

New Zealand Society of Animal Production online archive

This paper is from the New Zealand Society for Animal Production online archive. NZSAP holds a regular annual conference in June or July each year for the presentation of technical and applied topics in animal production. NZSAP plays an important role as a forum fostering research in all areas of animal production including production systems, nutrition, meat science, animal welfare, wool science, animal breeding and genetics.

An invitation is extended to all those involved in the field of animal production to apply for membership of the New Zealand Society of Animal Production at our website www.nzsap.org.nz

[View All Proceedings](#)

[Next Conference](#)

[Join NZSAP](#)

The New Zealand Society of Animal Production in publishing the conference proceedings is engaged in disseminating information, not rendering professional advice or services. The views expressed herein do not necessarily represent the views of the New Zealand Society of Animal Production and the New Zealand Society of Animal Production expressly disclaims any form of liability with respect to anything done or omitted to be done in reliance upon the contents of these proceedings.

This work is licensed under a [Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License](http://creativecommons.org/licenses/by-nc-nd/4.0/).



You are free to:

Share— copy and redistribute the material in any medium or format

Under the following terms:

Attribution — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.

NonCommercial — You may not use the material for [commercial purposes](#).

NoDerivatives — If you [remix, transform, or build upon](#) the material, you may not distribute the modified material.

<http://creativecommons.org.nz/licences/licences-explained/>

Quantitative genetic selection for twinning rate in ewes

P.R. AMER AND L. BODIN¹

Abacus Biotech Limited, PO Box 5585, Dunedin, New Zealand

ABSTRACT

Data from 19 recorded sheep flocks were included in this study involving 324 thousand lambings from the 1970's up until the 2004 lambing season. The genetic correlation between number of lambs born, and a triplet trait coded as 1 for ewes lambing triplets or higher multiples, and 0 for ewes lambing singles or twins was estimated separately over 13 data sets. Genetic correlation estimates ranged between 0.78 and 0.95 with all but two dataset estimates differing from 1.00 by two or more standard error intervals. Flock differences in the relationship between mean NLB and the proportion of ewes lambing twins were also investigated through an analysis of sire mean results. Strong evidence was found for within flock genetic variation in twinning incidence that is independent of mean NLB. This is different to the clear relationship that exists between mean litter size of a group of ewes and the proportion that lamb twins. There were also meaningful differences across-flocks in the proportions of ewes lambing twins after accounting for the effects on twinning percent of flock mean litter size. Our analyses suggest that simple selection strategies such as screening in twin lambing ewes from a commercial flock, and/or, only using twin-born rams in the breeding flock, will be relatively ineffective for improving twinning rates. A recommendation arising from the study is that genetic evaluation tools for twinning be made available to New Zealand sheep breeders. These tools would allow breeders to select for decreased triplets without compromising genetic progress in other traits including mean number of lambs born.

Keywords: Prolificacy; sheep; estimated breeding value; heritability.

INTRODUCTION

Over the last decade there has been a steady increase in the national lambing percentage by an average of 1.5 lambs tailed per 100 ewes joined per annum resulting from: superior genetics, fertility vaccines and management techniques. However, as pregnancy rates increase, so to does the number of triplet pregnancies (e.g. Amer *et al.*, 1998). Triplets can be problematic as they have lower survival rates and either take longer to finish to target slaughter weights, or have lighter carcasses at the same slaughter age. The lower survival of triplet lambs is an impediment to farmers with high fecundity ewes achieving higher lambing percentages. In addition, higher rates of triplets could be a deterrent to farmers adopting technologies that can increase the fecundity of their flocks.

Some stud breeders select for, and market, rams based on a history of twinning in both the ram's mother, and paternal grandmother. Increasing the number of foetuses per ewe scanned by increasing twinning rates (with less of both singles and triplets) is perceived by these stud breeders to be advantageous compared with increases due to having more triplet and higher multiples of foetuses. Existing *ad hoc* methods for genetic improvement of twinning rate include

screening in twin lambing ewes from a commercial flock, and/or, only using twin-born rams in the breeding flock. Because of the complex genetic relationship between ovulation rate, conception rate and embryonic mortality, it is questionable whether the *ad hoc* efforts by stud breeders have been very successful. Further, Amer *et al* (1998) reported data from a flock with a long history of selecting only rams from twin litters, but where the proportion of twin bearing ewes remained only slightly higher than has been observed over very large numbers of surveyed flocks. It is unlikely that the genetic response in twinning percent in this flock has offset the lost selection progress in other economic traits that will have resulted from the reduced pool of candidates to select from.

A more sophisticated genetic approach to selection for twinning rate might be more efficient at achieving high twinning rates without the concomitant increase in higher order birth ranks. San Cristobal-Gaudy *et al.* (2001), using sophisticated Bayesian computational techniques, concluded that there may be opportunities to genetically select for the proportion of ewes lambing twins (and against those lambing with higher litter sizes). The key to any analysis of twinning rate is to separate the strong but complex inter-relationship between twinning rate and mean prolificacy.

¹Station D'amélioration Génétique des Animaux, Institut National de la Recherche Agronomique (INRA), BP 27, 31326 Castanet-Tolosan, France

The objective of this study was to determine whether or not there is evidence for genetic variation in twinning rate that is independent of mean prolificacy, and establish whether an industry genetic evaluation system could be used instead of *ad-hoc* strategies currently adopted by some sheep breeders.

MATERIAL AND METHODS

Data

Data from 19 New Zealand sheep flocks were used. In a number of cases, flocks with close genetic relationships and of similar breed were incorporated into combined datasets. Characteristics of the resulting 13 datasets are summarised in Table 1. Composite datasets involve animals containing a combination of breeds, for example, prolific breeds such as Finn and East Friesians are combined with the Texel breed and dual purpose breeds that have been present in New Zealand for more than 50 years. There were 8 Romney and 3 Composite datasets where the primary purposes of sold rams was to breed replacement females. An additional Composite flock had the primary purpose of selling terminal rams, while the Texel flock sold both terminal rams and rams to breed replacement females. In general, the range of birth years of ewes and the numbers of lambings was much higher for Romney datasets, relative to Composite datasets. The largest Composite dataset contained a number of years of lambs from the base, dual purpose purebred, flock. All records from hogget lambing were excluded from the analysis.

TABLE 1: Summary of dataset characteristics

Data set breed type	Mean NLB	Lambings	Ewe birth years
Romney	1.71	41352	1972-2002
Romney	1.86	77864	1973-2002
Romney	1.73	54188	1980-2002
Romney	1.82	56046	1972-2002
Romney	1.70	15428	1976-2002
Romney	1.59	33859	1974-2002
Romney	1.77	7095	1987-2002
Romney	1.65	8071	1976-2002
Composite	2.06	2092	1996-2002
Composite	1.83	15348	1976-2001
Composite	1.58	3521	2000-2002
Composite (Terminal)	1.75	2259	1989-2002
Texel	1.61	6966	1987-2002

Statistical methods

Data were analysed using ASREML (Gilmour *et al.*, 1999) to estimate fixed effects and variance components for two litter size traits. All

records for ewes with one or more missing parents were eliminated from the analysis. This is because some breeders “screen in” commercial ewes with twins into their recorded flocks. Since there are no records for those contemporaries of these ewes that did not have twins, the screening process has the potential to bias results. Because screened in animals usually have one or both parents missing, eliminating records of ewes with any missing parent should eliminate any such bias.

The first litter size trait considered was number of lambs born per ewe lambing (NLB). The definition of NLB used was similar to that used in SIL, the New Zealand sheep genetic evaluation system, with the exception that in this study, ewes joined but failing to lamb at all were coded as having missing records, as opposed to 0 lambs born with the SIL definition. The second litter size trait was defined by coding all ewes lambing triplet or higher multiple litters as 1, and all ewes lambing single or twin litters as 0. This trait is referred to as triplet percent (TRIP) because the incidence of quadruplet and higher multiples was very low (i.e. less than 1%).

Variance components including additive genetic, permanent environmental, and residual effects were first estimated individually for each trait by dataset. The three-way interacting effects of ewe lambing flock, lambing year, and age of ewe were also fitted to minimize the effects of environmental factors on the variance estimates. Variance estimates generated from univariate analyses were then used as starting values for bivariate analyses to determine genetic and residual covariances which could in turn be transformed to obtain genetic and phenotypic covariances between the two prolificacy traits. Where estimates of permanent environmental effects were not significantly different from zero in the univariate analyses, they were not estimated at all in the bivariate analyses. For some datasets, there were convergence problems when permanent environmental effects were included in the bivariate analyses. For these situations, the permanent environmental effects were fixed at the levels found in the univariate analyses, and the remaining parameters then estimated.

Estimation of flock differences

An analysis was carried out to determine whether there were apparent differences in the percentages of ewes lambing with various litter sizes after accounting for differences in mean litter size. A two-step analysis was necessary because of the part-whole relationships among mean number of lambs born, and the ewe litter size proportions within the group. Step 1 involved estimating the

mean number of lambs born and the proportions of ewes lambing singles, twins and triplets or higher multiples, and ewe group size, for groups of ewes with a common sire, birth flock, lambing year and ewe age category. Ewe age category is defined as ewes lambing as two tooth, versus ewes lambing at older (i.e. >2yo) ages. The results from all component datasets from step 1 were then combined into a single master dataset. Step 2 of the analysis involved fitting polynomial (order 4) regression equations to the data from step 1 using standard weighted least squares procedures. Ewe litter size proportions were regressed on group mean NLB, both within birth flocks, and across all birth flocks available from the datasets. The weighting factors were based on the number of ewes in each group.

Example BLUP evaluation

Best Linear Unbiased Prediction (BLUP) was used to estimate breeding values for NLB and TRIP for an example flock. Breeding values for TRIP were then corrected for NLB breeding values using linear regression and taking the residuals (TRIP*) as a negative indicator of an animals genetic propensity for a high rate of twins after accounting for affects due to mean NLB.

RESULTS

Table 2 shows the estimates of heritabilities, genetic correlations and phenotypic correlations derived from the variance component estimates from each of the datasets. The datasets are listed in Table 2 in order of decreasing probability of the genetic correlation between NLB and TRIP being statistically different from 1 (based on the number of standard error intervals that each estimate lies from 1). Genetic correlations between TRIP and NLB ranged from between 0.78 and 0.93, with a weighted average of 0.91. The estimate of rg was greater than two standard error intervals from 1 for all but two of the datasets. For one additional dataset, no genetic correlation could be estimated due to a failure for the solutions to converge in the variance component estimation process.

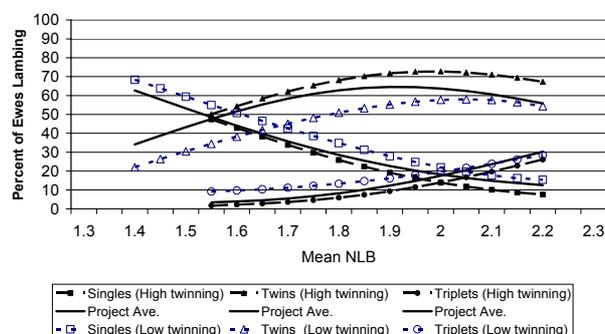
The weighted average of the estimates of heritabilities for NLB and TRIP were 0.061 and 0.036 respectively. The highest heritability estimate of 0.135 was for TRIP in a Composite flock. The lowest heritability for TRIP was also in a Composite flock. Phenotypic correlations were always lower than the genetic correlation estimate from the same dataset. This is a statistical artifact of the part whole relationship between the two traits.

TABLE 2: Heritability estimates for mean number of lambs born (NLB-h²) and triplet percent (TRIP-h²), as well as phenotypic (rp) and genetic (rg) correlations between the two traits (standard errors in brackets) for 13 datasets. Weighted averages are also presented with weightings based on standard errors.

Breed type	NLB-h ²	TRIP-h ²	rp	rg
Romney	0.059 (.006)	0.032 (.008)	0.50 (.00)	0.79 (.03)
Romney	0.086 (.006)	0.073 (.005)	0.62 (.00)	0.92 (.02)
Romney	0.051 (.005)	0.032 (.004)	0.54 (.00)	0.86 (.02)
Romney	0.070 (.006)	0.046 (.004)	0.60 (.00)	0.92 (.02)
Composite (Terminal)	0.103 (.017)	0.063 (.010)	0.50 (.01)	0.78 (.07)
Romney	0.051 (.009)	0.039 (.008)	0.50 (.01)	0.80 (.07)
Composite	0.105 (.009)	0.135 (.010)	0.64 (.01)	0.95 (.02)
Texel	0.136 (.028)	0.095 (.025)	0.49 (.01)	0.78 (.09)
Romney	0.038 (.005)	0.011 (.003)	0.39 (.01)	0.82 (.08)
Romney	0.067 (.011)	0.051 (.013)	0.54 (.01)	0.85 (.06)
Composite	0.097 (.035)	0.074 (.028)	0.78 (.01)	0.93 (.04)
Romney	0.036 (.012)	0.017 (.008)	0.40 (.01)	0.88 (.18)
Composite	0.038 (.013)	0.013 (.011)	-	-
Weighted average	0.061	0.036	0.57	0.91

Figure 1 plots the average, highest twinning, and lowest twinning flock polynomial relationships estimated for percent singles, twins and triplets, on group mean NLB. The highest twinning flock has the highest curve for percent twins and the lowest curves for percent singles and percent triplets. The highest and lowest twinning flocks both involve very substantial numbers of ewes lambing. Therefore, the flock differences shown in Figure 1 are unlikely to be just the result of random variation occurring within small flocks.

FIGURE 1: Polynomial functions plotted for percent single, twin and triplet lambing ewes plotted against average litter size (NLB) for the best (highest twins), project average and worst (lowest twins) flocks.

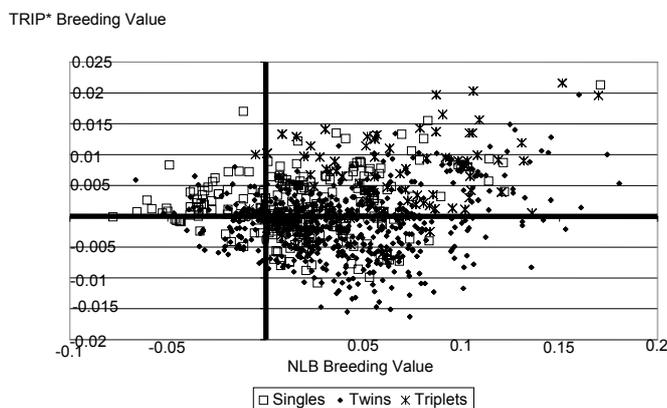


The highest and lowest twinning flocks differ by approximately 15 percent points in the proportion of ewes lambing twins across a wide range of mean values for NLB. While the highest twinning flock was Romney, and the lowest

twinning flock was a Composite (results not shown), there was a large overlap between Romneys and Composites in their maximums for twinning proportion. In other words, some Romney flocks with a history of selection and genetic progress in mean NLB (without consideration of twinning) have comparably low rates of twinning at any given mean NLB, as do some of the Composite flocks.

Figure 2 shows estimated breeding values of young rams for TRIP* (ie triplet proportion after linear correction for NLB breeding value) and NLB. Animals in the lower right hand quadrant of Figure 2 are expected to be economically most desirable (i.e. high mean NLB without a high incidence of triplets). While twin-born lambs are most commonly represented in this quadrant, there are significant numbers of single and triplet-born lambs which are also in this desirable quadrant, and many twin-born lambs that are in other less desirable quadrants. Being born as a twin is therefore not a reliable indicator of being of high genetic merit for twinning rate.

FIGURE 2: Plot of estimated breeding values from an example flock for triplet percent adjusted for NLB breeding value (TRIP*) against NLB breeding value for young rams without daughters with lambing records. Young rams born as singles, twins and triplets are indicated separately.



DISCUSSION

The estimates of genetic correlations between NLB and TRIP observed in this study provide strong evidence for within flock genetic variation in twinning incidence. Despite this, the majority of variation observed across the 324,000 lambings in this study was closely linked to average litter size (i.e. the percentage of ewes with twins is maximum at a group mean lambing percent of between 1.8 and 2.1 lambs born per ewe lambing). Furthermore, accurate information on

litter size distribution for a sire's progeny group does not eventuate until a ram used in the breeding program has significant numbers of daughters with litter size recorded. Therefore, progress from genetic selection for twinning rate is expected to be modest. Based on the data reported, it can be estimated that approx 0.25 % to 0.4 % less ewes lambing triplets per year of selection at the same mean lambing percentage could be achieved when a stud breeder sacrifices 20-30% of progress for other traits (data not shown). Thus, after 12 years of selection, a breeding flock having 8% of ewes lambing triplets might expect to have 3 to 5% of ewes lambing triplets if mean number of lambs born per ewe lambing has not changed.

It has long been known that breed variation exists in the distributions of litter sizes at comparable mean numbers of lamb born. Icelandic sheep have been identified as having high proportions of ewes with twin ovulations and high rates of embryo survival leading to higher incidences of ewes lambing twins than expected for British breeds of sheep (Hanrahan, 1989). Several Norwegian breeds of sheep and Texels from the Netherlands have also been implicated as having above average rates of twinning (Hanrahan, 1989). In contrast, Finn sheep have been shown to have a greater variation in ovulation rate and higher embryo mortality than Romanov sheep (Hanrahan, 1986). Both of these factors are expected to lead to a lower rate of twinning in Finn sheep relative to Romanov sheep at comparable mean litter sizes. Induced ovulation has also been identified as leading to an increased variability of litter size (Bodin *et al.*, 1989). It is unclear whether the large differences in ewe litter size distributions across-flocks observed in this study are due to genetic (including breed type) or environmental effects. However, anecdotal observation suggests that at least some of the differences are genetic. This includes the fact that with purebred flocks where there has been a history of selection on twinning rate (using ad-hoc methods), the peak twinning proportions tended to be higher than in those flocks where there has been heavy emphasis on increasing mean NLB. There was substantial variation in merit for twinning rate across datasets of the Composite flock type which might reflect differences in their breed makeup.

Currently, the only option for BLUP genetic evaluation of litter size in New Zealand is for mean number of lambs born. The sophisticated approach to selection to reduce variance around the mean litter size used by San Cristobal-Gaudy *et al.* (2001) is not tractable for large datasets and would not be suitable for a routine genetic evaluation system as implemented via Sheep Improvement

Limited in New Zealand. From Figure 2, it appears that ad-hoc methods such as screening-in commercial ewes after lambing twins, or only using twin-born ram lambs in the breeding flock are inefficient at identifying animals with a high potential for twinning rate. This is because many twin-born animals arise by chance from genetic lines where twinning rate is lower than average. Similarly, some single and triplet-born animals arise by chance from genetic lines where twinning rate is higher than average. It is therefore recommended that genetic evaluation tools for twinning (adjusted for group mean litter size) be made available to New Zealand sheep breeders. This should initially be on a within flock basis. Careful consideration of how best to adjust the TRIP estimated breeding values to be independent of mean NLB will be required before the triplet trait genetic evaluation can be incorporated into industry-wide across-flock genetic comparisons of animals based on aggregate indexes of all traits of economic importance. The relatively simple trait definition for TRIP as defined here could be readily introduced as a new trait for genetic evaluation, with minimal modification to existing software. Ideally, breeders concerned about twinning rates should apply downward selection pressure to the TRIP estimated breeding values after accounting for affects of estimated breeding values of mean NLB.

ACKNOWLEDGEMENTS

The authors gratefully acknowledge the research funding provided by Meat & Wool New Zealand, and by Sheep Improvement Limited, to undertake this study. We are also very grateful to the owners of the 19 participating flocks for making their data available for analysis, and for making a financial contribution to the study.

REFERENCES

- Amer, P. R.; McEwan, J. C.; Dodds, K. G.; Davis, G. H. 1998: Economic values for ewe prolificacy and lamb survival in New Zealand. *Livestock Production Science*. 58: 75-90
- Bodin, L.; Elsen, J.M. 1989: Variability of litter size of French sheep breeds following natural or induced ovulation. *Animal Production*. 48:535-541
- Gilmour, A. R.; Cullis, B. R.; Welham, S. J.; Thompson, R. 1999: ASREML Reference Manual. *NSW Agriculture Biometric Bulletin No. 3*, NSW Agriculture.
- Hanrahan, J.P. 1986: Reproductive efficiency in sheep. *In: Smith, C.; King, J.W.B.; and McKay, J. ed. Exploiting New Technologies in Animal Breeding: Genetic Developments*. Oxford, Oxford University Press. pp 59-70
- Hanrahan, J.P. 1989: Altering reproductive rate in sheep: some genetic and non-genetic options. *In: Dyrmondsson, O.R.; Thorgeirsson, S. ed. Reproduction, growth and nutrition in sheep*. Reykjavik, Agricultural Research Institute and Agricultural Society. pp 49-55
- San Cristobel-Gaudy, M.; Bodin, L.; Elsen, J.M.; Chevalet, C. 2001: Genetic components of litter size variability in sheep. *Genetic Selection Evolution*. 33:249-271.