Estimates of Genetic Parameters and Genetic Trends for Production Traits of Inner Mongolian White Cashmere Goat

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ABSTRACT : Two different animal models, which differ in whether or not taking maternal genetic effect into account, for estimating genetic parameters of cashmere weight, live body weight, cashmere thickness, staple length, fiber diameter, and fiber length in Inner Mongolia White Cashmere Goat were compared via likelihood ratio test. The results indicate that maternal genetic effect has significant influence on live body weight and cashmere thickness, but no significant influence on the other traits. Using models suitable for each trait, both genetic parameters and trends were analyzed with the MTDFREML program. Heritability estimates from single trait models for cashmere weight, live body weight, cashmere thickness, staple length, fiber diameter and fiber length were found to be 0.30, 0.07, 0.21, 0.29, 0.28 and 0.21, respectively. Genetic correlation estimates from two-trait models between live body weight and all other traits (-0.06~0.07) was negligible, as were those between fiber diameter and all other traits (-0.01~0.03) except cashmere thickness (0.19). Cashmere weight and staple length had moderate to low genetic correlations with other traits (-0.24~0.39 and -0.24~0.34, respectively) except for live body weight and fiber diameter. Cashmere thickness had a strong genetic correlation with fiber length (0.81), and low genetic correlation with other traits (0.19~0.34) except live body weight. Genetic trend analysis suggests that selection for cashmere weight was very effective, which has led to the slow genetic progress of cashmere thickness and fiber length due to their genetic correlations with cashmere weight. The selection for live body weight was not effective, which was consistent with its low inheritability. *(Asian-Aust. J. Anim. Sci. 2006. Vol 19, No. 1 : 13-18)*

INTRODUCTION

China is the largest producer of cashmere, with yields accounting for 50% the world's total production. The Inner Mongolian White Cashmere Goat (IMWG) is one of the major cashmere goat breeds in China. The cashmere produced by the IMWG is characterized by its brightness, color, elasticity, thin diameter, and feel. With the increasing demand for cashmere in domestic and foreign markets in recent years, cashmere production from the IMWG has steadily increased. To help ensure the sustainable development of the breed and the steady improvement of its performance, what we should do imminently is to unfold systemic breeding work.

The estimation of genetic parameters is an important aspect of animal breeding. However, only a few reports focus on cashmere goats (Pattie and Restall, 1989, Baker et al., 1991; Bigham et al., 1993; Bishop and Russel, 1996; Li et al., 2001; Zhou et al., 2002) and in these reports the numbers of animals in the data set were commonly small, from hundreds to thousands. In order to estimate genetic parameters, we must first construct an appropriate statistical model. For production traits, an important question is whether maternal genetic effects should be included in the model. The objective of this study is to first construct an appropriate statistical model for the production traits of the IMWG, then, using those results, obtain estimates of the various genetic parameters and analyze potential genetic trends after many years' selection.

MATERIALS AND METHODS

Animals and traits

The data used in this study was collected from the Aerbasi White Cashmere Goat Breeding Farm in Inner Mongolia, China. The farm was founded in 1984 and is the main breeding base for IMWG in Inner Mongolia. Since 1992, regular performance testing has been conducted at the farm. Between April and May each year, data are collected for cashmere weight (CW), live body weight (LBW) after shearing, cashmere thickness (CT), staple length (SL), fiber diameter (FD), and fiber length (FL). Cashmere thickness refers to the natural bending length of the fiber, while fiber length denotes the stretched unbent length. The details about the management of the animals, the measurement of the traits, and the collection of the data had been described in a previous study of Zhou et al. (2003). The characteristics of the data used in this study are summarized in Table 1.

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Table 1. Numbers of animals and records for each trait with means and standard errors

Trait[a]	No. animals with records	No. records	Mean	SE
CW (g)	5,289	12,208	529.7	4.794
LBW (kg)	5,048	11,514	28.5	0.067
CT (cm)	4,941	12,193	5.52	0.008
SL (cm)	5,274	11,854	16.86	0.035
FD (μm)	3,608	5,010	13.59	0.016
FL (cm)	3,607	5,008	9.17	0.020

[a] CW = cashmere weight, LBW = live body weight, CT = cashmere thickness, SL = staple length, FD = fiber diameter, FL = fiber length.

Statistical analysis

Statistical models : Analysis of variance (SAS GLM) was used to determine which of the systemic environmental effects had significant influence on the traits. The results indicated that sex, age, year, and flock had a significant effect on the traits. Treating these effects as fixed effects, two repeatability animal models (with and without maternal genetic effect) were used to estimate the genetic parameters and trends:

$$y = X\beta + Z_a a + Z_p P + e \qquad\qquad I$$

$$y = X\beta + Z_a a + Z_m m + Z_p P + e \qquad\qquad II$$

where y is the vector of observations, β is the vector of fixed effects with incidence matrix X, a is the vector of direct additive genetic effects with incidence matrix Z_a, m is the vector of maternal genetic effects with incidence matrix Z_m, p is the vector of permanent environmental effects with incidence matrix Z_p, and e is the vector of random residual effects. Expected values and covariance structures for random effects were assumed as follows:

$$E(y) = X\beta, E(a) = E(m) = E(p) = 0,$$
$$var(a) = A\sigma_a^2, var(m) = A\sigma_m^2, var(p) = I_p\sigma_p^2,$$
$$var(e) = I_e\sigma_e^2, cuv(a'm') = A\sigma_{am},$$
$$cov(a, p') = cov(a,e') = 0$$

where A is the numerator relationship matrix, I_e and I_p are identity matrices with orders equal to the number of animals in the pedigree and number of animals with records, respectively, σ_a^2, σ_m^2, σ_p^2 and σ_e^2 are the variance of direct additive genetic effect, maternal genetic effect, permanent environmental effect, and residual, respectively, and σ_{am} is the covariance between direct and maternal genetic effect.

Model comparison and parameter estimation : For each trait, the maximum likelihood values for the phenotypic values under the two models were calculated using MTDFREML (Boldman et al., 1995), with a criterion for iteration convergence set at 10^{-9}. To ensure that the maximum was global rather than local, different starting values were used and the corresponding maximum likelihood values were compared. Taking the largest of the values, the two models were then compared using a likelihood ratio test (Kendall and Stuart, 1979), with the test statistic as

$$LR = -2ln \frac{L_{MAX} \mid model\ I}{L_{MAX} \mid model\ II}$$

$$= [-2ln (L_{MAX}|model\ I)] - [-2ln (L_{MAX}|model\ II)]$$

where LR is the likelihood ratio value, L_{MAX}|model I and L_{MAX}|model II are the maximum likelihood values under model I and model II, respectively. It should be noted that model I is a sub-model of model II. The LR follows x^2 distribution with degrees of freedom equal to the difference between numbers of parameters to be estimated under the two models. It is easy to see that under model II two more parameters (σ_m^2 and σ_{am}) are to be estimated than under model I, leading a LR with 2 degrees of freedom. If the two models differ significantly, then the maternal genetic effect has a significant impact on the trait, and model II would represent the appropriate statistical model for the trait.

After determining suitable models for each of the traits, the estimates of the variance components were then obtained from these models. Genetic correlations were also estimated using the MTDFREML program (Boldman et al., 1995), but with two-trait models where both were suitable for the corresponding traits.

Genetic trend analysis : Estimates of breeding values were obtained under models suitable for each trait, with the averages of estimates of breeding values in the birth year used as measurement of genetic trend.

RESULTS AND DISCUSSION

Comparisons of different models

For live body weight and cashmere thickness, highly significant difference (p<0.01) between model I and model II was found (the LR values were 41.34 and 15.91, respectively), indicating that the maternal genetic effect was significant for both traits, although more so for live body weight. For cashmere weight, staple length, fiber diameter, and fiber length, no significant difference (p>0.05) between the two models was observed (the likelihood ratios were 5.66, 4.73, 0.002, and 0.99, respectively), implying that maternal genetic effect had little impact on the four traits. The results obtained here are similar to those of Bishop and Russel (1996) who analyzed the inheritance of fiber traits in a crossbred population of cashmere goats where animal body weight was affected by maternal genetic effect, while fiber diameter and fiber length were not.

Table 2. Estimates of variance components based on single-trait models[a]

Trait	Model	σ_a^2/σ_y^2	σ_m^2/σ_y^2	σ_p^2/σ_y^2	σ_e^2/σ_y^2	r_{am}
CW	I[b]	0.30		0.15	0.55	
	II	0.28	0.02	0.15	0.55	0.08
LBW	I	0.10		0.31	0.59	
	II[b]	0.07	0.07	0.27	0.60	-0.19
CT	I	0.20		0.14	0.66	
	II[b]	0.21	0.03	0.12	0.66	-0.23
SL	I[b]	0.29		0.31	0.40	
	II	0.33	0.01	0.28	0.40	-0.39
FD	I[b]	0.28		0.09	0.63	
	II	0.28	0.00	0.08	0.63	-0.98
FL	I[b]	0.21		0.21	0.58	
	II	0.19	0.01	0.21	0.59	-0.09

[a] σ_y^2 = phenotypic variance; σ_a^2 = direct additive genetic variance; σ_m^2 = maternal genetic variance; σ_p^2 = individual permanence environmental variance; σ_e^2 = residual variance; r_{am} = correlation between direct additive and maternal genetic effect.

[b] Suitable model for this trait.

Estimates of genetic parameters under single-trait model

Estimates of variance components (expressed as ratio to phenotypic variance) of each trait obtained under their suitable models are given in Table 2. Estimates obtained under the other model are also listed for comparison. From Table 3 we can see that, in general, the heritability (h^2), ratio of permanent environmental variance to phenotypic variance (σ_p^2/σ_y^2), and ratio of residual variance to phenotypic variance (σ_e^2/σ_y^2) estimated under the two different models show little difference. The permanent environmental effect accounts for a large proportion in all of the traits, while the maternal genetic effect accounting for some proportion of live body weight ($\sigma_m^2/\sigma_y^2 = 0.07$) and cashmere thickness ($\sigma_m^2/\sigma_y^2 = 0.03$), in consist with the results presented in Table 2.

To compare our estimates of heritability with those from other studies, the results from them are summarized in Table 3. Obviously, our estimates for each trait are close to those from Li et al. (2001) and Zhou et al. (2002), but lower than those from other studies. These may happen because of the differences in the genetic structure of different breeds, the definitions of the traits, the models used for analysis, and the environment the population subjected to. It should be noted that the number of animals included in the data used in our study is far more than those in other studies.

**Table 3.** Summary of estimates of heritability from different studies

Resource	Breed	Method	Traits			
			CW	LBW	FD	FL
Our study	Inner mongolia white cashmere goat	REML	0.30	0.07	0.28	0.21
Pattie and Restall (1989)	Australian cashmere ggoat	half-sib analyses	0.61	0.28	0.47	0.70
Baker et al. (1991)	New Zealand cashmere ggoat	REML	0.57		0.82	
Bigham et al. (1993)	New Zealand cashmere goat	REML	0.62	0.39	0.99	0.57
Bishop and Russel (1996)	Crossbred cashmere ggoat	REML	0.28	0.35	0.61	0.43
Bishop and Allain (2000)	Scotland cashmere goat	REML	0.59	0.25	0.64	0.57
Li et al. (2001)	Inner mongolia white cashmere goat	half-sib analyses	0.26	0.16	0.14	0.15
Zhou et al. (2002)	Inner mongolia white cashmere goat	REML	0.28	0.10	0.32	0.23

Table 4. Estimates of genetic correlations from bivariate-trait model

Trait 1[a]	Trait 2[a]	r_a	r_m	r_{a1m2}	r_{a2m1}	r_p	r_e
CW	LBW	-0.06		0.01		0.25	0.18
	CT	0.39		0.02		0.45	0.27
	SL	-0.24				-0.08	0.09
	FD	0.03				0.51	0.04
	FL	0.25				0.31	0.18
LBW	CT	-0.03	-0.16	0.22	-0.29	0.09	0.17
	SL	0.07			-0.27	0.03	0.12
	FD	0.03			-0.08	0.31	0.01
	FL	0.04			-0.43	-0.19	0.18
CT	SL	0.34			0.03	0.30	0.22
	FD	0.19			0.15	0.31	0.06
	FL	0.81			0.36	0.86	0.15
SL	FD	0.09				-0.28	0.01
	FL	0.27				0.11	0.06
FD	FL	-0.01				0.43	-0.06

Table 5. Comparison of estimates of genetic correlations among four traits obtained from different studies

Trait 1[a]	Trait 2[a]	Our study	Pattie and Restall (1989)	Baker et al. (1991)	Bigham et al. (1993)	Bishop and Russel (1996)	Bishop and Allain (2000)	Li et al. (2001)	Zhou et al. (2002)
CW	LBW	-0.06	-0.18		-0.34	0.13	0.03	-0.19	0.25
	FD	0.03	0.62	0.61	0.81	0.83	0.79	0.35	0.02
	FL	0.25	0.87		0.92	0.76	0.84	-0.20	0.36
LBW	FD	0.03	-0.06		-0.25	0.03	0.03	0.32	0.41
	FL	0.04	-0.31		-0.32	0.02	0.02	-0.18	0.18
FD	FL	-0.01	0.51		0.75	0.60	0.60	-0.31	-0.19
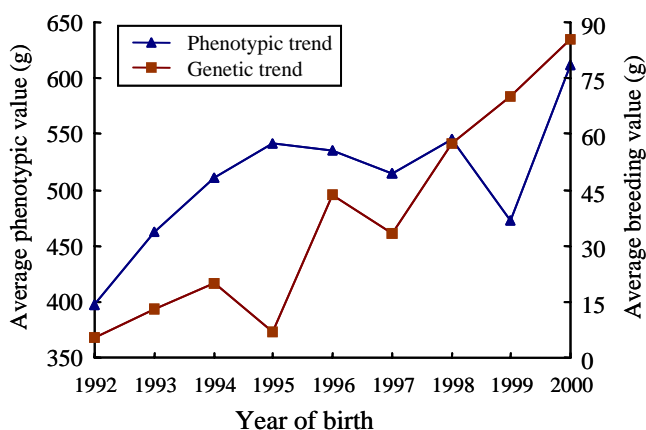
Figure 1. Phenotypic and genetic trend of cashmere weight.
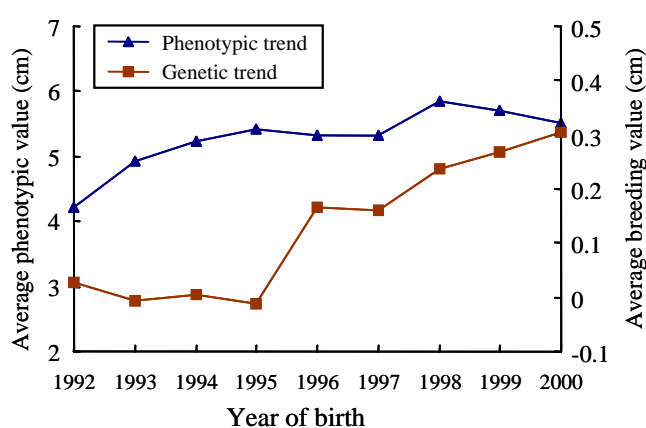
Figure 3. Phenotypic and genetic trend of cashmere thickness.
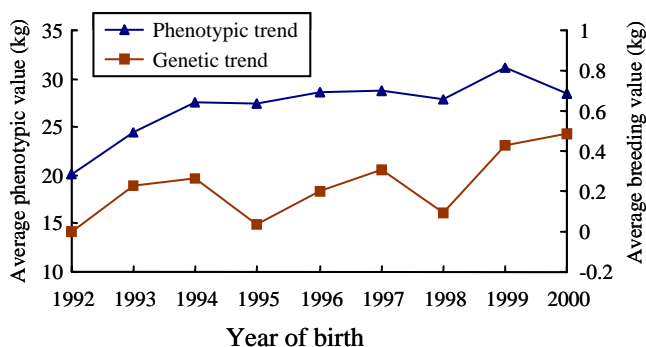
Figure 2. Phenotypic and genetic trend of live body weight.

Genetic correlations estimated under bivariate-trait model

Genetic correlations between any two traits were estimated using a bivariate-trait model, in which both models were suitable for the corresponding traits. The results are presented in Table 4. Generally, the genetic correlations among these traits were low ($|r_a|<0.40$) except that between cashmere thickness and fiber length, for which a strong genetic correlation (0.81) was observed. Particularly, the genetic correlations between live body weight and all of the other traits (-0.06-0.07) were nearly negligible. The same were observed between fiber diameter and the other traits (-0.01-0.09) with the exception of cashmere thickness (0.19).

For comparison, estimates of genetic correlations among the four production traits obtained from this and other studies are summarized in Table 5. The results differ markedly except for the genetic correlation between body weight and all other traits, which was generally low to negligible. The largest differences are in the estimates of genetic correlations between cashmere weight and fiber diameter and between fiber diameter and fiber length, where the estimates of ours and Zhou et al. (2002) were very low or nearly zero, while the estimates from other studies were relatively high (0.61-0.83 and 0.51-0.75, respectively). Again, these differences may be due to the differences in the genetic structure of different breeds, the sample size, the definitions of the traits, the models used for analysis, and the environment the population subjected to.

Estimates of phenotypic and genetic trend

Phenotypic and genetic trend from 1992 to 2000 for the 6 traits are illustrated in Figures 1-6. For cashmere weigh (Figure 1), the total increase over the nine-year time span for phenotypic and genetic levels was about 200 g and 80 g, respectively. In general, selection for cashmere weight was effective, and significant genetic improvement was obtained. For live weight body (Figure 2), a slow increase was observed in the phenotypic level, likewise little if any change in the genetic level. Although live body weight was one of the major selection traits in the population, little genetic improvement was obtained. This could be due to the low heritability (0.07) of live body weight. For cashmere
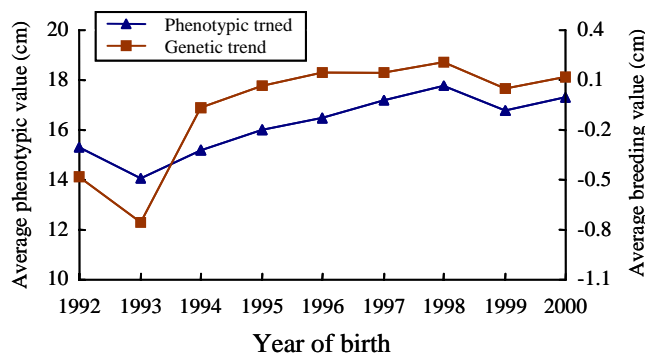
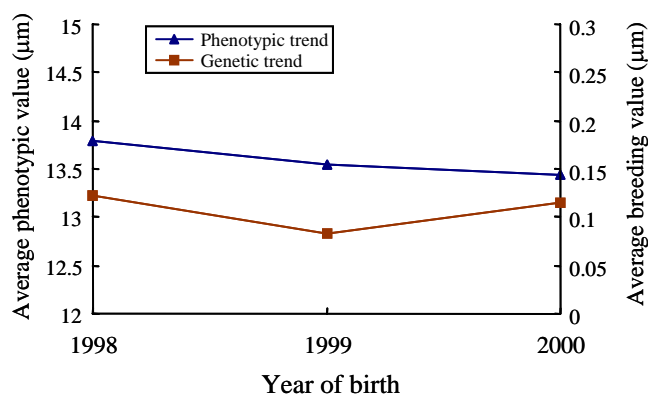**Figure 4.** Phenotypic and genetic trend of staple length.

Figure 5. Phenotypic and genetic trend of fiber diameter.

Figure 6. Phenotypic and genetic trend of fiber length.

breeding value increased about 0.15 cm. This may have resulted from the slight positive genetic correlation (0.26) between fiber length and cashmere weight.

IMPLICATIONS

Results of this study suggest that maternal genetic effect is not significant for cashmere weight, staple length, fiber diameter, and fiber length, but is highly significant for live body weight and cashmere thickness. Using models suitable for each trait to estimate genetic parameters, the results were quite different from those obtained in other studies. One very interesting difference was that the strong genetic correlation between cashmere weight and fiber diameter found in other studies wasn't found in this study. This could indicate that fiber does not necessarily become thicker with the increase in cashmere weight, which is in favor of genetic improvement for the two traits. The analysis for genetic trend shows that selection for cashmere weight was very effective, leading to slow genetic progress in cashmere thickness and fiber length. Of special interest was that fiber didn't become thicker with increases in cashmere weight. Further, the selection for live body weight was not effective, which was consistent with its low estimated heritability.

thickness (Figure 3), a slow ascending trend happened both at the phenotypic and the genetic levels. The total increase over the nine-year period was about 1 cm and 0.3 cm for the phenotypic and genetic levels, respectively. The genetic trend for cashmere thickness was similar to that observed for cashmere weight, possibly due to the relatively higher genetic correlation (0.39) between the two. For staple length (Figure 4), the phenotypic and genetic change showed similar patterns with slow ascending trends. The total increase over the nine-year period in phenotypic and genetic level was 2 cm and 0.7 cm, respectively. Staple length has little economic value in cashmere goats, and was not considered in the breeding program. This has led to a slow gentle change in this trait. For fiber diameter (Figure 5), data for only three years was collected. During that time, there was a slow decrease (about 0.3 cm in total) in the phenotypic level, with almost no change in the genetic level. Although the genetic correlation between fiber diameter and cashmere weight has been found to be high in other studies, it was barely visible in this study. Even though there was a significant increase in cashmere weight, the fiber didn't become thicker, which is just what we want. For fiber length (Figure 6), again data for only three years was available. During that time, the phenotypic and genetic trend changed in reverse direction. The average phenotypic value decreased about 0.11 cm, whereas the average
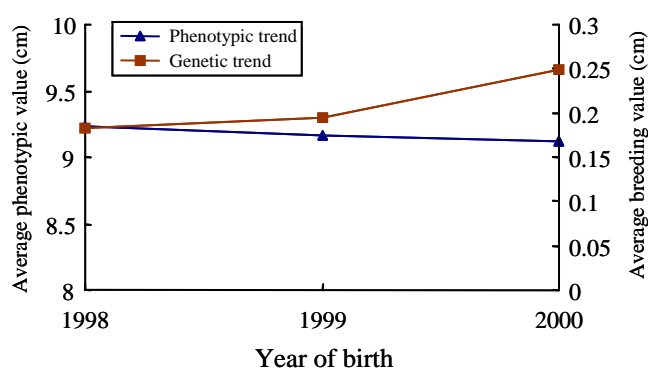
REFRECENCES

Baker, R. L., B. R. Southey, M. L. Bigham and S-A. N. Newman. 1991. Genetic parameters for New Zealand cashmere goats. Proceedings of the New Zealand Society of Animal Production. 51:423-428.

Bigham, M. L., C. A. Morris, B. R. Southey and R. L. Baker. 1993. Heritabilities and genetic correlation for live weight and fiber traits in New Zealand cashmere goats. Livest. Prod. Sci. 33:91-104.

Bishop, S. C. and D. Allain. 2000. Selection for fiber production in Angora and Cashmere goats. Proceedings of the 7th International Conference on Goats, Tours, France. 1:197-202.

Bishop, S. C. and A. J. F. Russel. 1996. The inheritance of fiber traits in a crossbred population of cashmere goats. Anim. Sci. 63:429-436

Boldman, K. G., L. A. Kriese, L. D. Van Vleck, C. P. Van Tassell

and S. D. Kachman. 1995. A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances. US Department of Agriculture. Agricultural Research Service.

Kendall, M. and A. Stuart. 1979. The Advanced Theory of Statistics. Vol. 2. Inference and Relationship. 4th ed. Macmillan, NY.

Li Jinquan, Wang Feng, Yin Jiun, Liu Shaoqing, Zhang Yongbin, Zhao Congfa and Wulan Bateer. 2001. Study on genetic parameters for several quantitative traits of Inner Mongolia Cashmere Goats. Hereditas, 23(3):211-216.

Pattie, W. A. and B. J. Restall. 1989. The inheritance of cashmere in Australian goats. 2. genetic parameters and breeding values. Livest. Prod. Sci. 21:251-261.

Zhou, H. M., D. Allain, J. Q. Li, W. G. Zhang and X. C. Yu. 2003. Effects of non-genetic factors on production traits of Inner Mongolia cashmere goats in China. Small Rum. Res. 47:85-89.

Zhou, H. M., D. Allain, J. Q. Li, W. G. Zhang and X. C. Yu. 2002. Genetic parameters of production traits of Inner Mongolia cashmere goats in China. J. Anim. Breed. Genet. 119:1-6.