	44.64	141.36	19.84	59.52
Mortimer SS10	3.4668	3.9162	5.1146	219	249	324	32.1	113.42	14.98	53.5
Mortimer DP7	3.2736	4.3896	5.5056	222	299	375	76.88	153.76	37.2	71.92
Russell	4.14	4.44	5.26	283	303	360	20	76	8	30
Silcock	1.5836	1.8618	2.4182	107	127	164	19.26	57.78	14.98	40.66
Kain	4.2926	4.8006	5.7912	292	326	394	33.02	101.6	17.78	53.34

Appendix 12 Individual break-even points for terminal stud operations.

	GS_low	GS_high
Bradford	19	87
Bull	33	116
Carter	26	77
Fischer	26	79
Keiller	15	60
Long	14	48
Michael	10	39
Milne	14	61
Price	13	52
Watt	12	48

Appendix 13 Individual break-even points for maternal stud operations.

	GS_low	GS_high
Arney	37	165
Bull	43	215
Carter	32	142
Keiller	44	147
Pearce	30	108

Appendix 14 Individual break-even points for Merino stud operations with conventional and early selection.

	Conventional		Early	
	GS_low	GS_high	GS_low	GS_high
Coddington	44.64	146.32	52.08	171.12
Michael	101.68	369.52	148.8	468.72
Mortimer SS10	72.76	233.26	107	374.5
Mortimer DP7	84.32	312.48	255.44	510.88
Russell	32	120	36	138
Silcock	83.46	303.88	162.64	468.66
Kain	83.82	281.94	177.8	535.94

Appendix 15 Individual results and intermediate calculations and genetic gain per year with and without genomic selection for terminal sire stud operations

	Accuracy male		Accuracy female		Superiority male		Superiority female		Genetic gain per year	
	no GS	GS	no GS	GS	no GS	GS	no GS	GS	no GS	GS
Bradford	0.54	0.68	0.54	0.54	2.71	3.42	1.41	1.41	1.15	1.35
Bull	0.64	0.75	0.64	0.64	3.95	4.61	1.59	1.59	1	1.13
Carter	0.71	0.79	0.71	0.71	3.46	3.83	1.92	1.92	1.04	1.11
Fischer	0.7	0.73	0.7	0.7	3.72	3.88	1.95	1.95	1.09	1.13
Keiller	0.72	0.74	0.72	0.72	4.16	4.3	7.82	1.82	1.22	1.25
Long	0.71	0.79	0.71	0.71	4.74	5.3	1.99	1.99	1.2	1.3
Michael	0.72	0.74	0.72	0.72	4.25	4.38	2.03	2.03	0.91	0.94
Milne	0.68	0.7	0.68	0.68	3.59	3.7	2.08	2.08	1.09	1.11
Price	0.71	0.74	0.71	0.71	3.17	3.27	2.25	2.25	1.01	1.03
Watt	0.71	0.74	0.71	0.71	3.92	4.04	2.07	2.07	1.08	1.1

Appendix 16 Individual results and intermediate calculations and genetic gain per year with and without genomic selection for maternal sire stud operations

	Accuracy male		Accuracy female		Superiority male		Superiority female		Genetic gain per year	
	no GS	GS	no GS	GS	no GS	GS	no GS	GS	no GS	GS
Arney	0.56	0.66	0.56	0.56	6.88	8.06	3.66	3.66	2.2	2.45
Bull	0.52	0.64	0.52	0.52	7.39	9.09	3.36	3.36	2.23	2.59
Carter	0.56	0.66	0.56	0.56	6.6	7.72	3.33	3.33	3.19	3.55
Keiller	0.56	0.66	0.56	0.56	7.4	8.72	3.37	3.37	2.04	2.3
Pearce	0.52	0.54	0.52	0.52	6.37	6.68	3.55	3.55	1.49	1.54

Appendix 17 Individual results and intermediate calculations and genetic gain per year with and without genomic selection for maternal sire stud operations

	Accuracy male		Accuracy female		Superiority male		Superiority female		Genetic gain per year	
	no GS	GS	no GS	GS	no GS	GS	no GS	GS	no GS	GS
Coddington	0.43	0.53	0.43	0.43	11.34	13.97	4.71	4.71	2.31	3.7
Michael	0.3	0.36	0.3	0.3	7.99	9.59	3.51	3.51	1.68	1.91
Mortimer SS10	0.63	0.71	0.63	0.63	9.62	10.84	3.89	3.89	2.27	2.48
Mortimer DP7	0.38	0.51	0.38	0.38	8.9	11.96	3.6	3.6	2.1	2.62
Russell	0.52	0.68	0.52	0.52	7.31	9.52	2.49	2.49	1.47	1.8
Silcock	0.54	0.69	0.54	0.54	8.89	11.36	3.52	3.52	2.03	2.44
Kain	0.43	0.52	0.43	0.43	11.59	14.02	5.8	5.8	3.31	3.77

Appendix 18

Workshop “Potential use of genomic tools in sheep breeding”
April 27-28, 2011
Liaison Centre, CSIRO Livestock Industries, New England Highway, Armidale

AGENDA
Wednesday 27 April

2.00	Welcome, Introduction, Objectives
2.15	Potential values of genomic selection to sheep breeding programs
2.45	Evaluating cost-benefit of breeding program investment
3.15	Afternoon tea
3.45	Value of genomic selection for stud and commercial rams
4.15	Approach to evaluating case studies
	Overview of input data for case studies
	Parameters evaluated by software
	Example of presentation of the case study results
	Summary slides of result
	Discussion on methods and principles to approach individual case studies SD
5.00	Close
6.00	Dinner at the Powerhouse

Thursday 28 April

9.00	Discussion of results of individual case studies
10.30	Morning tea
10.00	Optimizing the use of genomic technologies
	genotyping strategies
	age structure
	trait recording
12.00	Lunch
12.30	Discussion on further improvements and next steps
2.00	Close

Appendix 19

Workshop “Potential use of genomic tools in sheep breeding – Follow up workshop”
September 8, 2011
Mantra Tullamarine, Melbourne

AGENDA

8.00	Welcome, Introduction, Objectives (Alex / Sam)
8.15	Introduction into genomic selection (Julius)
9.00	Value of genomic selection for stud and commercial rams (Case studies) (Sonja)
10.00	Morning tea
10.15	Group discussions of case studies
10.45	Overview of case study results and key messages (Sonja)
11.15	Who gets the benefit from genomic selection? NPV for stud and commercial sector (Julius)
12.0	Lunch
1.00	Optimisation of age structure and genotyping strategy (Sonja / Julius)
2.00	Discussions of key messages, consequences, next steps (Alex / Sam)
3.00	Close

Appendix 20 – Example report

Workshop
“Potential use of genomic tools in sheep breeding”

Results breeder’s case studies
THE VALUE OF GENOMIC SELECTION FOR STUD AND COMMERCIAL MERINO RAMS

Case Study : Breeder’s name

Table1 Information supplied by the breeder

	Stud
No of rams	
No of ewes	
Lambing %	
Mortality % birth to weaning	
Mortality % weaning to adult	
No of rams sold for breeding per year	
Mating ratio (Ewe : ram)	
Traits recorded for selection	
Birth	
Weaning	
Post weaning	

Approach 1 - How much can I afford to spend on a DNA test?

Formulas

Formula 1

Value of a superior ram (in $)= $(SD_{Obj} \times i \times Acc) \times no\ of\ progeny \times CDE$

Formula 2

Add $ Value per ram = Value of superior ram $_{GS}$ – Value of superior ram $_{noGS}$

Formula 3

Break even = $\dfrac{Add\ \$\ value\ per\ ram}{no\ of\ test\ per\ ram\ sold\ (or\ selected\ within\ stud)}$

Results

Table 2 Selection intensities (i), standard deviation of the breeding objective (SD_{Obj} in $), cumulative discounted expressions (CDE) for stud (conventional and early selection) and commercial operation and generation intervals for males (L_m) and females (L_f)

Parameter	
SD_{Obj}	
CDE_{stud}	
$CDE_{commercial}$	
i_{stud}	
$i_{commercial}$	

Table 3 Index accuracies (Acc) of using phenotypic information only (no GS) and adding genomic information (GS) of varying accuracies (acc_low and acc_high) and superiority of stud and commercial rams (in $)

Information for selection	Acc	Superiority Stud	Superiority Comm
no GS			
GS_{acc_low}			
GS_{acc_high}			

Table 4 Value of superior rams and additional commercial dollar value gained per ram using a selection index with phenotypic information only (no GS) and with the inclusion of genomic information (GS) of varying accuracy

	Value of superior ram (in $)			Add $ value per ram	
	No GS	GS $_{acc\_low}$	GS $_{acc\_high}$	GS $_{acc\_low}$	GS $_{acc\_high}$
Stud ram					
Commercial ram					
Total					

Table 5 Break even point (Total)– How much can a breeder afford to spend on a DNA test.

	Add $ per DNA test	
	GS $_{acc\_low}$	GS $_{acc\_high}$
Stud ram		
Commercial ram		
Total		

Approach 2 Genetic gain per year per commercial ewe joined

(only presented for GS high_acc)

Formulas

1) Superiority = $SD_{BO} * i * Acc$

Calculated for males and females and with and without genomic selection

2) Genetic gain / year = $(superiority_m + superiority_f) / (Lm + Lf)$

Calculated with and without genomic selection

Parameters

Table 1 Standard deviation of the breeding objective (SD_{BO}), selection intensities (i_m and i_f) and generation interval for males and females (L_m and L_f)

Parameter	
SD_{BO}	
i_m	
i_f	
L_m	
L_f	

Results

Table 2 Accuracies and superiority of selection and genetic gain per year without genomic selection (no GS) and with genomic selection (GS) for males (m) and females (f)

	Acc_m	Acc_f	Superiority male	Superiority female	Genetic gain / year
no GS					
GS					

Glossary

SD_{obj}	Standard deviation of the breeding objective. Derived from the distribution of your SheepGenetics index. This number does not change
CDE	Cumulative discounted expression. The discounted sum of the expression of a sires' genes across years and generations. The younger a sire is used the higher the CDEs. CDEs are higher in stud rams than commercial rams, because the stud rams genes are also expressed at a commercial level.
i	Selection intensity. This number relates directly to the proportion of individuals selected in a flock.
Acc	Accuracy. This can be specified for males (m) and females (f).
GS	Genomic selection (genomic information can be of high or low accuracy in this study (acc_high and acc_low)
GS_{acc_high}	Genomic selection with genomic information of high accuracy. High accuracy is what we will achieve around 2013. Low accuracy is a bit lower of what we currently achiev. The accuracy of genomic information depends on the number of animals in the reference population.
L	Generation interval. The average age of parents at the birth of their progeny. This can be specified for males (m) and females (f)

Appendix 21 – Conference paper AAABG 2011

THE VALUE OF GENOMIC SELECTION FOR STUD AND COMMERCIAL MERINO RAMS

S. Dominik[1], J.H.J. van der Werf[2] and R.G. Banks[3]

[1]CSIRO Livestock Industries, New England Highway, Armidale, NSW 2350
[2]School of Environmental and Rural Science, University of New England, Armidale, NSW 2351
[3]MLA, c/- Animal Science, University of New England, Armidale, NSW 2351

SUMMARY

The additional value that can be gained from selecting stud and commercial rams based on genomic information was evaluated for Merino studs using two different breeding objectives. Selection index theory and gene flow methodology were used to contrast the accuracies and selection responses of indexes using phenotype information only, with those using additional genomic information of either high or low accuracy and selecting males at one year of age. With the inclusion of genomic information and earlier selection index accuracies increased and an additional 11–64% in commercial dollar value per ram could be gained from genetic improvement. The breakeven point for DNA testing was evaluated to be between \$13.04 and \$64.48, depending on the breeding objective and the accuracy of the genomic information.

INTRODUCTION

Genomic selection is being implemented in dairy industries internationally (Loberg and Duerr 2009). Various factors have contributed to this success, including the hierarchically integrated structures of the industry, the high accuracy that can be achieved in genomic breeding values, the sex limitation of the economically important traits, and the high value of bulls. In the beef industries, the economic benefit to a stud breeder of using genomic selection has been evaluated as ranging between 20-41%, depending on the breeding objective (Van Eenennaam 2011). The implementation of genomic selection in the Merino and terminal sire industries has been estimated to increase response to selection by up to 40%, depending on the accuracy of the trait breeding values (van der Werf 2009), and it is now trialled with industry flocks (Ball pers. comm.).

In the sheep industry genetic improvement is generated by a large number of stud breeding operations (approximately 1,000 active studs across terminal, dual-purpose and Merino sectors), each dependent on their commercial clients' operations, and thus varying in management practices and breeding objectives making potential gains from genomic selection quite variable. The aim of this study is to evaluate the economic benefits of genomic selection at the level of individual breeding operations for a range of production system of the stud's clients. The additional economic value gained through the inclusion of genomic information in selection was evaluated for rams that were either used as stud replacements or for rams sold for commercial use.

MATERIALS AND METHODS

Structures of stud and commercial operations. Two Merino stud operations were modelled using two different breeding objectives, reflecting their commercial clients' production system. One stud uses a MerinoSelect Merino 14% (M14%) index (www.sheepgenetics.org.au). This index includes reproduction and yearling and adult wool and body weight traits, but places most selection emphasis on reduction of fibre diameter while keeping clean fleece weight constant. The commercial clients of this stud run self-replacing fine wool Merino flocks, keeping a proportion of wethers for two years for wool production before selling them.

The second stud uses the MerinoSelect Dual Purpose 7% (DP7%) index (www.sheepgenetics.org.au). DP7% includes reproduction traits, yearling fat and eye muscle depth and adult and yearling wool and body weight traits. It aims at small gains in clean fleece weight, moderate reduction in fibre diameter and high gains in body weight and reproduction. The commercial clients of this stud produce dual purpose Merino sheep. Wool is of medium fibre diameter and 40% of ewes are mated to terminal sires for prime lamb production. No wethers are kept for wool production.

Economic value. The economic value of selecting a ram for stud replacement or for commercial use was evaluated by calculating index accuracies with and without genomic information using selection index theory (Lande and Thompson, 1990) and the value of selection differential of rams to commercial progeny. Accuracies and resulting trait responses for the Merino studs were evaluated using only phenotype information in the selection index (no GS) and contrasted with the responses after additionally including genomic information (GS) in the index. Rams were selected at 18 months of age. The genomic information was either of high ($r^2_{high}=h^2$) or low accuracy ($r^2_{low}=0.25^* h^2$). The accuracy (r^2) reflects the proportion of genetic variance explained by genomic information for each individual trait and is dependent on the number of individuals with both genotypic and phenotypic records (Goddard, 2009). All rams weaned in the nucleus were genotyped. Trait heritabilities ranged from h^2 = 0.6 for fibre diameter to h^2 = 0.06 for number of lambs weaned. As yearlings, animals were measured for fibre diameter and the coefficient of variation of fibre diameter, clean fleece weight and body weight. For DP7%, yearling fat and eye muscle depth were also measured at the same time. Phenotypic and genetic parameters and economic weights for the breeding objectives, DP7% and M14%, were obtained from SheepGenetics. The value of using a genetically improved ram per unit of index superiority was calculated from the cumulative discounted expressions (CDE) using the gene flow method (Hill 1974). CDE sum the proportions of genes of a selected ram that are expressed in commercial progeny over age classes. An annual discount rate of 7% was assumed. The economic value of the genetic superiority of a stud replacement ram or a commercial ram was calculated by multiplying the index superiority ($i^* \sigma_{Index}$, with i = selection intensity and σ_{Index} = standard deviation of the index) of selected rams by the CDE and the number of life time progeny, as previously described by Van Eenennaam *et al.* (2011). The additional dollar value per DNA test was obtained by dividing the genetic improvement benefit (in \$) per ram from GS over no GS by the number of DNA tests conducted per ram sold or used within the stud. This figure provides an estimate for the breakeven point for the application of genomic selection in a Merino operation as modelled in this study. This study did not estimate cost per ram.

Table 1. Flock structure of Merino stud operation

	Stud parameters
Weaning rate (%)	100
Ewe replacement (%)	20%
Mortality % male / female	2 / 2
No of age classes male / female	5 / 2
No of animals genotyped	All nucleus weaned males
Rams sold for breeding per year (%)	20
Rams selected for breeding within stud (%)	4
Mating ratio (Ewes : Rams)	50:1
Cumulative discounted expressions stud / commercial	1.30 / 0.45
No of lifetime progeny per commercial ram	100

RESULTS & DISCUSSION

The selection accuracy of two year old males ($r_{SelMales}$) increased with increasing accuracy of the genomic information (Table 2). It ranged from $r_{SelMales}$ = 0.37 – 0.60 for M14% and from $r_{SelMales}$ = 0.40 – 0.53 for DP7%. The inclusion of highly accurate genomic information increased selection accuracies of two year old males by 64% for M14% and by 32% for DP7%. The selection accuracies for DP7% were overall lower, because the selection index is highly dominated by the number of lambs weaned, which is a lowly heritable trait.

Table 2. Standard deviation of the breeding objective (σ_A) and the selection index (σ_{Index}), and selection accuracies of two year old males ($r_{SelMales}$) achieved for two breeding objectives (M14% and DP7%) using family information only (no GS) or adding genomic information (GS) of varying accuracies (r_{low} and r_{high})

Breeding objective (σ_A in \$)*	Information for selection	$r_{SelMales}$	σ_{Index}
M14% (3.99)	no GS	0.37	1.47
	GS r_{low}	0.44	1.76
	GS r^2_{high}	0.60	2.41
DP7% (4.53)	no GS	0.40	1.82
	GS r^2_{low}	0.44	2.01
	GS r^2_{high}	0.53	2.40

The benefit of incorporating genomic information into the selection index could be observed in the additional commercial dollar value gained (Table 3). The added value ranged from 1–32% for DP7%, depending on the accuracy of the genomic information and from 11–64%, for M14% (Table 3). The resulting additional values in this study vary more widely than the predictions for a fine wool and meat sheep breeding objective calculated by van der Werf (2009), or for beef cattle, where the predicted added value from genomic selection ranged between 55-158% (van Eenennaam 2011).

Table 3. Value of genetic improvement per ram using a selection index with phenotypic information only (no GS) and with the inclusion of genomic information (GS) of varying accuracy (r_{low} and r_{high}) and the additional commercial dollar value gained per ram from including genomic information

		Value of genetic improvement (in $)			Additional $ value per ram*	
		No GS	GS r^2_{low}	GS r^2_{high}	r^2_{low}	r^2_{high}
Stud	M14%	2,058	2,464	3,374	406 (+20%)	1,316 (+64%)
	DP7%	2,548	2,814	3,360	266 (+11%)	812 (+32%)
Commercial	M14%	93	111	152	18 (+20%)	59 (+64%)
	DP7%	115	127	151	12 (+1%)	37 (+32%)

*percent of value of genetic improvement without GS in brackets

The breakeven point of the additional gain per DNA test from genomic selection ranged between $13.04 and $64.48, depending on the accuracy of the genomic information and the breeding objective of the stud (Table 4). For a beef cattle scenario, the breakeven point was higher, as can be expected, ranging between $143 - 258 (van Eenennaam 2011), mainly because the genetic variation in profit per head in beef cattle is higher than in sheep. In this study, the additional value per DNA test ranged between $4.16 and $11.84 for commercial rams and between $18.48 and $52.64 for stud rams, depending on the breeding objective and the accuracy of the genomic information. The additional value per DNA test was low with the inclusion of genomic information of low accuracy, but it was around three times as much when genomic information was of high accuracy. The values in this study provide conservative estimates, because it was assumed that all rams born were genotyped. An optimised genotyping strategy would reduce the numbers of animals tested and increase the additional value gained per DNA test. The value is also highly dependent on the proportion of stud born males sold as commercial rams and would also be influenced by the age at which animals are genotyped and subsequently selected, which was not varied in this study.

Table 4. Additional value per DNA test ($) gained from stud and commercial rams bred with M14% or DP7% breeding objective

		Additional $ per DNA test	
	Breeding objective	GS r^2_{low}	GS r^2_{high}
Stud	M14%	16.24	52.64
	DP7%	10.64	32.87
Commercial	M14%	3.65	11.84
	DP7%	2.40	7.31
Total Value	M14%	19.89	64.48
	DP7%	13.04	40.18

CONCLUSIONS

The breeding objective and the accuracy of genomic information strongly influence the additional economic benefit that can be gained from using genomic selection for stud and commercial Merino rams. The breakeven point of the additional benefit from genomic selection provides an estimate of potential maximum cost to an individual breeder for application in the Merino industry. It was low for genomic information of low accuracy. The additional benefit of using genomic technology could be increased by optimising the genotyping strategy. This study is an important step in developing cost-effective strategies for implementation of genomic testing at the stud level. Further work will be needed to account for optimisation of generation intervals, and to examine the impact of the degree to which prices paid for flock rams reflect their genetic merit.

ACKNOWLEDGEMENTS

This work was funded by Meat and Livestock Australia. The authors would like to thank Andrew Swan for his advice.

REFERENCES

Goddard, M. (2009) *Genetica* **136**: 245-257.
Hill, W.G. (1974) *Anim. Prod*. **18**: 117.
Lande, R. and Thompson, R. (1990) *Genetics* **124**: 743.
Loberg, A. and Duerr, J.W. (2009) *Interbull Bull*. **39**: 3
van der Werf, J.H.J. (2009) *Proc. Assoc. Advmt. Anim. Breed. Genet*. **18**: 38.
van Eenennaam, A.L., van der Werf, J.H.J. and Goddard, M.E. (2011) J. Anim. Sci. **89**: 307.

Appendix 22 Workshops

As part of the project two workshops were held for participating breeders.

The aims of the workshops were

1) provide an understanding on genomic technologies and how they work
2) provide an understanding on the economic benefits to the sheep industries in general
3) provide an understanding the benefits to each individual breeders
4) provide an understanding of the influencing factors of industries and individual benefits

Participants

The workshop targeted top breeders from the maternal, terminal and Merino industry sector. Workshop participants were invited by SheepGenetics and MLA. A wide range of ages were represented within the participants. The only female who participated in the case studies was unable to attend any of the workshops. Four breeders represented two studs (e.g. Poll Dorset and Border Leicester). Most breeders would have other sectors to their agricultural operation (e.g. Angus stud, cropping, pig production). The list of participating breeders can be found in appendix 1.

Workshop content

The agenda for workshops 1 and 2 are presented in appendices 18 and 19. Introductory presentations provided background on genomic technologies and more specifically on single nucleotide polymorphism (SNP) markers and their application in genetic evaluation. This was followed by an explanation on the methodology of the assessment of the case studies. All participating breeders received a report outlining the gains with and without the application of genomic technologies (example report shown in Appendix 20). Group work enabled breeders to discuss and share their results, followed by questions, clarifications and comments. Each workshop was wrapped up with a session to collect key learning and key messages (Table A1 – A3). After workshop 1, feedback was collected within industry groups (terminal, maternal, Merino, science). Several suggestions were made to improve the case studies. Within the scope of this project, the majority were implemented and case studies re-run for workshop 2. Key messages provide a comprehensive benchmark for the level of knowledge that participants had at the completion of workshops 1 and 2.

Table A1 Comments and key messages from breeders of workshop 1

	Comments and key messages
Merino breeders	• Assume that there is a gain, but there needs to be a good process to make these gains clear to the clients • Early identification of early fleece weight real benefit • Segregation of age groups • SNP chip – what is the package for Merino breeders can pedigree be included and what are the most valuable traits to Merino breeders • Most would have best accuracy that the proportion tested can be dropped, but data on ASBVs still needs to be there • Average per head tested about $25 • The relationship of doing a proportion of the ewes and see what the benefits, in particular in combination with reproductive technologies
Maternal	• Reports need to be more informative and include the input parameters and intermediate results • Generation intervals • Take account of age structure • Sensitivity analyses • Impact of the effect of testing various proportions • Collaboration within industry ideals (IMF) – information on how breeding values relate to consumer • Traditional selection / Early selection – some of the terminals/maternal mate early already as traditional selection
Terminal	• Most of the traits are covered with the phenotypic info. In the short term no benefit of GS, but in the long term e.g eating quality will be worthwhile • Sensitivity analyses – effect of management tools, maybe provide a tool that breeders can play around with • Play with proportions genotyped (include proportions of males and females) • Altering generation interval • Effect of using ram lambs only • Testing rams every year will have an effect – what is the compounding effect on that over several years • Break up of age groups – effect on the model • Genetic merit of AI sires to take into account (maybe better than your ram lambs and effect of that) • Pedigree in the SNP panel would add value, smaller chip • Comparison GS and phenotyping or GS only • Cost of test will drive testing regime • getting industry used to what is coming – great idea to create a prototype index

Table A2 Overall comments and key messages and science group feedback of workshop 1

	Comments and key messages
Science group	• With tools like SheepObject – we can design prototype indexes for the future (e.g. including eating quality) which can demonstrate some of the unkown benefits of genomic selection • We need to have a better metric around performance $ per ewe in stud or commercial sector, or $ per unit of genetic gain – you can work out what the total value to the industry is – unit can be index points or dollars or desired gains or standard deviation of index • How to deal with outside sires – model that looks at accuracy and selection intensity as an outcome – add to the report • How do we deal with accuracy – we need to check the model • decision support tools that helps to pin point the critical control points • Utilising inbreeding – statistic might become different when we work out the relationship between animals re-evaluated through genomics • Investment in INF – Metric that tells you the relationship of your sire to the INF data set • We need to include cost for management benefits
Overall feedback	• We need to get people thinking about the future traits – Merino breech wrinkle, GFW and micron also – great marketing tool that this much improvement can be made • We can fast track benefits for people because genomics is going to give us great benefits. Before the advantages for Merino were not clear. • Get a presentation as marketing tool if possible? • Useful to tie it back to the significance of the INF and the opportunity to calibrate. To get confidence from stud to commercial you get a consistent story and they need to know how the package has been derived, which needs to have the knowledge where these breeding values come from • Messages need to consider the time frames that they can deliver in • Take home message – all the things that genomics will give you are possible, but not yet (Mark Mortimer). It all still is in the development phase. • We are about to go into pilot phase 2 – breeders genotype a proportion of their flock, 10-15 young rams (6mo), 3 rams need to be used within that year as verification. Real life version about some of the questions that have come up about how many to genotype. • For the maternal traits some of the good accuracies are still missing to get the most out of genomics. But if animals can be picked young for reproduction – this is where the gain comes in. Reflection on this take home message: Future reference populations, leave males intact to get scrotal circumference. The $uperBorder information on these traits can feed into the reference population (which means that all rams need to be genotyped). • The main messages are not just about our case studies, but it is all about the benefit to the industry, which is obvious in the discussions. Participants should think about their preparedness to make their case study information public • Main questions how to optimise phenotyping and genotyping. Answer there are some specific questions and some general questions.

Table A3 Key messages from participants of workshop 2.

Issue	Key messages
Benefit of genetic gain from genomic technologies to the stud breeder	The numbers presented a useful guideline, but there are other benefits that have not been taken into account • Reputation of a stud • Getting more rams above average index for sale • Not carrying all culls; management benefits • Pedigree test • Minimisation of risk (more accurate selection) • Product development; e.g. currently eating quality traits don't actually have $ benefit • Process of genomic information is set up and it is easy to add traits of interest • Increased confidence in ram purchases to clients
R&D questions	• Application of genotyping: proportions and which animals to genotype • What if the sheep industries move to a structure like dairy? Does the sheep industry need a change in structure to get the maximum benefit out of genomic selection? • Modelling if it is economically justified to measure feed efficiency in the INF • Genomics of feed efficiency, pigmentation, foot rot, genetic defects, e.g. HypoTrichosis in White Suffolk, undershot jaws, etc.
How to distribute the results from R&D	• Once road tested the technology will run itself • A sales strategy is required for breeders clients
Other comments	• Greatest return for investment in Merinos – problem that funding bodies are not prepared to spend money to get the most out of the biggest opportunity • The advantage of genomics in Merinos needs to be highlighted in their role in the crossbred lamb industry • Run model on using hogget rams in the terminal sector • Spreadsheet that let breeders play with options

Subjective overall assessment of the workshops

The workshops provided a good platform to use the “champion-approach”. By targeting top representatives of the various industry sectors, a flow of information from these champions to their clients and other breeders can be expected in the future. The participating breeders were well chosen to enhance the learning outcomes of the workshop settings. Prior knowledge, attitude to risk and uptake of the information differed, which generated constructive discussions about the information presented and how it links in with individual stud operations and industry. The case studies provided material that participants could relate to. It is unlikely that breeders will try to reconstruct the numbers presented in the reports, but working through it in a focussed manner during the workshop, helped to outline the important factors on-farm that influence the benefit of genomic technologies. However, participants suggested the development of a tool (e.g. excel spreadsheet) that links the various on-farm factors and allows exploration of their relationships. Overall, participants’ feedback appeared positive.

Recommendations

The case studies have highlighted a range of areas that would add to the knowledge of how much on-farm benefit can be gained from genomic technologies in the maternal, terminal and Merino sectors of the sheep industries.

- Development of an on-farm tool to explore the benefits of genomic technologies
- Optimisation of on-farm characteristics to gain most benefit from genomic technologies
- Optimisation of phenotyping and genotyping
- Investigate if the structure of the sheep industries have to change (e.g. hierarchical concept of the current dairy industries) to get the most benefit out of genomic technologies
- Explore other indicators of benefit of genomic technologies than used in this study (i.e. genetic gain per year and break-even point)
- Have an annual update on the developments in the area of genomics and messages from current research to industry

Bibliography

Dominik, S., van der Werf, J.H.J. and Banks, R. (2011) Proc. Assoc. Advmt. Anim. Breed. Genet. **19**: 323.
Hill, W.G. (1974) *Anim. Prod*. **18**: 117.
Lande, R. and Thompson, R. (1990) *Genetics* **124**: 743.
van der Werf, J.H.J. (2009) *Proc. Assoc. Advmt. Anim. Breed. Genet*. **18**: 38.