

GENOMIC SELECTION AND THE SHEEP COOPERATIVE RESEARCH CENTRE (CRC) NUCLEUS FLOCK

J.H.J. van der Werf

Co-operative Research Centre for Sheep Industry Innovation, Homestead Building, UNE, Armidale
NSW 2351

School Environmental & Rural Science, University of New England, Armidale NSW 2351

SUMMARY

Genomic selection is a new DNA based method of selecting animals for breeding. The test reveals DNA differences between animals for thousands of genetic markers. Prediction of an animal's genetic merit is based on DNA comparison with a group of reference animals with trait measurements as well as a DNA profile. A sustainable use of genomic selection by sheep breeders requires cheap genotyping combined with reliable predictions. A reference group of at least 2000 animals is needed. This is hard to achieve for smaller breeds, but feasible with some coordinated planning. For a dual purpose breeding objective that focuses on improvement of wool and meat we expect genomic selection can increase the annual rate of genetic gain by ~15%.

INTRODUCTION

Animal breeding research in the last decade has been dominated by the potential of genomic selection. Genomic selection refers to the selection of animals based on information obtained from a DNA test, also known as a genomic test. The DNA test provides information about pedigree and breed content, information about single gene traits such as horned-polledness and genetic defects and the test allows prediction of genetic merit for traits of economic importance. Genomic selection is not a silver bullet but an additional tool in breeding programs. The accuracy of genomic prediction in Australian sheep is currently comparable with the information obtained from a measurement on the animal itself or from a few progeny. The advantage of a genomic test is that the information is available early in life and even for traits that are hard to measure on-farm. Therefore, genomic selection can help achieve higher rates of genetic improvement, especially for traits that are otherwise hard to improve, e.g. reproductive rate, lifetime wool productivity and lamb carcass and eating quality.

Genomic testing has developed rapidly since the introduction of the first SNP-chip around 2006. Especially dairy breeding programs have completely changed. This is because the benefit is largest for dairy breeding as milk production cannot be measured on bulls and for sire selection a genomic test at a young age is an attractive alternative to a progeny test. A shorter generation interval along with abandoning progeny testing allows almost a doubling of the rate of genetic gain while the breeding program costs can be reduced. In sheep the benefit is smaller because 1) most traits in sheep can be measured on all animals and early in life, 2) the accuracy of the genomic test is lower because there is less information available due to smaller reference groups and 3) the profit per sheep is a lot lower than the profit per dairy cow so it is harder to justify investment in a genomic test for individual sheep. However, there are also significant benefits for sheep breeders.

This paper reviews the various aspects of implementing genomic selection in sheep breeding programs, including an estimate of the increased rates of genetic gain, the size and structure of reference populations that are needed, and the costs and benefits for individual breeders that invest in

genotyping and additional trait measurement. Currently, genomic testing is not available for the Dohne breed in Australia and this paper maps out a route to overcome the hurdles that prevent that.

What is genomic selection? Genomic testing involves collection of DNA samples on young breeding animals, usually via a drop of blood on a small card. These samples are sent for genotyping and based on information from tens of thousands of DNA markers (single nucleotide polymorphisms - SNPs) an estimate can be made of the breeding value, by comparing the DNA information on the tested animal with that of a reference population of animals that have information on DNA as well as phenotypes. The comparisons of DNA patterns can be seen as making comparisons with related individuals, similar to pedigree relationships. Animals related to those with a high phenotypic performance are expected to have a higher genetic merit. But rather than having just a handful or known relatives, as is the case with pedigree, genomic testing allows comparisons with thousands of other animals, each having a small relationship with a target animal to be predicted.

The Sheep CRC has demonstrated that genomic selection works. The CRC Information Nucleus Flock (INF) was set up to measure many animals and genotype them at the same time (van der Werf *et al.* 2010). Between 2007 and 2011, 18,000 lambs were born and measured for many traits, including growth rate, carcass composition, assorted wool traits and worm egg counts. About 10,000 lambs were measured for carcass traits and about 5000 animals for wool and reproductive traits. Using this resource as a reference population, we showed that breeding values could be predicted with accuracy between 25 and 50%. This was demonstrated by correlating the progeny test results of widely used rams with their genomic test prediction. Since 2011 we have delivered genomic predictions to breeders for the major breeds such as Merino, Poll Dorset, White Suffolk and Border Leicester.

Various Australian studies have reported on the genomic prediction accuracies achieved in real data (Daetwyler *et al.* 2010, Daetwyler *et al.* 2012, Moghaddar *et al.* 2013). Accuracies generally varied from 0.2 to 0.5. Genomic predictions are breed specific. It is not possible to obtain accurate genomic predictions if the reference population does not contain animals from the same breed as the animal that is predicted. Essentially, the relationships between animals from different breeds are too small to base any predictions on. Although the INF used 16 Dohne sires between 2009 and 2011, delivering almost 700 progeny, still more are needed to allow accurate predictions. The aim is to have information on about 2000 progeny, before genomic predictions are likely to be reliable.

Potential benefits. Traits with a moderate heritability that are easy to measure are relatively easy to improve. If traits can be measured cheaply, on both sexes and before time of first selection, the accuracy of estimating breeding value (EBV) at first age of selection can be high. In that case, genomic testing will have limited benefits as the increase in selection accuracy due to the genomic test will only be small. Table 1 compares the accuracy of estimated breeding value of 18 month old rams when estimated with and without the use of genomic information. The table shows that the selection accuracy is increased particularly for traits that could not be measured at the time of selection. The accuracy of the overall dual purpose index is increased by 46%. The result is that breeders can be more confident in selecting young rams, and therefore would allow more rams to be used in their stud. In practice it means that more young rams will appear in the top when ranking them. The overall effect of selecting rams at a younger age but with a higher accuracy will be an increased rate of genetic gain of 14%. The additional gain is higher for those traits that are hard to measure on young animals, i.e. adult traits and reproductive rate. The benefit would also be large for carcass traits that are normally not measured without slaughter.

Table 1. The effect of genomic selection (GS) on the accuracy of estimated breeding value (EBV) for a number of sheep traits when selecting young rams at 18 month of age

Trait	EBV accuracies of young males at 18 months		
	W/o GS*	With GS	%difference
Birth Weight	0.32	0.48	48%
Post Weaning Weight	0.67	0.79	17%
Post Weaning Eye Muscle	0.66	0.70	6%
Post Weaning Fat	0.58	0.64	9%
Adult Weight	0.49	0.69	41%
Adult Clean Fleece Weight	0.55	0.69	25%
Number of Lambs Weaned	0.17	0.28	60%
Dual Purpose Index	0.24	0.35	46%

*W/o: without

Reference populations. Accurate genomic predictions require a reference population of animals that have been measured for the traits of interest and that have also been genotyped. The predicted accuracy depends on the size of the reference population, but also on the diversity of the breed. A diverse breed such as Merino requires a much larger reference population than a more homogeneous breed such as the Border Leicester, because on average the relationships among the animals are much lower in diverse breeds.

Reference populations can be created for that purpose, such as the CRC Information Nucleus Flock and its successor, the Meat Livestock Australia (MLA) resource flock, and the Beef Information Nucleus (BINs) in various beef cattle breeds. Setting up a specific reference flock is required for traits that are not normally measured on farm, such as carcass and eating quality traits. Reference populations could also be created by contracting a number of breeders to record some key traits such as reproduction and adult wool attributes. If these traits were recorded in the past, than genotyping the sires with larger numbers of progeny could serve as a reference. This has been the case in the dairy industry. However, using progeny tested sires as a reference is only possible for traits already measured on-farm, i.e. easy to measure. Moreover, in small breeds it is not possible to find hundreds sires with progeny measured for weaning rate or adult fleece traits. Therefore, to build a reference population for the Dohne breed, a number of animals need to be genotyped and phenotyped for the appropriate traits each year. Measurement and genotypes on individual animals can be combined with genotypes of sires combined with phenotypes on many of their progeny. In the current MLA resource, flock the number of Dohne sires tested per year is about 10 and together they have about 100 offspring. However, these progeny are crossed with merino and therefore essentially count for a half. More genotyping of animals in industry flocks is needed before enough animals are recorded for a reference population.

Animals to be tested in the reference populations should be selected from a diverse genetic background within the breed, but also from family lines that can be expected to contribute to the future gene pool in that breed. There needs to be a balance between merit and diversity. A good strategy is to measure and genotype progeny from young sires of high genetic merit, yet these sires are relatively

unrelated to each other. The number of progeny tested per sire should be small because smaller progeny groups allow testing of more sires, which is desirable from a genetic diversity as well as an 'industry engagement' point of view.

Strategies for implementation. To assist breeders in their decision to invest in genotyping their selection candidates, we modeled predicted benefits and balanced them against the associated cost of genotyping. In a number of individual case studies those models were discussed with breeders and findings were presented and discussed with a wider audience of progressive breeders with an interest in the technology.

For individual breeders, there are various ways to save on genotyping costs. Firstly, genotyping of females is less efficient due to the lower selection intensity in females. Secondly, breeders can apply two-stage selection. Genotyping only about 20% of a young sire crop, would give more than 80% of the additional benefits of genomic selection when genotyping all males.

An important factor is whether breeders are able to mate their stock within the first year (at 7 months of age) as genomic information is relatively more beneficial for genomic estimated breeding value accuracies of younger breeding animals. Whether a breeder can afford testing depends also on the proportion of his stud-born rams that he can sell, and how much of the benefit is actually received by the breeder. Most of the benefit occurs in the commercial flocks where the offspring of the improved rams are more profitable. Typically, breeders only capture a small percentage of those benefits through increased ram prices. However, we found that even under such conservative assumptions, the break-even price of a genomic test is well above the current price of about \$50. It is expected that the price of genomic test will reduce further in the near future.

CONCLUSION

Sheep breeding programs can benefit from genomic selection by increasing rates of genetic gain, with more emphasis on traits that are otherwise hard to improve. Since prediction do not extend across breeds, and a reference population is required for each breed. This makes it hard to implement genomic predictions for small breeds. The sheep CRC is currently working on a whole genome sequence to check whether the information will allow prediction of genomic breeding value across breeds. This could be useful especially for the smaller breeds. However, in the meantime it is advisable to genotype well recorded animals and sires with recorded progeny.

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