



Genetic and phenotypic parameters of body weights in Saudi Aradi goat and their crosses with Syrian Damascus goat

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ABSTRACT

Genetic and phenotypic parameters were estimated from 1358 kids of Saudi Aradi goats (A) and their crosses with Syrian Damascus (D) in two experimental stations in Saudi Arabia between 2005 and 2010. Such crossbreeding plan resulted in four genetic groups of AA, DD, $\frac{1}{2}D\frac{1}{2}A$ and $\frac{3}{4}D\frac{1}{4}A$. The analysis of data was carried out by using a mixed animal model to find out every combination of pairs of traits. The five fixed effects included in the mixed model were location of the experiment, genetic group, year-season of birth, type of birth, and sex; the random effects for each two traits were the additive genetic effects for each of the two traits and the random error (temporary environmental effect). Cross-bred kids of $\frac{1}{2}D\frac{1}{2}A$ and $\frac{3}{4}D\frac{1}{4}A$ were heavier for all body weights relative to Saudi Aradi kids. The lower values observed in all weights for $\frac{3}{4}D\frac{1}{4}A$ kids compared to those in $\frac{1}{2}D\frac{1}{2}A$ are expected, which would confirm the fact that the estimates of direct heterosis were positive for the majority of weights studied. Medium to high heritability estimates were obtained for weights, ranging from 0.12 at the 8th week to 0.41 at birth. The increase in estimates is commensurate with age: from the weight in the 8th week to the weight in the 24th week. Genetic correlation estimates were generally medium to high, ranging from 0.40 to 0.99. Genetic correlations between adjacent body weights were higher than those between non-adjacent estimates. Phenotypic correlations were positive, and generally of lower significance than the genetic correlations.

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1. Introduction

Goat breeding programs have been generally based on measures of growth traits because they are highly heritable and easy to measure (Shrestha and Fahmy, 2007b; Devendra, 2010). However, rapid growth during the first stage of growth will minimize the cost which will provide more profits to the farmers. Studies on genetic parameters in goats have shown that body weights are moderately heritable (Shrestha and Fahmy, 2007b; Mugambi et al., 2007). Estimates of additive genetic and environmental components of (co)variances for economically important traits in

goats are needed to get true and unbiased prediction of genetic values, to predict direct selection responses, and to develop economic multi-trait selection indices (Van Vleck, 1993; Hofer, 1998; Hanford et al., 2005, 2006). Multi-trait animal models are preferable relative to single-trait animal models for getting unbiased (co)variances and genetic parameters and these estimates are needed to estimate the breeding values and to compare responses from different selection programs (Thompson, 2008). Also, knowledge of genetic and phenotypic relationship among economic traits is necessary in formulating an effective selection program. In goats, attempts to estimate genetic parameters using multi-traits animal models are scarce (Shrestha and Fahmy, 2007a,b). The Saudi Aradi goats and the Syrian Damascus are the most desirable goats in Saudi Arabia. The color of Aradi goats in northern Saudi Arabia is usually

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Table 1
Numbers of kids and summary statistics for body weight traits (kg).

Body weight	N	Mean	Standard deviation	Minimum	Maximum
0-week	1358	3.75	0.86	1.20	6.75
4-week	1122	8.20	2.20	3.10	17.94
8-week	987	11.61	3.26	4.85	24.65
12-week	922	14.78	4.09	5.54	27.75
16-week	877	17.69	4.55	5.50	34.50
20-week	880	20.20	4.99	8.40	42.00
24-week	835	22.99	5.36	8.60	45.75

black, and the average adult weight is 40 kg for the females and 51 kg for males; moreover, the adult has an average length of 75 cm, height of 66 cm, and heart girth of 76 cm (Bhattacharya, 1989). Performance of Damascus goats could record an average 174 and 157 g/day daily gain from birth to weaning (80 days), for male and female kids, respectively. Furthermore, Damascus bucks could attain 87.75 kg in weight and the does 53.60 kg, and milk yield of 380–880 kg/lactation (ACSAD, 1996).

The aim of this study was estimate heritabilities, in addition to genetic and phenotypic correlations. A multi-traits animal model is used for kid body weights in Saudi Aradi goats (A) and in their crosses with Damascus goats (D).

2. Materials and methods

2.1. Breeding plan

A crossbreeding program between Aradi Saudi goats (A) with Damascus goats (D) was conducted in Jouf Dairy Experimental Station, north of Saudi Arabia, and Meat Experimental Station at Qassim University, central Saudi Arabia. Does of Aradi goats were randomly divided into two groups, 120 does in each experiment. Each group of Aradi does was subdivided into two subgroups to be artificially inseminated from the semen of elite bucks of the same breed, and of Damascus breed. In both experiments, does of Damascus breed were randomly inseminated from bucks of the same breed to produce purebred kids. Moreover, crossbred does of $\frac{1}{2}D\frac{1}{2}A$ were backcrossed with Damascus bucks to get the genetic group of $\frac{3}{4}D\frac{1}{4}A$. Accordingly, the breeding plan permitted the production of four genetic groups: AA, DD, $\frac{1}{2}D\frac{1}{2}A$ and $\frac{3}{4}D\frac{1}{4}A$ in each experiment separately. The semen of bucks was randomly assigned to inseminate the does.

2.2. Management and feeding

All does in the present study were ear-tagged and housed in a semi-shaded/open front barn. Goats were fed a commercial pelleted diet and alfalfa hay. The amount of pellets and hay was calculated according to the nutrition requirements for goats, which is based on the animal age and the production status. Water, straw, salt and minerals were freely supplemented to all animals. Animals were fed *ad libitum* individually.

3. Data and models of analysis

Body weight of 1358 kids of Saudi Aradi, Damascus, and their crosses fathered by 69 sires and mothered by 134 dams was taken at birth, and quadra-weekly thereafter up to 24 weeks of age. Variance and covariance components and genetic parameters were estimated using the DFREML program fitting two-trait animal model. The GLM procedure in the SAS 9.1 program was used to detect the fixed effects, locations of the experiments (Qassim and Jouf), genetic group {Aradi (A), Damascus (D), $\frac{1}{2}D\frac{1}{2}A$, and $\frac{3}{4}D\frac{1}{4}A$ }, year-season of birth (1–18 level), type of birth (single – twin – triplet or more), and sex to be included in the model (SAS, 1999). Additive genetic effect for each trait,

co-variances between each two traits, and the residual were used as random effects. Variance components were estimated by multi-traits derivative-free restricted maximum likelihood program (MTDFREML; Boldman et al., 1995). The convergence criteria used in this analysis were the variance of $-2 \log$ likelihoods in the current simplex used in the derivative-free REML algorithm. This approach should ensure that a global, rather than a local, maximum likelihood estimate is obtained. The convergence was assumed when the variance of likelihood values in the simplex was less than 10^{-8} . In addition, restarting each analysis was performed with different starting values in order to avoid convergence to local maxima. All estimates were based on several restarts until $-2 \log$ likelihoods did not change up to 2 decimal points. The mixed animal model used in analyzing the data was:

$$Y = Xb + Z_a u_a + e$$

where $Y = n$ by 1 vector of records; b = the fixed effects in the model; u_a = the vector of direct animal genetic effects; X and Z_a = the incidence matrices relating records to the fixed effects and additive genetic effects, respectively, and e = the vector of the residual effects.

The variance and co-variance structures for the model were as follows:

$$\begin{bmatrix} a_1 \\ a_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a_1}^2 & \sigma_{a_1 a_2} & & \\ \sigma_{a_2 a_1} & A\sigma_{a_2}^2 & & \\ & & In_1 \sigma_{e_1}^2 & \sigma_{e_1 e_2} \\ & & \sigma_{e_2 e_1} & In_1 \sigma_{e_2}^2 \end{bmatrix}$$

where A = the numerator relationship matrix; In_1 and In_2 = identity of the matrix of order that is equal to the records of trait 1 and 2, respectively; $\sigma_{a_1}^2$ and $\sigma_{a_2}^2$ = the direct genetic variance for trait 1 and trait 2, respectively; $\sigma_{a_1 a_2}$ = the covariance between direct genetic variance effect for trait 1 and trait 2; $\sigma_{e_1 e_2}$ = the covariance between residual effect for trait 1 and 2; $\sigma_{e_1}^2$ and $\sigma_{e_2}^2$ = the error variance for trait 1 and 2, respectively.

4. Results and discussion

The summary statistics for body weights in the present study are shown in Table 1. Kid body weights were 3.73, 8.20, 11.61, 14.78, 17.69, 20.20, and 22.99 kg at 0, 4, 8, 12, 16, 20 and 24 weeks of age, respectively. However, wide phenotypic variations in all weights were observed.

Analyses of variance showed that the fixed effects of location of the experiment (Qassim and Jouf), genetic group

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