

Contract session: Application of genetic technologies to the New Zealand sheep industry

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Introduction

The contract session, “Sheep Improvement Limited (SIL) - the first 10 years”, was presented at the 2009 NZSAP conference (Newman 2009). This described the establishment and subsequent development of Sheep Improvement Ltd (SIL), and documented the range of traits recorded and the genetic improvement achieved since SIL began in 2000. Six years later, SIL continues to be the main delivery mechanism for genetic improvement in the New Zealand Sheep industry, with an expanded range of traits recorded and with many breeding values informed by results from genomic tests. These genomic tests have been developed from significant investment over several decades and are beginning to deliver on the promise they hold for genetic improvement. The International Sheep Genomics Consortium (ISCG), of which Ovita was a member, developed single-nucleotide polymorphism (SNP) genomic panels needed for the estimation of molecular breeding values (mBV). This research has enabled Ovita, the Pastoral Greenhouse Gas Research Consortium (PGGRc) and the FarmIQ Primary Growth Partnership to develop and deliver genomic breeding values through SIL to the New Zealand sheep industry. mBVs have been ‘blended’ with the quantitative estimated breeding values (eBVs) already available through SIL, and appropriate economic models, to provide the sheep industry with the greatest suite of tools it has ever had to achieve genetic improvement. This contract documents the developments made to achieve this.

Ovita – developing the framework for genomic selection

The Ovita Foundation for Research Science and Technology programme was established in 2002 as the sheep genomics biotechnology consortium between Beef + Lamb New Zealand and AgResearch, with the aim of developing new DNA technology for the New Zealand sheep industry. Ovita moved from a microsatellite gene discovery platform, with 250 DNA markers across the sheep genome, to the new single-nucleotide polymorphism (SNP) platform with tens to hundreds of thousands of markers (Kijas *et al.* 2012). SNP technology provided a genomic selection tool that would allow improved accuracy for a new range of traits, hitherto in the too-hard basket because they were either poorly recorded in SIL, measured late in an animal’s life or were difficult to measure on farm. Genomic predictions were developed, ultimately for use with the Sheep50K SNP product, in groups of animals that were intensively phenotyped and genotyped, and these prediction equations could be applied to SNP results in the

wider breeding population without the need to phenotype animals.

Genomic predictions have been developed for New Zealand Romney, Coopworth, Perendale and terminal and maternal Composite breeders to date. The technology works best where the animals are closely related to those in the training and validation sets, and the technology is not easily transferred across breeds.

Ovita developed and implemented genomic selection including a number of poorly recorded traits (facial eczema, lamb survival, dagginess, adult ewe live weight and ewe longevity) or traits not recorded in SIL (flystrike, pneumonia) and then developed technologies that allowed these to be cost effectively implemented in industry. Additional solutions included rapid high quality DNA extraction from tissue sampling units, the SNP Parentage Plus assay and cheaper low density chips (Sheep5K), all coupled with appropriate software for the development of across-flock and -breed blended genomic breeding values (gBVs) available in SIL. From this technology development, other research investments (e.g. FarmIQ) have made advances in developing higher density SNP chips to expand the range of traits measured and accuracy of prediction.

In addition to the Sheep5K and Sheep50K SNP panels, Ovita has developed a number of commercial DNA tests, namely WormSTAR, i-SCAN 2, Parentage Plus and CARLA. WormSTAR is a DNA test to identify sheep with genetic resistance to internal parasites and that shed fewer eggs onto pasture. i-SCAN 2 is a DNA test to detect carriers of Ovine microphthalmia, a genetic defect which causes blindness. Parentage Plus is a test to establish an animal’s pedigree based on SNP DNA markers. CARLA is a test to measure immunity to internal parasites from a saliva sample, based on the presence of antibodies to a molecule found in internal parasite larvae.

Resources developed in Ovita were collated at the end of the programme. These include phenotypes, nearly all of which are available through SIL, and DNA samples and tissues accessioned in the AgResearch Genophyle database and reconciled with the SIL database. SNP chip 5, 50 and 600K genotypes are available as flat files with metadata recorded in the Genophyle database.

Ovita genomic predictions

The ovine SNP ‘50K’ chip used by Ovita was developed by Illumina and ISGC, and became available in January 2009. The chip reports results for 53,903 putative SNPs spread across the genome (including the X chromosome). Ovita genotyped animals using this 50K

SNP chip to establish ‘training’ sets for a genomic selection programme. These animals were predominantly industry sires from the major dual-purpose breeds in New Zealand with large numbers of well-recorded progeny. At the end of June 2013, genotypes for 13,468 SIL recorded sheep were quality-control checked and available for use (Dodds et al. 2014).

Animals were divided into four breed groups, namely Romney, Coopworth, Perendale and composite. Animals were considered a ‘pure’ breed if they were at least 75% of that breed based on the breed composition in SIL, or ‘composite’ if they were more than 30% (combined) of these three breeds.

A SIL genetic evaluation, comprising some 4.4 million animals from 322 relevant flocks, was run to produce eBVs for training the genomic predictions. The pedigrees stored in the SIL database were corrected where necessary, based on genotyping results. The resulting eBVs had their parental contributions removed (to avoid double counting in the analysis) and were rescaled (‘deregressed’) to the phenotypic scale. Adjusted eBVs were retained for analysis if they achieved a target reliability threshold. Genomic prediction was based on ‘genomic BLUP’, whereby the usual animal relatedness matrix was replaced by a relatedness matrix calculated from the SNP results (Van Raden 2008). The prediction model also accounted for some breed differences by fitting the first six principal components of the genotypes. Adjusted eBVs with higher reliability were given more emphasis in the analysis.

Genomic predictions were validated by comparing them with adjusted eBVs from breed sets of the youngest available animals, which were initially withheld from the prediction training. The accuracy, defined as the correlation between predicted BV and true BV, was calculated from this comparison, and directly from a genomic BLUP analysis. Accuracies for 20 SIL index traits ranged from 0.12 to 0.66 for lamb fleece weight in Perendales and 12-month fleece weight in Coopworths, respectively, and averaged 0.37 (Auvray et al. 2014). Predictions were withheld for some breed/trait combinations when they did not reach a target level of significance in validation set comparisons.

Commercial breeders can obtain mBV predictions by genotyping their animals with either the ‘Sheep50K’ SNP chip, or with a lower density Sheep5K chip with missing SNPs ‘imputed’ (Browning & Browning 2009). Genomic predictions are currently combined (‘blended’) with eBVs to give a genomic BV (gBV).

Current research goals are to develop predictions in a wider set of breeds and to allow genomic predictions using all available genotypes and trait records in a single analysis.

Sheep Improvement Limited

SIL is the national performance recording service for New Zealand sheep. The SIL Advanced Central Evaluation (SIL-ACE) national across-flock and breed analysis has been performed since 2004 (Young & Newman 2009). SIL-ACE is an opt-in analysis and now routinely includes 352

flocks, comprising 60% of active flocks in SIL and 80% of animals in the most recent birth-cohort. Improved genetic connections between flocks and increased recording of traits have led to increasing genetics gains. Genetic trends for terminal sire and dual-purpose “overall” indexes are currently 42 and 86 cents per year, respectively.

SIL economic indexes are used widely in industry, but there is some confusion amongst ram breeders and buyers due to naming of indexes. SIL “overall” indexes share a common name within sheep type, but differ in what they comprise depending on what traits a flock or flock group are collecting and evaluating. As well, wide variation in the amount or type of genetic information presented in the ram buying marketplace is causing confusion among users. SIL is introducing industry standard indexes for the main sheep types (terminal and dual-purpose) to address this issue. These are based on existing indexes, but have a fixed set of objective traits and a small, fixed set of “indicator” traits. For terminal breeds, the objective traits are lamb survival, lamb growth and meat yield. For dual-purpose breeds, the objective traits are reproduction, lamb survival, lamb growth + adult size, meat yield and wool production.

SIL developments follow three themes – “Better breeding objectives”, “More accurate evaluations”, and “Matching genetics to user needs”. Better breeding objectives will include key traits that influence farm profit, e.g., maternal longevity and body condition score. Economic indexes will specifically consider performance on hill country. Whether genetics are better adapted to hill country than low country will also be studied

At the same time, genetic evaluations will be more accurate, earlier, as genotype data are used to increase accuracies of pedigree and eBVs. SIL plans to move to a single, all-SIL evaluation run once a week. A number of projects are focused on this outcome, including developments to account for crossbreeding, inbreeding, and screening-in of animals.

Addressing the issue of data quality and the speed in which data are collected, validated and added to SIL is another focus for the future. Smart tools for collecting and adding data to the SIL database will be developed to speed up collection of performance data, reduce manual entry and rapidly identify discrepancies. Support services will focus more on data quality and less on data transfer.

Genetic information will be simpler to use and more relevant to farmers and associated industry groups. One development underway is the Farm Genetic Plan which will align genetic merit of a flock with actual performance to better inform future genetics purchases.

FarmIQ meat quality genomics

FarmIQ is a joint New Zealand government and industry Primary Growth Partnership, whose mission is to add value to the red meat sector by improving understanding of the relationship between on-farm and in-plant operations with an animals’ meat yield and quality. The aim of the genetics programme in FarmIQ is to deliver high-quality

genetic and genomic breeding value predictions for growth, meat yield and eating quality in terminal sire flocks.

FarmIQ commissioned a high density (HD) SNP chip, which was developed in conjunction with Illumina and ISGC, and released in 2013 as the *Ovine Infinium® HD SNP BeadChip*. ISGC and FarmIQ developed the HD SNP chip following the re-sequencing of 73 diverse breeds from around the world and utilised the recently released sheep genome assembly (OARv3.1). The HD chip contains around 600K SNPs.

The FarmIQ programme has used this HD chip for genome wide association studies and multi-breed genomic predictions for meat quality traits in New Zealand composite terminal sire breeds. FarmIQ is currently beta-testing results in commercial terminal sire breeding flocks to ensure the system is accurate, practical and cost-effective.

PGGRC methane genetics

Methane emissions from ruminants, (primarily sheep and cattle), contribute around 31% of annual anthropogenic greenhouse gas (GHG) production of New Zealand. The Pastoral Greenhouse Gas Research Consortium (PGgRc) is supported by the livestock industry to research methane mitigation methods including vaccines, inoculants, feedstuffs and breeding strategies for lower emitting animals.

Divergent selection lines for high and low methane emissions have been established by the PGgRc as a research tool to investigate the genetic component of methane emission. They have shown that methane production is heritable and repeatable. The level of methane produced has been shown to be influenced by the genetics of individuals in these selection lines, and that genetic selection is feasible (Pinares-Patiño *et al.* 2011). Sheep are measured for their gross methane emissions and for methane yield per unit dry matter intake (DMI). Initial estimates of heritability (and repeatabilities) are 0.29 ± 0.05 (0.55 ± 0.02) and 0.13 ± 0.03 (0.26 ± 0.02) for gross emissions (g CH₄/day) and for methane yield (g CH₄/kg DMI) respectively. The high and low selection lines currently differ by around 8% in methane yield after 1.5 generations.

There is some evidence for physiological differences between selection lines, with the low emitting selection line animals tending to have smaller rumens, higher lean yield and higher killing out percentage (Elmes *et al.* 2014, Bain *et al.* 2014). Correlations with production traits have been investigated and have shown to be either slightly positive or neutral, with the exception of wool production. The genetic correlation of methane yield with FW12 is -0.32 ± 0.11 , i.e. lower methane emissions are associated with higher fleece weights. While the correlation is negative, the result is economically favourable.

Respiration chambers are a very accurate, but expensive method to measure methane emission, and are not practical on a commercial scale. Alternative predictors are required for implementation in a breeding programme. There are a number of alternative techniques. It is possible to do brief measurements in a respiration chamber. Methane

research is based on methane and carbon dioxide measured every 6 minutes over a 48 hour period, but the individual measurements are highly correlated. Simple portable PAC chambers have been designed to take one hour measures of CH₄ and CO₂ on-farm. Around four measures are needed to predict gross methane and methane yield with the equivalent accuracy to a respiration chamber. Rumen microbial profiles can be used to predict methane emissions. DNA sequence data of rumen microbial contents gives an estimate of the abundance of sequences assigned to each microbial taxa. Measurement of volatile fatty acids has some predictive ability. Low emitting animals tend to have higher amounts acetate in rumen samples and in circulating blood plasma. Finally, genomic prediction has been shown to have a prediction accuracy of around 50%, based on molecular breeding values predicted from HD genotypes from around 1600 animals.

Gaseous emissions could be included in selection indexes in the near future. Total emissions of CO₂ and CH₄ measured in respiration chambers are highly correlated with dry matter intake ($r=0.98$). This means that greenhouse gases could be incorporated into the current selection indexes primarily as a proxy for feed intake to increase efficiency. This would deliver immediate benefit to the industry whilst ensuring that the NZ sheep industry has a mitigation strategy in place in the event of a carbon tax being imposed on ruminant selection.

Economics of breeding

Economic values for SIL traits are all calculated as the dollar value for a unit change in the trait, all other traits being equal. This has served the industry well in weighting traits according to the economic return. However, economic considerations are not the only driver in ram breeder and buyers decisions. Farmers may be prepared to, for example, sacrifice some profit in order to simplify management. As such, a farmer's preferences may differ from the optimum calculated through economic theory. The uptake of genetic selection tools could be improved if farmer preferences are taken into account when designing breeding objectives.

Farmers' trait preferences have been analysed, mainly in developing countries (poor market data/ valuation of non-market traits), to inform the design of breeding programmes by understanding what kind of animals farmers would like to have. Farmer characteristics are thought to have a strong influence on farmers' preferences for improvements in traits.

Farmers' preferences are known to be highly variable and not accounting for this variability might bias the estimate of these preferences in the sense that the average preferences might not reflect the preferences of a large proportion of farmers.

There are many statistical tools to analyse the variability of preferences for trait improvements, by determining if there are groups of farmers that can be identified with specific patterns of preferences and with particular characteristics. Choice experiments, where participants are asked to choose between two scenarios to

determine the trade-offs they are willing to make, can be used to analyse a wide range of issues related to farmer preferences for trait improvements. As an example, choice experiments are being used to study how people deal with complexity of information on genetics. Another example is the use of choice experiments to identify farmer groups and use that information to design selection indexes which cater to the industry in question.

Results from this work will be used to inform the next generation of breeding objectives.

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