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.

Genetic parameters for New Zealand cashmere goats

R.L. BAKER, B.R. SOUTHEY, M.L. BIGHAM[1] AND S-A.N. NEWMAN[2]

MAF Technology, Ruakura Agricultural Centre, Hamilton, New Zealand.

ABSTRACT

Genetic and phenotypic parameters were estimated for some components of cashmere production using data obtained from goats born in 1987 and 1988 from flocks participating in a sire reference scheme. A total of 33 sires and 841 progeny were included in the analysis. Heritability estimates of weaning and yearling liveweights from univariate restricted maximum likelihood (REML) analyses were $0.14\pm.10$ and $0.22\pm.15$, respectively. Heritabilities were estimated for four fibre traits recorded at the yearling shearing using a multivariate REML analysis. Heritability estimates were $0.31\pm.14$ for fleece weight, $0.64\pm.21$ for yield of down, $0.57\pm.19$ for down weight and $0.82\pm.23$ for down diameter. There was an unfavourable positive genetic correlation between down weight and down diameter of $0.61\pm.17$ in agreement with Australian estimates. Genetic correlations of yearling liveweight with down weight and fibre diameter were slightly negative and also indicated unfavourable relationships. The implications of these parameters for the development of breeding plans and selection indices for cashmere goats are discussed.

Keywords Goats, cashmere, heritability, fibre, selection index.

INTRODUCTION

The developing cashmere goat industry in New Zealand has demonstrated considerable interest in developing performance recording, genetic improvement programmes and group breeding schemes. In an attempt to foster these developments the Ministry of Agriculture and Fisheries operated a sire reference scheme (SRS) for cashmere goats in 1987 and 1988 (Baker and Parratt, 1987). Since 1989 this SRS has been operated by a group of goat farmers (Goat Genetic Services), with Ruakura personnel analysing the data for goats born in 1989. While the numbers of contributing flocks to the 1987 and 1988 schemes were less than originally hoped, breeding values were provided to those involved in 1989. At the same time a useful data set was available for estimation of genetic parameters for two liveweights and four fibre traits recorded at the yearling shearing.

There have been relatively few published reports on the inheritance of cashmere production (Millar, 1986; Pattie *et al.*, 1990). The genetic parameters in this paper are the first New Zealand estimates.

MATERIALS AND METHODS

Source of Data

In 1987 a total of 12 flocks enrolled in a sire reference scheme and data were collected from 8 of these flocks. A number of participants had very poor artificial insemination (AI) conception rates to the two reference sires and opted not to continue. Two further flocks were deleted from analysis because of insufficient progeny from the reference sires. Six flocks continued with the scheme in 1988 but again considerable problems with AI were encountered. Data were analysed from just two of these flocks, both of whom had participated in the scheme in 1987.

Data Recorded

Participants in the SRS were asked to record the sire, dam, birth date, sex, birth rank and weaning rank of each kid. Live weights were recorded at weaning and as yearlings. At the yearling shearing (July-August) the fleece was weighed and then analysed at the Whatawhata Fibre Laboratory for yield of down, down weight and down diameter.

TABLE 1 Overall means, range of flock means, residual standard deviations (RSD) and coefficients of variation (CV) for the live weights and fibre traits.

Trait	Number of records	Overall mean	Range of flock means	RSD	CV(%)
Weaning wt. (kg)	841	13.9	10.9-17.4	2.7	19.4
Yearling wt. (kg)	442	18.2	14.1-29.7	2.9	15.9
Fleece wt. (g)	654	258	180-375	74.4	28.8
Yield of down (%)	623	35.9	31.2-40.2	10.5	29.2
Down wt. (g)	623	93	71-139	42.6	45.8
Down diameter (micron)	624	15.8	14.9-17.7	1.0	6.3

Data Analysis

Preliminary analyses were undertaken for each trait using least squares fitting the fixed effects of flock-year, sex, birth-rearing rank, date of birth and all first order interactions. Based on these analyses paternal half-sib heritabilities were estimated for each trait using a univariate restricted maximum likelihood (REML) analysis including the significant fixed effects from the least squares analyses and sire as a random effect. The four fibre traits were also included in a multivariate REML analysis with flock-year-sex, birth-rearing rank and date of birth as fixed effects and sire as a random effect. A multivariate REML analysis including all six traits was also undertaken but, because some flocks had not recorded yearling weight, this analysis had problems with convergence. Breeding values had been estimated for each trait using a univariate reduced animal model BLUP analysis. The correlations among sire breeding values were calculated to provide another approximate estimate of genetic correlations.

RESULTS

Some basic statistics on the structure of the data set are given in Table 1. From the total of 841 kids with weaning weights recorded only 53% of these were recorded for yearling weight and 74% of those weaned had down weight and down diameter recorded. In several cases participants opted to measure fibre traits just on male kids and some participants just measured white kids because of the cost of the fibre tests (about $20 per fleece tested). The down must be less than 18.5

microns to qualify as cashmere fibre and the mean of all records at the yearling stage was 15.8 microns with a range of flock means from 14.9 to 17.7 microns.

Heritability estimates from the univariate REML analyses ranged from low to moderate for the two live weights and from moderate to high for the fibre traits (Table 2). The number of progeny per sire ranged from 6 to 165 for weaning weight and from 4 to 55 for down weight.

TABLE 2 REML paternal half-sib heritability estimates.

Trait	Heritability ± standard error[1]
Weaning weight	0.14±0.10
Yearling weight	0.22±0.15
Fleece weight	0.25±0.13
Yield of down	0.52±0.19
Down weight	0.45±0.17
Down diameter	0.79±0.23

[1] 33 sires included in each analysis, except for yearling weight where 29 sires were represented

Genetic and phenotypic correlations among the four fibre traits are given in Table 3. In all cases the heritabilities from this multivariate REML analysis were slightly higher than those estimated from univariate analyses (Table 2). However, the relativities of the size of the heritabilities did not change, with down diameter being highly heritabile (0.82±0.23) and fleece weight moderately heritable (0.31±0.14). The genetic

TABLE 3 Heritability estimates (on the diagonal - underlined), genetic correlations (below diagonal), phenotypic correlations (above diagonal) for the four fibre traits from a multivariate REML analysis.

Trait	FW	YLD	DWT	DD
Fleece weight (FW)	<u>0.31±0.14</u>	0.05	0.66	0.24
Yield of down (YLD)	0.05±0.30	<u>0.64±0.21</u>	0.70	0.32
Down weight (DWT)	0.47±0.23	0.86±0.08	<u>0.57±0.19</u>	0.42
Down diameter (DD)	0.13±0.30	0.30±0.27	0.38±0.28	<u>0.82±0.23</u>

correlation of most practical economic significance in Table 3 is that between down weight and down diameter which is positive (0.38±0.28), and therefore unfavourable if a cashmere breeder wishes to increase down weight and decrease down diameter simultaneously. This particular genetic correlation estimate is not significantly different from zero because of its large standard error. When a multivariate analysis was undertaken including weaning weight with the four fibre traits, the genetic correlation estimated between down weight and fibre diameter was then 0.63±0.17 (P<0.01).

It is possible that the estimation of the genetic correlation between down weight and diameter could be affected by deriving it from a multivariate analysis which included fleece weight and down yield because of the part-whole relationships among fleece weight, yield and down weight (D. Garrick, *pers. comm.*). This was tested by undertaking a multivariate REML analysis which just included down weight and diameter. The genetic correlation estimate was now 0.61±0.17, which is higher than the estimate of 0.38±0.28 derived from the 4 trait REML analysis but similar to the estimate from the 5 trait REML analysis which included weaning weight (0.63±0.17). The most reliable estimate of this genetic correlation from this data set is 0.61±0.17.

The phenotypic correlations among weaning weight, yearling weight, down weight and down diameter were all close to zero and ranged from -0.09 to 0.04. The genetic correlations among these same traits were all very imprecisely estimated in the multivariate REML analysis that was undertaken including all six traits. For example, the genetic correlations of yearling weight with down weight and down diameter were -0.25±0.48 and -0.35±0.44, respectively. To further investigate

the genetic associations among live weights and fibre traits correlations among sire breeding values (27 df) were calculated and are shown in Table 4. With the exception of the negative correlation in Table 4 between fleece weight and yield of down all correlations among the four fibre traits were of similar magnitude to the REML genetic correlation estimates in Table 3. The correlations in Table 4 of yearling weight with down weight and down diameter were slightly negative - i.e. -0.17 and -0.14, respectively.

DISCUSSION
Heritabilities

The original analysis of this data set, to produce breeding value estimates for participants in the SRS, involved assuming a heritability estimate for each trait for the BLUP analyses. The only heritabilities for cashmere production available in 1989 were those that had recently been estimated in Australia and which were summarised and reviewed by Pattie *et al.* (1990). Some concern was expressed about the reliability and relevance of the relatively high heritability estimates for the fibre traits estimated in Australian cashmere goats, particularly those for down weight and down diameter. It is reassuring that the heritabilities from this New Zealand data set are very similar to the Australian estimates. The heritability for yearling down diameter (0.82±0.23) appears very high but this estimate is not significantly different from the Australian estimates which range from 0.47 to 0.70.

The high heritabilities for the main down production characteristics (i.e. down weight and down diameter), in conjunction with the high phenotypic coefficients of variation (Table 1) for all fleece traits

TABLE 4 Correlations among sire breeding values (27 df) for the two live weights and the four fibre traits.

Trait	WWT	YWT	FW	YLD	DWT
Weaning weight (WWT)	1.00				
Yearling weight (YWT)	0.40	1.00			
Fleece weight (FW)	0.43	0.10	1.00		
Yield of down (YLD)	-0.14	-0.20	-0.21	1.00	
Down weight (DWT)	0.07	-0.17	0.43	0.74	1.00
Down diameter	-0.19	-0.14	0.23	0.33	0.51

except fibre diameter, indicate that there is considerable genetic variation and scope for selection.

Genetic Correlations

The use of selection indexes requires reliable estimates of genetic correlations in addition to heritabilities, phenotypic standard deviations, and relative economic values. It is generally agreed that the three most important traits for maximising financial returns for cashmere goats among those traits measured in this study are down weight, down diameter, and yearling weight (Pattie *et al.*, 1990; Ponzoni and Gifford, 1990). In addition, a complete breeding objective would also include some measure of reproductive performance (e.g. number of kids weaned per doe mated). It is again encouraging to note the consistency of the published literature estimates of genetic correlations among yearling live weight, down weight and down diameter (Pattie *et al.*, 1990). The literature estimates of genetic correlations of yearling weight with either down weight or down diameter are consistently slightly negative (range -0.06 to -0.18). With one exception, the literature estimates of the genetic correlation between down weight and diameter are equally consistent (range 0.54 to 0.77). The exception was an estimate of 0.04±0.23 reported by Gifford *et al.* (1990). However, there seems little doubt that there is a moderately high positive genetic correlation between down weight and diameter, particularly as the realised genetic correlation following divergent selection for down weight and down diameter in separate sets of selection lines was 0.54 (Restall and Pattie, 1990).

Down Yield

The importance of yield of down as either a trait in a breeding objective or as a selection criterion has not been fully evaluated. The present pricing schedules include penalties for low yield when these fall below 20%, because of effects on processing costs. In the present study yield of down had a high heritability (0.64±.21), while Australian estimates range from 0.23 to 0.90 (Pattie *et al.*, 1990). If the flock mean was particularly low for yield of down there seems little doubt it would respond to selection. However, in most flocks which have flock means for yield of down ranging from 30 to 40%, this trait could be most easily handled by independent culling levels.

If it was decided to include down yield with down weight and other traits in a multiple trait selection index then the genetic correlation between down weight and yield must be interpreted correctly. Since yield is the ratio of down weight to fleece weight there is an automatic 'spurious' positive correlation between these traits due to the part-whole relationship. The same logic applies to the positive genetic correlation between fleece weight and down weight. It is therefore not correct to suggest that fleece weight can be used as a predictor of down weight to avoid the not inconsiderable cost of dehairing the fleece to estimate down weight (e.g. Gifford *et al.*, 1990).

CONCLUSIONS

It is clear both from the results reported here, and from similar studies in Australia, that there is considerable genetic variation among Cashmere goats for the main

down production characteristics and live weight. Sufficiently precise genetic parameters are now available to allow the estimation of breeding values by using multi-trait index methods and information from relatives. However, selection for high down weight will be accompanied by increased down diameter and possibly slightly reduced live weight. Restricted selection indexes can be used to prevent these undesirable changes, but typically they reduce the potential rate of genetic increase in down weight by 25 to 50%. Difficulties and costs of measuring down weight directly by dehairing the fleece can be partly overcome by indirect selection for down length (Pattie and Restall, 1987). Down length has a strong genetic correlation (about 0.90) with down weight (Pattie and Restall, 1989; M. Bigham and R.L. Baker, *pers. comms*). No indirect selection criterion is currently available to reduce the cost of measuring down diameter. However, sequential selection procedures can reduce the expense of measuring down diameter. Pattie and Restall (1987) have presented independent culling levels and two-stage selection indexes designed to achieve this.

REFERENCES

Baker R.L.; Parratt A.C. 1987. Genetic improvement in goats: Central testing and sire referencing. *Proceedings of the Ruakura Farmers' Conference 39*: 95-98.

Gifford D.R.; Ponzoni R.W.; Simon N.J.; Ellis F.C.; Levine R.; Milne M.L. 1990. Genetic parameters for production characteristics of Australian cashmere goats. *Proceedings of the Australian Association of Animal Breeding and Genetics 8*: 461-465.

Millar P. 1986. The performance of cashmere goats. *Animal Breeding Abstracts 54*: 181-199.

Pattie W.A.; Baker R.L.; Nicoll G.B.; Restall B.J. 1990. Breeding for cashmere and mohair. *Proceedings of the 4th World Congress on Genetics Applied to Livestock Production 15*: 167-176.

Pattie, W.A.; Restall, B.J. 1987. Breeding Cashmere in Australian feral goats. *Proceedings of the 2nd International Cashmere Conference*, Lincoln, New Zealand, pp 51-67.

Pattie, W.A.; Restall, B.J. 1989. The inheritance of Cashmere in Australian feral goats. 2. Genetic parameters and breeding values. *Livestock Production Science 21*: 251-261.

Ponzoni R.W.; Gifford D.R. 1990. Developing breeding objectives for Australian cashmere goats. *Journal of Animal Breeding and Genetics 107*: 351-370.

Restall B.J.; Pattie W.A. 1990. Response to selection for down weight and diameter in Australian cashmere goats. *Proceedings of the Australian Association of Animal Breeding and Genetics 8*: 475-478.