

CHALLENGES AND OPPORTUNITES FOR GENETIC IMPROVEMENT IN THE MERINO INDUSTRY

T.M. Fischer¹ and R.G. Banks²

¹Australian Wool Innovation Limited, 16-20 Barrack St, Sydney, NSW, 2000

²Meat and Livestock Australia, 165 Walker St, North Sydney, NSW, 2060

SUMMARY

Significant scope exists to increase the rate of genetic gain in the Merino industry. This paper discusses some of the reasons behind the rates of improvement being achieved as well as barriers to uptake of across-flock evaluation as a flock improvement technology. The paper will also discuss the significant opportunities that emerging technology may contribute to enhancing rates of gain as well as potential changes to breeding structures within industry.

INTRODUCTION

Sheep genetic evaluation systems in Australia have been very effective at generating genetic gain in flocks engaged in across flock benchmarking (Banks 2005, Kemper and Casey 2006) at rates sufficient to at least maintain pace with the cost-price squeeze present in Australian agriculture. Notwithstanding this, levels of genetic gain in Merinos could be higher than what has been achieved across stud flocks in industry (Banks, 2005). The variation in the level of genetic improvement across flocks is of equal concern, as it reduces the opportunity for improvement in commercial flocks and hence return on the investment in research, development and extension. Whilst certain individual flocks may be achieving close to what is theoretically possible, many flocks are still achieving gains well below their potential and many (up to 80%) are not even engaged in across flock benchmarking.

POTENTIAL RATE OF GENETIC GAIN

Kemper and Casey (2006) demonstrated that significant genetic progress has been achieved in the Merino breed over the past 25 years. Sheep Genetics Australia (SGA) estimates indicate the rate of gain in MERINOSELECT flocks is around 0.15 index standard deviations per year (R Apps pers. comm.), while Banks (2005) suggested that the leading flocks are improving at four times that rate of gain. Supporting this, comparing current progress in key Merino Traits (greasy fleece weight, fibre diameter) to the work of Atkins (1987) indicates that current rates of progress are around half of the possible rate. This suggests that there is considerable scope for improvement in the rate of genetic gain when considering the parameters that contribute to selection response within Merino flocks. For example:

- Heritability of the wool traits are moderate (e.g. staple strength 0.3) to high (e.g. fibre diameter 0.6)
- Selection intensity is high given flock sizes and use of artificial breeding is wide spread
- High levels of variation exists for most traits

However, there are a number of other factors embedded within the Merino industry which contribute to current rates of genetic gain:

Adoption

- Higher generation interval in Merinos than other sheep breeds as many traits under selection are not expressed until adult ages as well as the use of progeny testing (participation in sire evaluation or on-farm) before extensively using a sire
- Lack of pedigree in Merino flocks in SGA due to cost and difficulty of collection
- Selection emphasis on traits that are currently not objectively measured which ultimately limits the selection intensity
- Reduced measurement of objective traits due to cost of collection (e.g. staple strength)
- Belief in the industry that there is significant GxE interaction that limits effective selection

Furthermore, there are factors other than those affecting the selection response equation that impact rates of genetic improvement that warrant discussion. For example, the wool industry has a relatively long supply chain when compared to other agricultural industries. This has led to limited and often confusing data resulting in poorly informed industry direction and slower response when there is a change in the market, and as a result genetic selection is compromised. In addition, numerous factors contribute to wool value (at least 6 objective, 2 subjective) further complicating which direction to head.

There are also a series of factors considered as barriers to uptake of across-flock genetic benchmarking. These include:

- Handling large volumes of data for many traits (up to 33 at present) on large flocks as well as cost of collection for sufficient data quality
- Lower use of outside genetics compared to other breeds due to GxE concerns, use of specific types or bloodlines and other beliefs on breeding (Kaine *et al*, 2006)

FEASIBILITY AND COST OF ASSESSING GENETIC VARIATION

As mentioned, the cost and difficulty of collection of phenotypes and pedigrees is an impediment to uptake of across flock genetic evaluation in the Merino industry, as well as the rate of genetic improvement. This is likely to become an increasing issue in the future given many traits are either labour intensive (hence limited by labour cost and availability), expensive (e.g. staple strength) or difficult to measure (e.g. worm egg count). In MERINOSELECT there are Australian Sheep Breeding Values (ASBVs) for wool, growth, carcase, internal parasite resistance and reproduction traits at the various different age stages (33 traits). Uptake of measurement for each trait group in Table 1 is variable and likely to be a function of cost, difficulty and overall importance in the breeding objective. It is estimated that it costs up to \$40 per animal to collect a full suite of measurements, however the cost of measurement for most animals in the MERINOSELECT database is \$15-20 as very few animals are measured for all traits (R Apps, pers. comm.). There is also interest from industry for additional traits such as visual wool quality, conformation and breech traits to be added which could equate to 25 extra traits. If the list expands or if the labour shortage worsens, trait measurement will become more expensive and more difficult. Given this, perhaps consideration needs to be given to strategies for optimal measurement of traits at the farm level, potentially with individual studs having nucleus and multiplier sectors with different levels of measurement embedded.

If we consider the proportion of genetic variation explained and accuracy of that information relative to cost, Table 2 illustrates cost and accuracy of genetic information obtained from conventional methods. Comparing this with genotypic information which is currently available for sheep through testing, the cost for an individual test is around \$20 per animal and the genetic variation explained is around 10% for a given trait. In the future, it is anticipated that high density genotype information will explain a large proportion of variation for many traits with the same accuracy of breeding values based on own performance records (60%) or perhaps even progeny test accuracy (>80%). Comparing the cost relative to variation explained and accuracy, currently the most cost effective way of assessing genetic variation is through conventional means (phenotypes). In the future it is likely that SNP based technology will explain more variation with higher accuracy, however cost will be a critical factor determining uptake.

Table 1 – Traits and proportion of animals measured in MERINOSELECT

Information Source	Variable	Wool	Growth	Carcase	Parasites	Repro	Total
Conventional phenotypes and measurement	Proportion of animals measured	>90%	>75%	15%	10%	10%	
	Number of traits	7	1	2	1	3	33
	Number of ages	3	4	1	3	1	

Table 2 – Cost per head, genetic variation explained and accuracy of breeding values based on phenotypic information.

Information Source	Variable	Wool	Growth and Carcase	Parasites	Repro	Pedigree	Labour	Total
Conventional phenotypes and measurement	Cost/head	\$10	\$5	\$5	\$5	\$5	\$10	\$40
	Variation Explained	100%	100%	100%	100%			100%
	Accuracy*	70%	60%	50%	40%	~90%		~60%

*Accuracy estimate based on an animals with own performance records only

OPPORTUNITIES FOR THE MERINO INDUSTRY THROUGH EMERGENCE OF NEW TECHNOLOGY – A PARADIGM SHIFT?

With the highly anticipated emergence and application of SNP chip technology in the beef (Hayes *et al.*, 2006) and dairy (Tier *et al.*, 2007) industries, work is underway to generate a similar tool for R&D in sheep (Maddox *et al.*, 2006) and subsequently apply whole genome selection in industry flocks. Tier *et al.* (2007) demonstrated the ability of SNP technology coupled with the appropriate algorithm to produce breeding values with 80% accuracy on dairy bulls with no phenotypic or progeny information. As with any DNA based technology, the testing can be done at birth, hence significant gains are possible in terms of generation interval as well as improved accuracy. Based on this potential alone, it is predicted that whole genome selection will be the next major technology

Adoption

advance in animal breeding since across flock BLUP evaluation was implemented. The other advantage is that the traits that can be incorporated into such a chip are limited only by the data available, hence selection for traits that have not been possible up until now could become routine provided that there are reliable sources of the appropriate “calibration” data. Validation of such a technology in the sheep industry is to be conducted in the Sheep CRC Information Nucleus Flocks.

Given the potential for increased gain, it is likely that those breeders that adopt the technology fastest and are able to make effective use of it will be in an advantageous position. It is also possible that such technology will change industry breeding structures, for example, large commercial operations could collect blood for SNP analysis and calculation of breeding values on their animals without the extensive measurement protocols that are required in stud breeding today. However, it is unlikely that SNP technology will obviate the need for measurement altogether. It is anticipated that there will be an optimal investment at the industry and individual breeder level for core and hard to measure traits. In turn, this may drive rationalisation and separation of businesses based on their ability to manage intensive recording and allow them to differentiate themselves. It is possible we may see two levels emerge; “nucleus” studs with heavy recording and use of SNP chips, and “multiplier” studs with very limited on-farm recording and pedigree and use of lower density chips.

Furthermore, if the ratio of genotyping relative to cost increases in a similar manner to that which has been witnessed in human genomics and analogous to increases in computing power in the IT industry, then it is predicted that the volume of information generated (genotypes) will double every few years with no real change in cost. Acknowledging the time lag between generation of enhanced tools that provide additional information and the application of that to industry, the real challenge will lie in the analysis, interpretation and explanation of the data to industry.

CONCLUSION

The scope for improvement in the rate of genetic gain in the Merino breed is considerable. The potential benefits for Merino flocks from emerging SNP technology is greater than in other sheep breeds because of the greater potential to reduce generation interval (time lag due to progeny testing), reduce cost (from progeny testing and recording in large flocks) and improve accuracy of genetic information. It is possible that breeding structures will rationalise as a result of the increased difficulty and cost of recording and SNP based tools that will enable nucleus flocks to become smaller with more accurately characterised animals. Given these potential changes, industry will need appropriate guidance on which animals to phenotype and genotype in order to get the most value out of measurement and return on investment in genetics and genomics research and development.

REFERENCES

- Atkins, K.D. (1987) In: “Merino Improvement Programs in Australia”, editor B.J. McGuirk. Australian Wool Corporation, Melbourne, 1987. 1987:299
- Banks, R.G. (2005) *AAABG* **16**: 372
- Hayes, B.J., Chamberlain, A.J., Goddard, M.E. (2006) *Proc. 8th WCGALP*, 30-06.
- Kaine G., Lineham C., Rowbottom, B., (2006) “Sheep Breeding & Sire Selection”, AWI, 115 pp.
- Kemper K., Casey A. (2006), World Merino Conference Publication, 6 pp.
- Maddox, J.F., Dalrymple, B.P. McWilliam, S.M., McCulloch, A., Kirkness, E.F., Townley, D., Barris, W.C., Kijas, J.W., Ratnakumar, A. (2006) 30th ISAG
- Tier B., Crump R., Moser G., Solkner J., Thomson P.C., Woolaston A., Raadsma H.W. (2007) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **17**: 308.