



Estimation of Genetic Parameters for Wool Traits in Angora Rabbit

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ABSTRACT : Different genetic parameters for weaning weight and wool traits were estimated using restricted maximum likelihood (REML) in Angora rabbits. Total wool yield of first (I), second (II) and third (III) clips were taken as a separate trait under study. The records from more than 2,700 animals were analysed through fitting six animal models with various combinations of direct and maternal effects. A log likelihood ratio test was used to select the most appropriate model for each trait. Direct heritability estimates for the wool traits were found to be moderate to high across different models. Heritability estimates obtained from the best model were 0.24, 0.22, 0.20 and 0.21 for weaning weight, clip I, II and III; respectively. Maternal effects especially due to permanent environment had higher importance at clip I and found to be declining in subsequent clips. The estimates of repeatability of doe effect on wool traits were 0.44, 0.26 and 0.18 for clip I, II and III; respectively. Weaning weight had moderately high genetic correlations with clip I (0.57) and II (0.45), but very low (0.11) with clip III. Results indicated that genetic improvement for wool yield in Angora rabbit is possible through direct selection. Further, weaning weight could be considered as desirable trait for earliest indirect selection for wool yield in view of its high genetic correlation with wool traits. (**Key Words :** Angora Rabbit, Animal Model, Heritability, Maternal Effect, REML)

INTRODUCTION

Angora wool is third largest animal fibre produced, after sheep wool and mohair, with annual world production of about 8,500 tons. Presently, China dominates the International Angora wool market and contributes about 90% to the total world production of Angora wool (Schlink and Liu, 2003). India is marginal producer of Angora wool with estimated annual production of about 30-40 tons. Angora wool production is the most important economic trait in Angora rabbits and appears to be affected by a number of genetic as well as non genetic factors (Thebault et al., 1992; Allain et al., 1999; Katoch et al., 1999). Heritability estimates as genetic parameters for different wool traits in Angora rabbit are reported to be low to moderate (Garcia and Magofke, 1982; Caro et al., 1984; Allain et al., 1999; Katoch et al., 1999). Further, wool traits could be improved by direct and indirect selection methods in Angora rabbits (Allain et al., 2004; Rafat et al., 2007, 2008). Initial wool clips were found important in early

selection, due to their high genetic correlation with latter clips (Rafat et al., 2009) and significant genetic correlation exists between wool yield and corresponding body weight in Angora rabbits (Jelinek et al., 1980; Garcia and Magofke, 1982; Singh et al., 2006). Likewise, correlated responses for body weight after selection for fleece yield in Angora rabbits have been observed experimentally (Qinyu, 1992; Rafat et al., 2008). Animal models using Derivative Free Restricted Maximum Likelihood (DFREML) procedure are widely used to estimate the genetic parameters for different economic traits in livestock. However, there is limited information available on applicability of such an animal model procedure for wool traits (Rafat et al., 2009) and growth traits (Niranjana et al., 2010) in Angora rabbit. The objective of this study was, therefore, to estimate genetic components for wool traits using DFREML procedure with various combinations of direct and maternal effects in German Angora rabbit reared under sub-temperate Himalayan conditions.

MATERIALS AND METHODS

Different records of wool traits (Clip I, II and III) and weaning weight for German Angora rabbit were obtained for a period of nine years (2001 to 2009). About 40 to 60

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breeding females were maintained every year in a closed type flock, with a male to female breeding ratio of 1:5. Animals after weaning at 42 d of age were kept individually in all wire cages of standard dimensions under similar housing and management conditions. Rabbits were fed concentrate, containing 15 to 20% crude protein, in graded quantity from 30 to 140 g at different ages and seasonal grasses *ad libitum* (Bhatt and Sharma, 2009). Records of weaning weights were obtained at 42 d of age; whereas of clip I was obtained at 52 d of age and subsequent clips (II and III) after regular intervals of 75 days. Animals were sheared manually with scissors exactly on the defined day. The characteristics of the data structure are summarized in Table 1.

Initially, the data were analysed by least squares analysis of variance (SPSS, 2005) to identify the fixed effects with significance ($p < 0.05$) and such effects were included in the model(s). Further, (Co)variance components were estimated by DFREML (Meyer, 2000). Six different single-trait linear models, which accounts for different combinations of the direct and maternal effects were initially fitted for each trait.

$$\text{Model 1: } y = X\beta + Z_a a + \varepsilon$$

$$\text{Model 2: } y = X\beta + Z_a a + Z_m m + \varepsilon \\ \text{with Cov}(a_m, m_o) = 0$$

$$\text{Model 3: } y = X\beta + Z_a a + Z_m m + \varepsilon \\ \text{with Cov}(a_m, m_o) = A\sigma_{am}$$

$$\text{Model 4: } y = X\beta + Z_a a + Z_{pe} pe + \varepsilon$$

$$\text{Model 5: } y = X\beta + Z_a a + Z_m m + Z_{pe} pe + \varepsilon \\ \text{with Cov}(a_m, m_o) = 0$$

$$\text{Model 6: } y = X\beta + Z_a a + Z_m m + Z_{pe} pe + \varepsilon \\ \text{with Cov}(a_m, m_o) = A\sigma_{am}$$

Where:

y is a vector of animal record for weaning weight, clip I, II and III yields,

β is a vector of fixed effects for the trait consisting of

sex (2 levels), year of birth (9 levels) and season of birth (4 levels: January-March, April-June, July-September, October-December),

a is a random vector of direct additive genetic effects of animal for the trait,

m is a random vector of maternal additive genetic effect of animal for the trait,

pe is a random vector of permanent environmental effect of dam for the trait,

ε denotes vector of residual effect.

The X , Z_a , Z_m and Z_{pe} are association matrices and A is the numerator relationship matrix between animals. The σ_{am} denotes the covariance between direct additive genetic and maternal genetic effects. Assumptions for variance (V) and covariance (Cov) matrices involving random effects were

$$V(a) = A\sigma_a^2, V(m) = A\sigma_m^2, V(c) = I\sigma_c^2, \\ V(e) = I\sigma_e^2, \text{ and } Cov(a,m) = A\sigma_{am}$$

Where, I is an identity matrix and σ_a^2 , σ_m^2 , σ_c^2 and σ_e^2 are additive direct, additive maternal, maternal permanent environmental and residual variances, respectively. Different genetic parameters *viz.* direct (additive) heritability (h^2), total heritability (h^2_t), maternal genetic heritability (m^2), maternal permanent environment (c^2), direct maternal correlation (r_{am}) and maternal repeatability for doe performance across the year (t_m) were estimated as per standard formula (Niranjan et al., 2010). Most suitable univariate model was identified by Likelihood ratio test (LRT) for each trait (Meyer, 1992). Differences in log-likelihood for the two models were compared for significance level ($p < 0.05$) by chi-square distribution and the degree of freedom considered was equal to the difference in the number of (co)variance components of these models.

In bivariate analysis for the estimation of genetic correlations between two traits, the best models from the single trait analysis were combined with appropriate covariance between random effects in the model. Estimates of genetic, phenotypic and environmental correlation between different economic traits were obtained by REML using a derivative free algorithm fitting an animal model DFREML (Meyer, 2000).

Table 1. Data structure for weaning wt. and wool traits of German Angora

Record/parameter	Weaning weight	Clip I	Clip II	Clip III
No. of records	2,738	2,704	2,491	2,326
Sires with progeny records	148	148	146	146
Dams with progeny records	354	354	352	349
Least squares mean of trait (g)	717.43	22.01	90.13	148.34
Standard deviation (g)	165.12	6.60	20.94	25.50
Coefficient of variation (%)	22.15	26.11	18.59	13.62

RESULTS AND DISCUSSION

Least squares means along with the standard deviation (SD) and percent coefficient of variation for weaning weight and wool traits under study are given in Table 1.

(Co)variance components and genetic parameters estimated by different models for wool traits are presented in Table 2. The most appropriate model, which included direct additive and permanent environmental effects of the dam for traits under study, was model-4 according to likelihood ratio test.

Table 2. Estimates of (co)variance components (in gm²) and genetic parameters for Clip I, II and III

Trait	Estimates	Model-1	Model-2	Model-3	Model-4	Model-5	Model-6
CLIP I	σ_a^2	13.40	8.81	13.89	8.05	8.05	13.61
	σ_m^2	-	24.35	30.73	-	0.31	4.74
	σ_{am}	-	-	-9.71	-	-	-7.63
	σ_c^2	-	-	-	14.23	13.97	14.26
	σ_e^2	19.60	14.72	12.04	15.00	15.00	12.06
	σ_p^2	33.01	47.88	46.94	37.28	37.33	37.03
	h^2	0.41±0.04	0.18±0.04	0.30*	0.22±0.04	0.22±0.04	0.37*
	m^2	-	0.51±0.03	0.65*	-	0.01±0.04	0.13*
	r_{am}	-	-	-0.47*	-	-	-0.95*
	c^2	-	-	-	0.38±0.03	0.37±0.04	0.39*
	h_t^2	0.41	0.44	0.31	0.22	0.23	0.12
	t_m	0.10	0.56	0.52	0.44	0.44	0.40
	log L	-6,205.78	-6,355.69	-6,346.42	-6,008.79	-6,330.26	-6,319.06
CLIP II	σ_a^2	116.13	56.32	64.20	54.50	51.27	65.42
	σ_m^2	-	80.15	89.02	-	19.42	31.38
	σ_{am}	-	-	-18.84	-	-	-32.92
	σ_c^2	-	-	-	58.65	43.99	50.57
	σ_e^2	164.64	165.60	162.11	164.61	165.86	158.88
	σ_p^2	280.77	302.07	296.49	277.75	280.54	273.33
	h^2	0.41±0.05	0.19±0.06	0.22*	0.20±0.06	0.18±0.001	0.24*
	m^2	-	0.27±0.04	0.30*	-	0.07±0.02	0.11*
	r_{am}	-	-	-0.25*	-	-	-0.73*
	c^2	-	-	-	0.21±0.03	0.16±0.02	0.19*
	h_t^2	0.41	0.33	0.27	0.20	0.22	0.12
	t_m	0.10	0.32	0.29	0.26	0.28	0.24
	log L	-8,387.69	-8,647.12	-8,646.35	-8,323.91	-8,638.23	-8,635.00
CLIP III	σ_a^2	143.51	72.32	87.76	83.19	78.15	97.88
	σ_m^2	-	74.37	91.82	-	23.33	34.36
	σ_{am}	-	-	-27.62	-	-	-29.17
	σ_c^2	-	-	-	51.44	35.41	40.79
	σ_e^2	264.90	275.16	267.00	268.95	270.86	260.41
	σ_p^2	408.42	421.88	418.96	403.58	407.75	404.28
	h^2	0.35±0.05	0.17±0.06	0.21*	0.21±0.06	0.19±0.06	0.24*
	m^2	-	0.18±0.04	0.22*	-	0.06±0.06	0.09*
	r_{am}	-	-	-0.31*	-	-	-0.50*
	c^2	-	-	-	0.13±0.03	0.09±0.05	0.10*
	h_t^2	0.35	0.26	0.22	0.21	0.22	0.17
	t_m	0.09	0.22	0.21	0.18	0.20	0.18
	log L	-8,288.38	-8,527.02	-8,526.17	-8,262.75	-8,530.48	-8,529.37

Column in bold represents estimates from best model as per LRT.

* Indicates that the approximation used to define standard errors of parameter estimates failed.

Weaning weight

For weaning weight trait, model 4 was found best among six LRT based models (Data not shown). Estimates for additive direct (σ_a^2), maternal permanent environmental (σ_c^2), residual variance (σ_e^2) and phenotypic (σ_p^2) variances were 6514.94, 8528.26, 12275.44, and 27318.64; respectively for best model. Direct heritability (h^2) estimate for the weaning weight ranged from moderate (0.20) to high (0.41) for different models. However, it was moderate (0.24) for the model 4 and consistent to recorded previously (Niranjan et al., 2010). It makes the weaning weight a trait of choice for moderate genetic improvement through selection. Moderately high maternal permanent environment effect ($c^2 = 0.31$; model 4) indicated the importance of maternal care during early age in Angora rabbits. Similarly, high repeatability of doe performance ($t_m = 0.37$; model 4) increases the scope of selection for improvement in weaning weight trait through dam side and corroborate with earlier findings (Niranjan et al., 2010).

Clip yield

Analysis for the (co)variance components estimates of the clips (I, II and III) is presented in the Table 2. The direct heritability (h^2) estimates from all the models ranged from 0.18 to 0.41 for clip I and II and 0.17 to 0.35 for clip III; respectively. From the most appropriate model 4, however, moderate estimates of heritability for clip I (0.22 ± 0.04), II (0.20 ± 0.06) and III (0.21 ± 0.06) were found and were in agreement to moderate estimates derived from REML (Allain et al., 1999) and ASREML (Rafat et al., 2009) animal models in French Angora. Consistency in h^2 indicates about the maintenance of the genetic variability in latter clips, also. Moderate heritability estimates for clip I and II, and low for clip III (Garcia and Magofke, 1982) and contrastingly, very low (0.09) and very high (0.96) heritability estimates for clip I, II, and III in German Angora (Caro et al., 1984; Katoch et al., 1999) have also been recorded.

Maternal permanent environmental had an important effect on clip yields. Estimates of maternal permanent

environment (c^2) varied across the age, however with progressive decline. For best model (4), the c^2 estimate was found highest for clip I (0.38), which reduced to 0.13 for clip III. Similar decline for the m^2 across all the models was also observed. Estimates indicated that maternal effect was the maximum in clip I and decreased in subsequent clips with advancement of age. These observations were consistent to the higher maternal genetic heritability and permanent environment effect for growth traits in Angora rabbit (Niranjan et al., 2010). Results indicated the importance of the maternal genetic effect, as it accounts for significant portion of the total genetic variance. Study revealed a higher importance of maternal effect over additive genetic effect on the wool traits similar to growth traits in Angora rabbits (Niranjan et al., 2010). Estimates of h^2 , m^2 and c^2 , obtained from the more inclusive model (5) were 0.22, 0.01 and 0.37 for clip I; 0.18, 0.07 and 0.16 for clip II, and 0.19, 0.06 and 0.09 for clip III, respectively. However as per LRT, model 4 was significantly ($p < 0.05$) superior to all other models for all the wool traits. Estimates of r_{am} were high and negative for all the wool traits under study and were similar to early growth traits in German Angora (Niranjan et al., 2010). Negative σ_{am} could arise from genes having antagonistic pleiotropic effects on maternal performance and wool trait (Wilson and Reale, 2006). Total heritability estimates were also moderate in magnitude for all three clips using model 4, indicating scope for further genetic improvement in the trait. Similarly, estimates for t_m were 0.44, 0.26 and 0.18 for clip I, II and III; respectively. Moderate repeatability of the doe performance for wool traits in Angora rabbit indicate for further improvement through maternal selection.

Correlation estimates:

The most appropriate models (Model 4) from the single trait analyses for Clip I, II, III and weaning weight were used for bivariate analysis for estimation of genetic, phenotypic, and environmental correlations between different economic traits of Angora rabbit (Table 3). Estimate for direct genetic correlation between weaning

Table 3. Correlation estimates for Weaning wt., Clip I, II and III

Trait	Weaning weight	Clip I	Clip II	Clip III
Weaning weight		0.57±0.09 (1.00±0.01)	0.45±0.10 (1.00±0.03)	0.11±0.12 (1.00±0.95)
Clip I	0.73±0.01 (0.62±0.03)		0.39±0.15 (0.50±0.07)	-0.04±0.17 (0.27±0.10)
Clip II	0.48±0.01 (0.45±0.06)	0.44±0.01 (0.45±0.04)		0.30±0.17 (0.24±0.11)
Clip III	0.22±0.01 (0.26±0.04)	0.20±0.01 (0.28±0.04)	0.43±0.01 (0.52±0.03)	

Above the diagonal: genetic and permanent environmental (in parenthesis) correlations; value±SE.

Below the diagonal: phenotypic and residual (in parenthesis) correlations; value±SE.

weight and clip I was highest (0.57), however, it decreased in subsequent clips (0.45 in clip II and 0.11 in clip III). In similar study, Garcia and Magofke (1982) had observed abrupt decrease in genetic correlation of body weight at 65 d age with clip yields (I, II and III). Higher genetic correlation of weaning weight with initial two clips suggested that animals with above average weaning weight would tend to be above average in genetic merit for these clips. Thereby, it indicates that indirect selection for these clips on the basis of weaning weight is possible, as a high correlation between the body weight and wool production exists in Angora rabbits (Qinyu, 1992; Singh et al., 2006). Genetic correlation of clip I with clip II was moderate (0.39) and comparable to the earlier estimate (0.41) in Angora rabbits (Jaitner et al., 1988). While, the genetic correlation between clip I and III of German Angora was negative and the phenotypic correlation was positive and low (0.20). Similarly, a very low (close to zero) genetic correlation between clip I and clip III and others had been estimated in French Angora (Rafat et al., 2009). This possibly indicates that genetic factors determining clip I are different to those which determine clip III. The observation is in concurrence with the facts that clip traits are affected by different additive genes and the hair follicle development in the rabbit is not complete at the age when first shearing occurs (Rougeot et al., 1984; Rafat et al., 2009). The estimate of genetic correlation between clip II and III was moderate (0.30) and comparable to earlier estimate (0.26) in German Angora breed (Jaitner et al., 1988). Estimates of maternal permanent environmental correlation of weaning weight and wool traits were high and positive. However, these estimates were moderate (clip I and II) and low (clip I and III, clip II and III) among different clips. Decreasing permanent environmental effects of the dam indicates about depleting influence of maternal effects on clips at latter age. Estimates for phenotypic correlation between different traits were positive and low to high and were similar to the residual correlation estimates for the respective traits.

CONCLUSIONS

The heritability estimates for wool clips (I, II and III) trait in Angora rabbits were moderate and consistent. There was high genetic correlation between weaning weight and clip I, however, it decreased progressively in subsequent clips. Moderate genetic improvement is possible through selection on the basis of initial clips particularly clip I due to higher h^2 estimate. Further, selection of the Angora rabbits is possible earliest at weaning age, considering higher estimates of h^2 for weaning weight and higher genetic correlation with wool traits.

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