

DIRECT AND MATERNAL (CO)VARIANCE COMPONENTS AND GENETIC PARAMETERS FOR GROWTH TRAITS OF DORPER SHEEP IN SEMI-ARID KENYA

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ABSTRACT

Genetic and phenotypic parameters for lamb growth traits for the Dorper sheep were estimated from data obtained from the Sheep and Goats Station in Naivasha, Kenya. Traits considered were body weights at birth (BW0, kg), at 1 month (BW1, kg), at 2 months (BW2, kg), at weaning (WW, kg), at 6 months (BW6, kg), at 9 months (BW9, kg) and at yearling (YW, kg), average daily gain from birth to 6 months (ADG0–6, gm) and from 6 months to 1 year (ADG6–12, gm). Direct heritability estimates were, 0.18, 0.36, 0.32, 0.28, 0.21, 0.14, 0.29, 0.12 and 0.30 for BW0, BW1, BW2, WW, BW6, BW9, YW, ADG0–6 and ADG6–12, respectively. The corresponding maternal genetic heritability estimates for body weights up to 9 months were 0.16, 0.10, 0.10, 0.19, 0.21 and 0.18. Direct maternal genetic correlations were negative and high ranging between -0.47 to -0.94. Negative genetic correlations were observed for ADG0–6 and ADG6–12, BW2 and ADG6–12, WW and ADG6–12 and BW6 and ADG6–12. Phenotypic correlations ranged from 0.15 to 0.96. Maternal effects are important in the growth performance of the Dorper sheep though a negative correlation exists between direct and maternal genetic effects. The current study has provided important information on the extent of additive genetic variation in the existing flocks that could now be used in determining the merit of breeding rams and ewes for sale to the commercial flocks. The estimates provided would form the basis of designing breeding schemes for the Dorper sheep in Kenya.

Keywords: Annual trends; Dorper sheep; (Co)variance components; Genetic parameters; Growth traits

INTRODUCTION

The Dorper sheep breed, first introduced in Kenya in 1952, is widely adopted within pastoral/extensive and smallholder production systems due to its desirable growth potential and good mothering ability (Kiriro 1994; Kosgey et al. 2008). It is popularly crossbreed with the local Red Maasai breed for improved growth and reproductive efficiency (Kiriro 1994). In recognition of its productive potential, the Government of Kenya in collaboration with Food and Agriculture Organisation/United Nations Development Programme (FAO/UNDP) initiated a project in 1970 for genetic improvement of the Dorper and the Red Maasai sheep (Kiriro 1994). This programme involved both within breed selection and crossbreeding with the aim of combining the desirable attributes in the two breeds.

Continued genetic improvement of the Dorper sheep would be achieved through efficient management and enhancement of the program. The initial step in implementing a knowledge based genetic improvement program is accurate estimation of genetic and phenotypic parameters. Genetic parameters for growth traits of Dorper sheep using data from the Sheep and Goat Station (SGS) - Naivasha have previously been presented (Inyangala et al. 1992; Kiriro 1994). In those studies, it was assumed that there was no relationship between the dams and that the sires were mated randomly to the dams.

However, with regard to the mating structure at the station, sires were usually assigned to particular dams. Furthermore, maternal effects were not effectively accounted for in the evaluation of growth traits in those studies, a fact that has been acknowledged to result in overestimation of genetic parameters (Maniatis and Pollot 2002; Zamani and Mohammadi 2008). The objective of the current study was to estimate (co)variance components, genetic and phenotypic and parameters for the Dorper sheep breed under semi-arid conditions in Kenya. Implications of the study to future sheep breeding programmes are also discussed.

MATERIALS AND METHODS Data sources, flock management, selection and breeding

Data on growth performances of purebred Dorper sheep were obtained from the SGS-Naivasha- a government farm. The station is located approximately 100 km North West of Nairobi at an altitude of 1,829–2,330 m above sea level in agroecological zone IV classified as semi-arid (Kiriro 1994). The vegetation consists mainly of Kikuyu grass (*Pennisetum clandestinum*) with scattered trees of Acacia species. The average rainfall is 680 mm per annum. Rainfall distribution is bimodal with a peak in April and November. The average minimum and maximum temperatures are 8°C and 26°C, respectively. The relative humidity varies from 60% to 75%. The Station maintains two farms, Ol'Magogo and Top Farm, which are approximately 20 km apart. Animals were grazed on natural pastures during the day in both farms. Selection of parents for the next generation was based on weight of the animals and their physical conformity to breed type. Ewes were mated in April–May and October– November seasons to lamb in August–September and February–March seasons, respectively. Ewes were first joined to rams depending on their weight and the youngest age at first mating was 18 months. Lambs ran with the dams up to 3 months when they are weaned. Nursing dams were not supplemented with concentrates but all animals were provided with mineral licks and water ad libitum. All animals are routinely weighed at birth, months 1, 2, 3, 6, 9 and

12. Disease and parasite management was mainly prophylactic through regular dipping, drenching and vaccinations against notifiable diseases. Sick animals were usually treated.

Description of traits, data characteristics and analyses

Data were extracted from available growth performance records stored at the SGS. Growth traits considered were body weights at birth (BW0, kg), at 1 month (BW1, kg), at 2 months (BW2, kg), at weaning (WW, kg), at 6 months, (BW6, kg), at 9 months (BW9, kg) and at yearling (YW, kg), pre-weaning daily gain from birth to 6 months (ADG0–6, kg/day) and post-weaning average daily gain from 6 months to yearling (ADG6–12, kg/day; Table 1).

Table 53. Data structure, levels of significance for the various fixed effects, summary statistics and structure of the
models used in the final analyses for pre- and post-weaning growth traits

		Trait						Trait			
		Pre-weaning					Post-weaning				
		BW0 (kg)	BW1 (kg)	BW2 (kg)	WW (kg)	ADG0-6 (g/day)	BW6 (kg)	BW9 (kg)	YW (kg)	ADG6-12 (g/day)	
No. of records		2,602	2,120	2,287	2,084	1,782	1,838	1,557	1,477	1,368	
Overall mean		3.76	10.64	14.54	19.38	110.88	24.33	29.86	36.64	65.16	
SD		0.74	2.71	3.94	4.74	31.45	5.74	6.26	7.49	26.83	
No. of sires		56	56	55	54	50	50	54	54	51	
No. of dams		1,164	1,031	1,075	1,003	943	953	790	761	742	
Sex	F	***	*	***	*	***	***	***	***	***	
Flock	F	ns	*	***	***	***	***	***	***	ns	
Birth type	F	***	***	***	***	***	***	***	***	*	
Dam parity	F	***	***	***	***	ns	**	**	***	***	
Year of birth	F	***	***	***	***	***	***	***	***	***	
Weighing age	С	-	***	***	***	-	***	***	***	-	
Maternal environment	R	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark					
Direct additive genetic	Α	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark		\checkmark	\checkmark	\checkmark	
Maternal genetic	Α	\checkmark	\checkmark	\checkmark	\checkmark		\checkmark	\checkmark			
Direct-maternal effects	А	\checkmark		\checkmark							

Traits: BW0 birth weight, BW1 month 1 weight, BW2 month 2 weight, WW weaning weight, BW6 month 6 weight, BW9 month nine weight, YW yearly weight, ADG0–6 average daily gain 0–6 months, ADG6–12 average daily gain 6–12 months; type of factors: F fixed factor, C linear covariate, a random factor with relationship matrix, R random factor with identity matrix, ns not significant, $\sqrt{}$ fitted *P<0.05, **P<0.01, ***P<0.001

Data were edited for consistency of pedigree information and dates, discarding those with anomalies. Preliminary analyses to determine the significant fixed effects influencing growth performance were conducted using PROC GLM procedures of SAS (SAS 1998). Covariance components and genetic parameters for individual traits were estimated using various animal models based on restricted maximum likelihood procedures. All analyses were performed using MTDFREML computer programme (Boldman et al. 1995). Various univariate models with differed in the combinations of direct additive, maternal genetic and maternal environmental effects were implemented for each trait to determine the most parsimonious model to describe the data. The structures of the models used for the various traits in the final analyses are shown in Table 1.

The general mixed model fitted in this case was:

 $y = Xb + Z_1a + Z_2m + Z_3c + \varepsilon$ with cov $(a, m) \neq 0$

where y is a vector of observations on the specific trait of the animal; b, a, m and c the vectors of fixed effects including covariables, direct additive genetic effects, maternal additive genetic effects and maternal permanent environmental effects, respectively; X, Z_1 , Z_2 and Z_3 are the corresponding incidence matrices relating the fixed and random effects to y; and ε a vector of residuals. Total heritability (h²) was estimated by summing all the genetic $\sigma^2 \sigma^2 + 0.5 \sigma^2 + 1.5 \sigma$

effects expressed as a proportion of the phenotypic variance (

(total-additive / 2) i.e. $(a m a \sigma_P \sigma_P)$

Estimates at least two times higher than their corresponding standard errors were assumed to be significantly different from zero. Random effects were assumed to follow a normal distribution with mean zero and the general (co)variance structure:

c var[]=	$I\sigma_c^2$	$a^{A\sigma^2}$	$A\sigma_{_{am}}^{0}$	8
т	0	$A\sigma_{am}$	$A\sigma_m^2$	0
е	[0	0	0	$I\sigma^2$]

where *I* and *A* represent the identity and additive genetic relationship matrices respectively. A bivariate animal model was used to estimate the genetic and phenotypic correlations between traits.

RESULTS

Estimates of (co)variance components and genetic parameters

Table 2 presents estimates of (co)variance components and genetic parameters for pre- and post-weaning traits from the univariate analyses. Direct heritability estimates were low to moderate. Pre-weaning direct genetic heritability (h^2) estimates were, 0.18, 0.36, 0.32, 0.28 and 0.12 for BW0, BW1, BW2, WW and ADG0–6, respectively. Post- weaning h^2 estimates were 0.21, 0.14, 0.29 and 0.30 for BW6, BW9, YW and ADG6–12, respectively. Total heritability (h^2) was moderate to low. WW, BW6 and BW9 had low h^2 at 0.05, 0.04 and 0.07, respectively.

Maternal effects were significant for pre-weaning performance. WW had the highest maternal genetic heritability. Maternal genetic variance was not significant for YW, ADG0–6 and ADG6–12. Maternal environmental variances were significant for pre-weaning traits with maternal heritability (h^2) h2m estimated at, 0.12, 0.09, 0.05 and 0.03 for BW1, BW2, WW and ADG0–6, respectively. Moderate to high negative correlations between direct and maternal genetic variances were observed. Estimates for ram were -0.47, -0.67, -0.76, -0.94, -0.88 and -0.70 for BW0, BW1, BW2, WW, BW6 and BW9, respectively. Table 3 presents genetic and phenotypic correlations from bivariate analyses. Low to high genetic and phenotypic correlations were observed. Seture to 0.94, respectively. Negative genetic correlations were observed for ADG0–6 and ADG6–12, BW2 and ADG6–12, WW and ADG6–12 and, BW6 and ADG6–12.

DISCUSSION

Pre-weaning traits

This study presents estimate of variance components and genetic parameters using various models. There were significant maternal genetic and maternal environmental effects on pre-weaning growth performance. Various studies have reported the influence of these effects in early growth of lambs (e.g. Abegaz et al. 2002; Maniatis and Pollot 2002; Zamani and Mohammadi 2008). Failure to account for maternal effects has been shown to result in overestimation of direct heritability (Maniatis and Pollot 2002). Estimates of direct genetic heritability for BW0 in this study compare favorably with estimates from other studies (e.g. Neser et al. 2000; Vatankhah and Talebi 2008a). Rashidi et al. (2008) reported very low direct heritability estimate for BW0 of 0.04. Higher direct heritability estimates than in the present study have been reported for various sheep breeds (e.g. Al-Shorepy 2001; Abegaz et al. 2002; Gizaw et al. 2007; Vatankhah and Talebi 2008b). The differences among reported estimates are an indication of the genetic diversity of populations. Besides, variations in data structure and choice of models to fit the data would also be a potential source of varying estimates between this study and what has been reported in the literature for tropical sheep breeds. Estimates of heritability for pre-weaning growth performance are scarce in literature. Notter (1998) reported a direct heritability of 0.16 and 0.14, and 0.07 and 0.08 for 30 and 60-day body weight for the Suffolk and Polypay sheep breeds, respectively. Neser et al. (2000) reported a direct heritability of

0.27 for Dorper sheep for 42-day body weight.

1

^{am}/₂).

2

Component	Trait ^a								
	Pre-weaning					Post-weaning			
	BW0 (kg)	BW1 (kg)	BW2 (kg)	WW (kg)	ADG0-6	BW6 (kg)	BW9 (kg)	YW (kg)	ADG6-12
					(g/day)				(g/day)
q^2	0.07	2.24	3.80	5.04	70.12	4.97	4.29	12.43	173.70
я ²	0.06	0.63	1.20	3.57		4.78	5.40		
φ^2		0.74	1.01	0.99	20.45				
σ_{am}	-0.03	-0.79	-0.79	-3.98		-4.29	-3.35		
ρ^2	0.29	3.40	7.37	12.70	517.21	17.71	23.76	29.72	400.48
β^2	0.40	3.40	11.76	18.33	607.88	23.16	30.10	42.16	574.18
$h^2 \pm SE$	0.18 ± 0.01	0.36 ± 0.03	0.32 ± 0.03	0.28 ± 0.05	0.12 ± 0.05	0.21 ± 0.05	0.14 ± 0.05	0.29 ± 0.09	0.30 ± 0.09
$h^2_{\pm} SE$	0.16 ± 0.01	0.10 ± 0.02	0.10 ± 0.02	0.19 ± 0.04		0.21 ± 0.05	0.18 ± 0.06		
$c^2 \pm SE$		0.12 + 0.02	0.09 ± 0.02	0.05 ± 0.02	0.03 ± 0.01				
<i>r_{am}</i>	-0.47	-0.67	-0.76	-0.94		-0.88	-0.70		
h^2	0.21	0.40	0.27	0.05	0.12	0.04	0.07	0.29	0.30
$e^2 \pm SE$	0.74 ± 0.01	0.55 ± 0.04	0.63 ± 0.05	0.69 ± 0.07	0.85 ± 0.10	0.76 ± 0.10	0.79 ± 0.12	0.71 ± 0.14	0.70 ± 0.13

 Table 54. Estimates of (co)variance components and genetic parameters for the pre- and post-weaning growth traits from the univariate

 σ^2 direct additive variance, σ^2 maternal additive variance, σ^2 maternal permanent environmental variance, σ_{am} direct-maternal genetic covariance, σ_e^2 residual variance, σ^2 phenotypic variance, h^2 direct genetic heritability, h^2_m maternal genetic heritability, c^2 ratio of maternal permanent environmental effect, ram direct-

maternal genetic correlation, h^2 total heritability, e^2 ration of residual effect ^a See Table 1 for description of the traits

Correlations										
	ADG0-6	BW0	BW1	BW2	WW	BW6	BW9	YW	ADG6-12	
ADG0-6		0.19	0.47	0.60	0.71	0.94	0.73	0.66	-0.02	
BW0	0.29		0.50	0.45	0.37	0.35	0.28	0.25	0.06	
BW1	0.42	0.80		0.79	0.62	0.55	0.49	0.43	0.07	
BW2	0.63	0.57	0.92		0.76	0.65	0.59	0.52	-0.03	
WW	0.70	0.41	0.67	0.88		0.78	0.64	0.52	-0.04	
BW6	0.90	0.56	0.56	0.56	0.90		0.80	0.69	-0.01	
BW9	0.83	0.29	0.61	0.79	0.79	0.95		0.83	0.08	
YW	0.55	0.15	0.64	0.81	0.57	0.65	0.86		0.67	
ADG6-12	0.20	0.16	0.28	0.28	0.15	0.25	0.17	0.85		

 Table 55. Estimates of genetic and phenotypic correlations between growth traits^a from bivariate analyses

^a See Table 1 for description of traits

^b Genetic correlations below the diagonal, phenotypic correlations above the diagonal

Maniatis and Pollot (2002) estimated a direct heritability of 0.14 for 8 weeks' weight from a model that included maternal effects and a covariance between direct and maternal genetic effects. Comparatively, higher direct heritability estimates of 0.36 and 0.32 for BW1 and BW2, respectively, were reported in the present study. Heritability estimates for WW obtained in this study are comparable to what has been reported for various tropical sheep breeds fitting models that accounted for maternal effects (e.g. Abegaz et al. 2002; Gizaw et al. 2007; Vatankhah and Talebi 2008a, b; Zamani and Mohammadi 2008). Estimates of correlations between direct and maternal genetic effects were moderate to high and consistently negative for pre-weaning traits (Table 2).

Negative direct-maternal genetic correlations are common in the literature (e.g. Abegaz et al. 2002; Rashidi et al. 2008). High and negative genetic correlations were expected due to the small data size and data structure. The effect of data size and structure on the estimation of covariance between direct and maternal effects is well documented (Meyer 1997; Maniatis and Pollot 2003). The seemingly high estimate of direct-maternal correlation reported in this study should therefore be treated with caution. This estimate should be re-calculated once sufficient data is available from the ongoing recording at the SGS as well as data from other flocks participating in the recording scheme.

Post-weaning traits

Maternal genetic variances were significant for BW6 and BW9 but maternal environmental effects were found to be insignificant in this study for the post-weaning traits. Importance of maternal effects to growth performance has been reported to decline with age, with observed post-weaning maternal effects as a 'carry-over' of maternal influence until weaning (Maniatis and Pollot 2002). Heritability estimates for post-weaning traits reported in the present study are within the range of estimates reported in the literature (e.g. Abegaz et al. 2002; Vatankhah and Talebi 2008a). Moderate direct genetic heritability estimates for post-weaning growth traits for this population imply that it is possible to select for these traits for improved growth performance and high sale weights. However, this could be challenged by the fact that antagonism between direct and maternal genetic effects would complicate selection based on maternal genetic variation.

Genetic and phenotypic correlations

The genetic correlations from bivariate analyses between traits considered in this study ranged from 0.15 to 0.95, while phenotypic correlations ranged from -0.04 to 0.94 (Table 3). The value for the genetic correlation between BW0 and WW of 0.41 was comparable with that reported by Abegaz et al. (2002) but lower than other estimates in the literature (Gizaw et al. 2007; Rashidi et al. 2008). The high and positive genetic and phenotypic correlations between BW1 and BW2, BW2 and WW, WW and BW6 and BW9 and YW indicate that selection for one trait will result in the improvement of the other trait. Lacks of resources and resistance to labor-intensive innovations have been highlighted as some of the reasons for suboptimal data recording in the tropics (Kosgey et al. 2006). Minimal recording would reduce the expenses incurred, and may result in better and more accurate records. High and positive correlations between traits mean that only one of the traits can be recorded and selection on it will result in similar changes in the other trait.

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