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Application of Genomics to Breeding

M. J. Long

"Pendarra" White Suffolk Stud, ARDLETHAN N.S.W 2665

mdlong@bluemaxx.com.au

Introduction

The Australian sheep industry has undergone some significant changes in the past few decades. Many factors have brought about a dramatic fluctuation in sheep numbers from a peak of 170 million during the 1980's to the current level of around 75 million (Barker 2013). Droughts, fluctuating prices, the influence of technology in competing enterprises and a generational shift in attitudes toward rural expectations have all impacted the current sheep industry. In addition to the huge variation in sheep numbers, the genetic composition of the population has changed from a predominately Merino maternal base with 2-3 main breeds used for cross breeding, to the current population which contains a significant mix of diverse genetics specifically suited to a much wider range of commercial preferences. The development of composite genetics for specific environments or markets has allowed commercial producers to tailor genetics for their specific requirements.

Perhaps the most significant development in the Australian sheep industry has been the development of a comprehensive performance recording system, Lambplan and MerinoSelect, under the management of Sheep Genetics Australia (SGA) that has replaced the time honoured system of visual classing and assessment. Historically, genetic gain has been slow and inconsistent with some momentous "breeding fads" actually stalling or reversing genetic gain for several generations. A performance recording system that independently evaluates measurable traits producing Australian Sheep Breeding Values (ASBV's) has allowed for the consistent and rapid improvement across a range of commercially relevant traits that has been independently proven to increase profits across all breeds (Ramsay 2012).

The past 5-6 years has seen this advantage taken to the next level with the Sheep CRC using single nucleotide polymorphism (SNP) chip technology to identify DNA marker information and generating genomic breeding values that supplement ASBV's for traits that have been historically been measured and has made possible selection for a range of traits that are hard to measure or cannot be measured on a live animal. The immediate advantages of DNA testing young animals is obvious but the identification of commercially advantageous traits alone will not improve genetic gain; it is the deliberate application of this technology into breeding programs that allows for accelerated and reliable genetic gain.

Genomics for easy to measure traits

The use of ASBV's allows for the prediction of the genetic merit of animals based on a range of phenotypic measurements adjusted for external influences and estimations based on pedigree and linkages between relatives and across different breeding enterprises. Seedstock producers use this information to tailor their genetics with an emphasis on the commercially relevant core traits relating to carcase (Growth, Fat, Muscle), wool (Fleece Wt, Micron) and fertility traits. This has resulted in excellent genetic gain in the Australian sheep industry and allowed for confident selection of superior genetics based on accurate, independent analysis of large amounts of data across all breeds and environments. The more data collected and analysed, the more accurate the ASBV's on individual animals.

Inclusion of genomic breeding values, currently referred to as Research Breeding Values (RBV's), into this analysis increases the accuracy of the performance values, therefore increasing the confidence in selection of high performance individuals. It is the early measurement of these core traits that provides the greatest advantage. DNA analysis at an early age also allows for the prediction of lifetime performance across a number of commercial traits that would otherwise have taken years to collect and analyse therefore allowing more confident earlier use of these genetics in breeding programs than would have been the case if relying on phenotypic measurements alone. Earlier use of genetics and

faster genetic turnover delivers faster genetic gain. While the advantage gained for the core traits is minimal in Terminal genetics due to the current widespread use of young genetics and accurate ASBV's, it is the lifetime wool predictions in the Merino that will benefit most from DNA testing producing values for wool traits that may have taken 2-3 years to physically collect. The identification of the poll/horn gene marker is one test that is already being adopted in the Merino industry. One of the defining advantages of genomics is that, not only is it possible to gain early information on phenotypic traits that may take many years to physically measure, but we can also determine the impact of specific traits that contribute to lifetime profitability.

Genomics for hard to measure traits

Phenotypic traits that are easily measured have long been the focus of almost every structured breeding program. There are several traits that are hard to measure or almost impossible to physically measure on live animals and the use of DNA analysis has enabled breeders to confidently select for these traits. Predominately these traits relate to meat eating quality (Shear Force Tenderness, Intra Muscular Fat and Lean Meat yield), parasite resistance (Worm Egg Count), meat nutrition (Omega -3, iron, zinc), taste and shelf life properties, lifetime wool production traits (Adult Fleece Weight, Fibre Diameter, Staple Strength) and fertility (Number of Lambs Weaned). These traits, while some may not have obvious direct commercial impact to sheep producers, are vitally important to the processor, retailer and consumer. The consideration of these hard to measure traits into a breeding program is made possible through the generation of RBV's, based on significant research and the identification of DNA markers as part of the Sheep CRC program. The integration of RBV's into a sheep breeding program allows, not only consideration for phenotypic traits that are economically important to sheep producers, but consideration for those who handle and utilise the product after the raw product is sold off farm. This ultimately has significant impacts on the acceptability and market growth of the superior product and confidence to purchase the product in the commercial marketplace.

What Genomics means to the Industry

Clear advantages of utilising genomics for core traits alone are greater accuracy, earlier selection for superior animals and increased selection pressure which collectively results in faster genetic gain. Work in the dairy industry has shown genetic gain using genomics in a breeding program to be double that of traditional breeding systems (Scheffers 2012, Hayes 2009) and can result in profits more than twice that from non genomic based programs (Taubert 2011). Gains of this magnitude may not be achievable in the sheep industry as Lambplan/MerinoSelect is already achieving reasonable genetic gain but genomics will enable additional gains across a much wider range of traits to be realised. Screening for traits using DNA analysis on very young animals and the subsequent generation of RBV's will allow for all aspects of both phenotypic traits and hard to measure traits to be incorporated into a structured, multi-focused breeding program. While this provides benefit in traditional natural breeding programs, the use of artificial breeding techniques such as ET or JIVET/MOET will provide breeders with the confidence and means to quickly multiply superior genes resulting in significantly faster genetic gain and the accelerated spread of these superior genes throughout the sheep industry. Who ultimately benefits? Everyone within the Australian sheep industry from commercial sheep producers, right through to consumers.

The use of genomics adds to the accuracy and therefore confidence in any breeding program. What was historically a hit and miss approach to selection is now, with genomics, a measured calculation of all variables to achieve desired outcomes resulting in shorter intervals for adoption of superior traits and greater economic gain. Traditionally, relatively small selections of superior individuals were identified and test mated to evaluate the probability of producing superior progeny. The genetic worth of sires was primarily assessed using progeny testing and the result, good or indifferent, may have taken several years to determine. With the use of genomics, a much larger population of individuals can be screened and assessed at a significantly earlier age for superior genes without the guesswork of either visual selection or decisions made with limited information. While DNA screening would predominately be limited to screening of potential young sires, the obvious potential to also screen selections from the ewe flock and use targeted ET or JIVET programs becomes evident. The impact within a breeding operation of ewe genetics is limited due the smaller numbers of progeny produced;

to be able to enhance the influence of the maternal component within a breeding program only adds to the potential gains genomics offers.

One of the major constraints of any breeding program is the existence of correlations that can impede the progression of specific objectives within a breeding program. These correlations exist in all breeds but are especially important in the wool industry where many negative correlations exist between carcass traits, fertility and wool characteristics. However, within any population there are individuals that break the trend and the use of genomics allows seedstock producers to quickly and confidently identify individuals that break targeted correlations and allows breeding toward a multi-focussed breeding objective without sacrificing one trait against the other. Traditionally, these “curve benders” are the main reason why genetic gain has experienced phases of above average acceleration and identifying them was more good luck than good management. Identifying them earlier using genomic testing will only further accelerate the gains made through targeted selection for more than one trait.

Identification and consideration of correlations in a breeding program is vital to achieving specific breeding objectives. Without genomics this is predominately guesswork and to concentrate breeding aims on more than just a few traits would often lead to limited or no progression in the breeding program. The greatest benefit of genomics in this situation is the early identification of a range of selected and varied traits on live animals allowing for the selection of individual animals that have the right mix of traits all heading toward a targeted breeding objective. Genomics offers the unique opportunity to concentrate selection pressure on a specific trait and at the same time regulate the influence of negatively correlated traits to ensure genetic gain is not compromised. Genomic selection should not result in a major change of breeding goals but it will add another level of selection on which to make sire selections and consequently should improve the outcomes of selection decisions.

Genomics offers the opportunity to not only improve production traits but facilitates the development of product differentiation based on RBV's. The development of a niche market or branded product requires some strict assurances to maintain quality and consistency. Genomics offers a means to benchmark product excellence whether it is meat eating quality or wool quality that is being marketed. The development of benchmarks based on genomic RBV's are able to be independently applied across the whole industry and provide confidence to producers and consumers that whatever is claimed within the product description has been accurately verified through DNA testing. Genomic benchmarks for meat eating quality in Australia are a real possibility within a very short time frame and the same could be developed for a whole range of traits identifiable through the use of genomics.

The development of genomics and the subsequent collection and storage of DNA will become a significant asset for all livestock industries. As breeding lines become closer due to the extensive use of superior animals to multiply favourable genes, so too does the risk of proliferation of harmful or mutant genes. The existence of a data base of collected DNA will assist industry to identify and control the expression of these faults in the sheep industry thus alleviating the need to develop a new procedure for investigating the gene/s responsible. While research is currently looking at specific genes in relation to current priorities within the Australian sheep industry, the future will more than likely raise new issues and the existence of a substantial DNA collection will enable historical investigation of any new trait that may become relevant.

Management Advantages using Genomics

Constant collection of data to obtain ASBV's is time consuming and always has a human element that can result in inaccuracies with data collection. While some degree of phenotypic measurement needs to be maintained to retain the relevance and accuracy of RBV's, there is the opportunity to either reduce or temporarily cease phenotypic measurements and rely primarily on genomics to evaluate potential high performance individuals. This could be appropriate in a drought season where the genetic potential of a group of animals is not able to be achieved and rather than be cautious about selections based on animals that have not reached their potential, the use of genomics will provide

confidence in the selection of superior animals, regardless of the effect of a tough season. Genomics would also assist where decisions have to be made to reduce flock numbers due to a range of circumstances enabling the higher performing individuals to be retained based purely on genomic predictions. The requirement to retain all animals to gain a full complement of phenotypic measurements is avoided allowing management to better deal with situations where flock structure and size may require some hard decisions to be made.

Identification of superior individuals or selection pressure has traditionally been achieved by an initial selection of a significant number of potential candidates and the preferential feeding and constant evaluation over an extended period of time of these individuals which has an associated higher cost of both inputs and management. Genomics offers the cost advantage of significantly reducing the number of potential young high performance sires that need to be set aside and evaluated, therefore reducing both feed and time inputs into the management of the next generation of sires. This results in the same high selection pressure but with a reduced impact on management. Young sires can be assessed using genomics, incorporated into joining programs and have progeny on the ground well before traditional means of evaluation would have provided enough information and confidence to use these sires.

Genomics allows for some significant changes in the manner by which we manage our stud flocks. Rather than attempting to fit genomics into current management practices, we now have the opportunity to structure flock management around genomics. The use of genomics goes beyond identification of production traits, but also provides animal identification and parentage which has vast implications for time management and efficiencies on property. The use of syndicate joining has always had the weakness relating to the absence of reliable pedigree information. While an ideal process in which to test a selection of ram lambs, the inability to accurately determine pedigree or the complete loss of the pedigree of progeny negated any advantages gained. Single sire joining while ensuring reliable pedigree information is a relatively inefficient use of resources and has the potential to result in lower conception rates or complete failure. Genomics not only allows early selection of potential young sires, but the subsequent accurate progeny matching to these sires. It allows the development of more appropriate breeding programs that are easier to manage, have superior economies of scale and provide elevated rates of genetic gain. The use of genomics results in more efficient use of inputs and higher gains through better use of all resources on property.

Practical Application of Genomics: A Case study

TRADITIONAL SELECTION

Potential sires are selected from a select group of sires that have been fully performance tested to provide accurate performance figures and are joined to groups of ewes selected from computer modelling with the objective of breeding to a mid parent value accounting for the performance figures of the ewe. Consideration of commercially relevant traits is restricted to what can actually be measured or obtained from correlations. For a January/February joining, all the information on young sires is not usually completed when the decisions on which sires to use have to be made so predominately hogget sires are preferred.

All mating groups are to a single sire to ensure accurate pedigree and backup rams in any AI program are preferably single sire. If ram lambs are to be used, they are also single sire joined but the problem of potentially very low conceptions is always a concern, especially involving ewe lambs which potentially provide the greatest genetic gain. The property is not set up with enough smaller joining paddocks and this can compound the problem of single sire mating. The process of joining in single sire mating groups requires numerous secure paddocks, preferably not too large, and intensive management of these groups to ensure that all ewes are joined successfully and the ram is actually working. Lambing involves tagging three times a day and recording of data associated with lambing to ensure accurate pedigree, but at best it is still not one hundred percent accurate as some ewes will walk off with another ewe's lambs. The collection of all relevant data at lambing is crucial to ensuring the performance values attained are accurate and meaningful.

A typical data set required to gain ASBV's on a specific sire is as follows:

Stud ewe 075718 gives birth to a set of twins on the 16th June 2011. We know that she was joined on the 17th January to sire 075630 as part of a synchronised joining program. The birth was unassisted and the other twin survived and was reared as a twin. The birth weight of the ram twin (Tagged 119194) was 5.7 kg and the ewe twin was 5.0 kg. A weaning weight of 54.2 kg was recorded on the 24th October and a subsequent weight and scan measurement on the 23rd March recorded a weight of 60.5 kg with 3.5 mm of fat and a muscle depth of 36 mm.

All this information is submitted to SGA, analysed through the Lambplan data base and information returned by the end of March 2012 as listed in Table 1, nine months after the birth of the sire. Previous to this final detailed information, all ASBV's were based on weight measurements alone, the influence of pedigree and various correlations relating to phenotypic measurements collected.

Table 1. Typical reporting of ASBV results on an individual animal from Lambplan

Pendarra 119194

| Breeding and index values Analysis TERMINAL 15/04/2013 | | | | | | | |
|--|------|------|------|-------|-----------|--------|----------|
| Pendarra | Bwt | Mwwt | Wwt | Pwwt | Pfat | Pemd | SRC |
| 2303242011119194 | 0.07 | 2.61 | 7.33 | 12.25 | -0.02 | 1.64 | 130.7 |
| Sex 1 | | | | | | | Lamb2020 |
| Dob 16/06/2011 | | | | | Carcase + | 178.76 | 110.6 |

GENOMIC SELECTION

A group of potential young sires is selected from a large group using DNA testing in combination with breeding values for not only core traits but also hard to measure traits. Joining is not restricted to single sire mating due to the access of reliable parentage matching using genomics. This not only provides more accurate parentage but more efficient use of resources. Syndicate joining (more than one sire per ewe group) can be used to enable more efficient use of large paddocks, especially important to ensure good conception outcomes with ram lambs over ewe lambs and invaluable when the property is limiting in resources such as feed or water in a particular season.

Currently to gain a set of performance values on a sire using genomics, the same amount of phenotypic data is collected plus a blood sample is taken at weaning to provide all the information detailed in Figure 1 with better accuracies for the core traits and information on traits that are hard to measure. Information can also be gained on traits such as worm resistance which cannot be measured physically on the property due to low worm burden in a dry environment.

The advantage is that larger number of potential sires is able to be blood tested to ensure all potential candidates are fully evaluated for a range of traits exceeding what is traditionally available through phenotypic data collection. The blood cards are returned through SGA for analysis and the information is then available to be used by the end of November, five months after the birth of the lamb, therefore enabling genuine consideration for the use ram lambs for a January/February joining program.

The information required also allows for consideration of a whole new range of traits previously not possible with just phenotypic analysis and allows management decisions based on more accurate analysis of the complete genetic composition of the individual from genomic information combined with the actual measured performance of the animal. The influence of meat eating quality RBV's is a significant consideration in our breeding objectives and genomics allows a balanced approach to achieving breeding objectives.

SHEEP GENETICS

Research Breeding Values



PENDARRA

230324-2011-119194

Analysis type: TERM (15-Apr-13)

Project category: Pilot 3

| Trait Name | RBV | Acc | Avg | Trait Name | RBV | Acc | Avg |
|------------|-------|-----|-------|------------|-------|-----|-------|
| bwt | 0.1 | 86 | 0.3 | wwt | 7.5 | 89 | 8.3 |
| pwt | 12.4 | 71 | 12.9 | pemd | 1.8 | 74 | 1.4 |
| pfat | -0.3 | 71 | -0.6 | pfec | 33.7 | 30 | -2.9 |
| hcwt | 0.0 | 49 | 0.2 | cemd | -0.1 | 45 | 0.2 |
| cfat | 0.7 | 43 | -0.1 | imf | 0.9 | 48 | -0.0 |
| shearF5 | -2.8 | 44 | 0.1 | lmy | -1.2 | 45 | 0.1 |
| dress % | -0.0 | 47 | 0.0 | SRC \$ | 129.9 | 49 | 131.8 |
| Carcase+ | 181.9 | 68 | 182.2 | Lamb2020 | 109.7 | 55 | 111.2 |
| PollHorn | PP | | | | | | |

Figure 1. Research breeding values as a result of genomic testing

Collection of DNA has the potential to replace all phenotypic measurements with Genomics information alone. While this is a decision that will be up to individual breeders and we will continue recording all phenotypic measurements, it does provide an ideal opportunity during a tough season to make selections very early on which animals to retain rather than feeding the entire lamb drop through to obtain a complete set of meaningful phenotypic data resulting in huge savings on feed costs. In a situation where feed conditions have prevented the full genetic expression of traits, or lambs are being moved to a separate property, genomic testing provides additional confidence in selection of potential young sires that do not have the full complement of phenotypic measurements recorded. All these opportunities for better management and cost savings are possible through the well thought-out use of genomics in a breeding enterprise.

Conclusion

Genomics is the “Satellite Navigation System” for the Australian Sheep industry that will allow breeders to more accurately develop a genetic blueprint for achieving targeted outcomes and at the same time increase rates of genetic gain. It will allow breeders to navigate around issues that have previously been virtually impossible to resolve and provide new opportunities for future breeding programs and the development of new products.

Genomics also offers the opportunity to adjust flock management to increase efficiencies of both inputs and time. The overall contribution of genomics to industry is more consistent and accelerated genetic gain resulting in higher returns to producers and more consumer confidence in the products that the Australian sheep industry through its producers is marketing.

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