# GENETIC EXPRESSIONS AND ECONOMIC IMPACT OF PERFORMANCE RECORDING IN MULTI-TIERED SHEEP BREEDING SCHEMES

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## SUMMARY

This research initiative explores the value of performance recording in the multiplier flock of multi-tiered sheep breeding schemes integrating commercial and breeding structures. Discounted gene flow theory was used to model the flow of genes from the selected multiplier rams that are mated to commercial ewes. A model which predicts genetic trends and gene flows at an individual trait level was combined with trait economic values to aggregate the total industry benefits associated with alternate recording and selection strategies. While recording efforts and molecular technology adds significant costs to the breeding schemes, their application in multiplier flocks also adds considerable margins by increasing accuracy of selection with consequent higher rates of progress.

## INTRODUCTION

In New Zealand, the sheep breeding sector is part of a wider multi-tier structure. The majority of sheep breeding is structured in two tiers, nucleus and commercial, with the special case where an intermediate tier multiplies rams to be mated in commercial flocks; a multiplier tier. The highly varied production systems across the country require that breeders, and ultimately commercial farmers, have the ability to rank selection candidates on combinations of performance traits applicable to their systems. Recently, an increasing number of sheep breeder conglomerates and groups have been formed allowing larger investments in breeding program design. It is important to increase the accuracy of prediction, and consequently the rate of genetic progress, which in lower tiers is equal to the progress obtained in the nucleus, although more accurate selection in the multiplier will reduce the genetic lag that exists between nucleus and commercial flocks. Given the opportunity to integrate information flow across tiers through the application of new molecular and phenotype data collection technologies, higher genetic gains can also be achieved by expanding performance recording in the commercial flock. The role of multiplier flocks has increased due to demand for more productive and affordable rams which originate from flocks that apply up to date selection technology. In multi-tiered breeding schemes the informed selection of replacement ewes and rams for use in lower tiers results in added value to the commercial farmer. This research examines breeding scheme design and the integration of breeding and commercial performance data to achieve faster genetic gain. This study investigates the value of selection based on performance recording in the multiplier tier of a breeding scheme in which commercial sheep production is part of a vertically-integrated breeding structure.

## MATERIAL AND METHODS

This research was based on multiple trait deterministic simulation using New Zealand industry parameters. The primary focus was on meat sheep production for a commercial operation where there is limited use of terminal sires, which means that flocks in this operation are mainly using livestock selected for maternal traits. A number of scenarios based on different strategies for implementing recording in the multiplier flock were simulated and their benefits evaluated.

**Simulation scenarios.** The simulation scenarios accounted for the recording strategy, the use of genomic selection in the different tiers, selection and culling of candidates based on breeding index (full trait range) or production index (limited trait range), and alternative replacement

policies. The policies for replacing ewes in the nucleus flock assume candidates are available from two sources; young female hoggets from the nucleus flock, or older mixed-age proven ewes from the multiplier flock. Full recording practices and parentage were assumed within the nucleus flock, whilst simple trait performance recording, such as pregnancy scanning, live weight and body condition score, were assumed in the multiplier flock. The simulation scenarios modelled in this study were: *Base scenario*, no performance recording in the multiplier tier; *Scenario 1*, performance recording in the multiplier tier implemented in Year 1, including DNA parentage, the top 5% of rams tested on 50K SNP chip, the top 15% of rams tested on 5K SNP chip (Genomic Selection, GS), selection on a breeding index, and young female hoggets from the nucleus flock selected as replacements; *Scenario 2*, same recording as Scenario 1, but without GS; *Scenario 3*, performance recording in multiplier tier from Year 1 without parentage, and selection based on phenotypic performance of ewes and a phenotypic selection index; *Scenario 4*, same as Scenario 1, but with selection of mixed-age proven ewes to replace the nucleus flock; *Scenario 5*, same as Scenario 2, but with selection of mixed-age proven ewes to replace the nucleus flock; and *Scenario 6*, where GS is implemented based on genotyping of the flock, but without phenotypic recording.

**Genetic trends.** Average genetic trends were calculated for each trait in each tier based on deterministic prediction, for which calculations included trait specific genetic parameters and accuracies, selection intensity and generation interval. The calculation of genetic progress in ewes born in the nucleus before the base year of selection in the multiplier flock (Year 1) was assumed as a linear relationship between age at selection and the annual rate of genetic progress for the different traits. The average genetic merit of the flock was calculated based on recursive equations which account for the proportion of animals in each age class. The selection differential and consequent genetic progress was calculated using selection index theory principles combined with the methodology proposed by Ducrocq and Quaas (1988). The average genetic merit in the different tiers was calculated based on the reported response to selection values obtained from a selection index model from van der Werf (1999). These responses were converted into selection differentials which form the basis to calculate genetic trends across tiers and scenarios. The progeny merit in a given year for a specific trait is equivalent to the mean genetic merit of sires and dams selected to produce the progeny, calculated as described above, and the selection differential applied in the progeny. Accuracies of GS predictions were modelled as additional traits, genetically and phenotypically correlated with traits included in the selection index model (van der Werf, 2009).

**Discounted genetic expressions.** The discounted genetic expression coefficients (DGEs) account for the proportion of superiority transmitted over time to an individual's descendants through transfer of genes. The expressions of genes in different age classes, discounted at 7% per annum, were calculated through a series of transition matrices for a self-replacing ewe (Amer, 1999). In the current study, genetic expressions were used to model the flow of genes from multiplier rams once they pass into the commercial flock for mating. Discounted genetic expression coefficients for traits expressed at different time points were grouped as vectors (with dimension equal to the year of expression) of: annually expressed traits, traits expressed at end of life or cull traits in ewes, traits expressed at birth, and at slaughter in lambs. Age composition, and reproductive and survival rates used in the calculations of DGEs within the gene-flow model were obtained from industry data.

**Cost-benefit analysis.** Benefits were calculated across all tiers for the different scenarios. The genetic merit of cohorts combined with DGEs and trait economic values were used to generate the monetary impact observed in the commercial tier with and without recording in the multiplier flock for all scenarios. The total economic impact is presented as the additional benefits of the implementation of varying recording practices in the multiplier tier, relative to base scenario, after

accounting for the costs of parentage testing, genomic selection, electronic identification, recording, and genetic evaluation. The economic impact was estimated for a large commercial operation with 180,000 ewes lambing per year.

## RESULTS AND DISCUSSION

Within scenarios, there were significant differences in traits' selection differentials between tiers. Across scenarios, selection differentials were higher in the nucleus in comparison to the multiplier and commercial flocks, and they differed considerably between scenarios. The rates of genetic progress in the commercial tier of scenarios 1 and 4 were the highest, followed by scenarios 2, 5 and 6 which had similar rates. The rates of progress for scenarios 1 and 4, and for scenarios 2 and 5 were nearly identical. The lowest progress was achieved in Scenario 3. In time, genetic progress tended to stabilize and become constant across tiers, although differences in average merit (genetic lag) between tiers and between scenarios remained. These results also reflect the variation in the timing of actual expressions of traits; e.g. lamb birth trait impacts occur first, and cull ewe trait impacts occur last. Table 1 presents, for each trait, the genetic lag between the nucleus and the commercial flock in the different scenarios. A reduction of approximately two years in the lag between the nucleus and the commercial flock was achieved when recording was implemented in the multiplier tier for all scenarios, except for Scenario 3.

**Table 1. Genetic lag (years) in year 20 between the nucleus and the commercial tier in different scenarios, where Com$_c$ represents the commercial flock after recording is implemented in the multiplier.**

| Trait (Abbrev.) | Scenario 1 | | Scenario 2 | | Scenario 3 | | Scenario 4 | | Scenario 5 | | Scenario 6 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Com | Com$_c$ | Com | Com$_c$ | Com | Com$_c$ | Com | Com$_c$ | Com | Com$_c$ | Com | Com$_c$ |
| Carcase weight | 7.92 | 5.78 | 7.93 | 5.90 | 8.29 | 7.01 | 7.93 | 5.71 | 7.93 | 5.80 | 7.86 | 5.53 |
| Weaning weight | 7.92 | 5.78 | 7.93 | 5.89 | 8.36 | 7.48 | 7.93 | 5.72 | 7.93 | 5.82 | 7.86 | 5.54 |
| Number of lambs born | 8.79 | 6.63 | 8.79 | 6.59 | 8.99 | 6.79 | 8.78 | 6.65 | 8.77 | 6.93 | 8.74 | 6.39 |
| Ewe mature weight | 8.79 | 6.77 | 8.79 | 7.14 | 8.97 | 6.56 | 8.80 | 6.50 | 8.82 | 6.75 | 8.53 | 5.68 |
| Ewe BCS | 8.78 | 6.04 | 8.78 | 5.92 | 9.22 | 9.22 | 8.76 | 6.58 | 8.77 | 6.34 | 9.21 | 7.94 |
| Survival mat | 8.78 | 6.27 | 8.78 | 6.58 | 9.44 | 9.44 | 8.78 | 6.27 | 8.78 | 6.58 | 9.68 | 9.68 |
| Weaning weight mat | 8.79 | 6.65 | 8.79 | 6.59 | 9.44 | 9.44 | 8.79 | 6.59 | 8.77 | 7.00 | 8.65 | 6.09 |
| Stayability | 8.44 | 5.84 | 8.43 | 4.73 | 8.98 | 8.98 | 8.43 | 6.23 | 8.42 | 5.24 | 8.87 | 7.74 |
| Lamb survival | 8.00 | 5.80 | 11.1 | 11.1 | 11.1 | 11.1 | 8.00 | 5.80 | 11.1 | 11.1 | 8.00 | 5.80 |

Figure 2 presents the difference from the Base scenario of the cumulative net present value (NPV), estimated as the sum over time of the present values of benefits and costs discounted at 7% per annum. The NPV for scenarios 4 and 5 lie exactly underneath those for scenarios 1 and 2 respectively, as a consequence of nearly identical rates of genetic progress. Scenarios assuming parentage assignment (i.e. all scenarios but Scenario 3) presented an early spike in costs associated with DNA testing in the multiplier flock which stabilised over time. Yearly recording costs also include trait measurement, electronic identification (EID) and genetic evaluations. The marginal (relative to Base scenario) commercial flock benefit, which includes the multiplier flock as a significant component of the commercial operation, accumulated steadily after a delay and then stabilized after ten years as a constant flow of benefits. Benefits stabilized after a given number of years because genetic progress becomes constant. Losses are reversed after 5 – 7 years in all scenarios with exception of Scenario 3, and in the long run, annual benefits exceed annual costs by a factor of two. Scenario 3, which assumed phenotypic selection without parentage assignment, did not result in enough extra genetic progress to offset the performance recording costs.
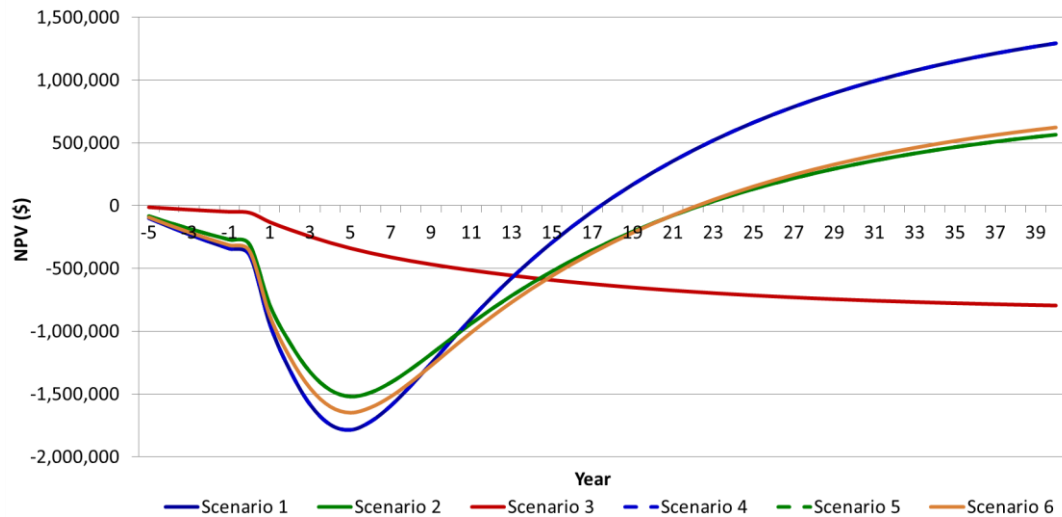
**Figure 2- Cumulative net present value across scenarios assuming different strategies of performance recording in the multiplier tier of multi-tiered breeding scheme.**

Selection intensity and age structure differences between scenarios assuming mixed-age ewe replacements did not result in changes in NPV when compared to the policy where young ewe lambs are selected as flock replacements. Results demonstrated that higher genetic progress can still be achieved through more accurate selection based on selection of proven mixed-age ewes.

The results demonstrated the potential that GS has to increase genetic progress in the breeding scheme. Increased progeny merit and reduced genetic lags were achieved in scenarios 1 and 4, which assume GS, when compared to equivalent scenarios without GS. The implementation of a GS strategy was cost-effective when including current costs of genetic testing. The strategy where GS without phenotypic recording is undertaken was promising, and its feasibility relies on the accuracy of genomic predictions.

**CONCLUSION**

The results of this study demonstrate that performance recording in the multiplier tier can reduce the long genetic lag between the nucleus and commercial flocks in multi-tiered breeding programs. The results also demonstrate that economic benefits can be generated by implementing recording in the multiplier tier. Such recording is justified if the breeding scheme captures all of the benefits through value added to slaughter lambs and replacement females produced in the commercial tier. The investment in genotyping was the major expense in the scenarios where it was applied. Strategies where proven mixed-age ewes are selected as replacements of the nucleus flock produce identical margins to those which select young ewes, offsetting eventual increases in generation interval. It is important to note that the biggest benefits came from a combination of full recording of functional traits plus parentage assignment.

**REFERENCES**
Amer, P. R. (1999). *New Zealand J. Agri.Res.*, **42**(3), 325–336.
Ducrocq, V. & Quaas, R.L. 1988. *J. Dairy Sci*, **71**: 2543-2553.
van der Werf, J.H.J. (1999). Multi-trait selection index MTINDEX20T model. http://www-personal.une.edu.au/~jvanderw/software.htm