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Estimation of genetic parameters for body weight traits and pelt quality score in Iranian Karakul sheep

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ABSTRACT

Genetic parameters for birth weight (BW), weight at 3, 6, 9 months of age (3MW, 6MW, 9MW), yearling weight (YW) and pelt quality score (PELT) were estimated in Iranian Karakul sheep. Data and pedigree information were obtained from the Breeding Station of Karakul sheep located in North Khorasan province in Iran from 1994 to 2009 on 5437 lambs descended from 193 sires and 1886 dams. Six different animal models were fitted, differentiated by including or excluding maternal effects, with and without covariance between maternal and direct genetic effects. The most suitable model amongst all six models was determined based on likelihood ratio tests for each trait. In addition, multivariate analysis was carried out among the considered traits to estimate the genetic and phenotypic correlations. Direct heritability estimates for BW, 3MW, 6MW, 9MW, YW and PELT were 0.21, 0.10, 0.14, 0.18, 0.21 and 0.004, respectively. All the phenotypic correlations estimates among body weight at different ages were positive. The estimates of phenotypic correlations for PELT-BW and PELT-3MW were low and positive while the remaining were low and negative. The estimates of direct genetic correlations between body weights were positive; whereas those among PELT and liveweights were negative. Current estimates of genetic parameters in Iranian Karakul breed may be used to design selection programme. Our results showed that improvement of growth performances seems feasible, as the studied traits were moderately heritable, although the heritabilities at 3MW and 6MW were quite low. However, selection for BW should be judicious in order to prevent unfavorable consequences on pelt quality. So, considering the high genetic correlations between 3MW and other body weight traits, the genetic improvement of 3MW should be one of the main selection goals.

1. Introduction

Sheep breeding constitutes the most important portion of Iranian livestock sector and a total of approximately 50 million head of sheep, belonging to more than twenty breeds and sub-breeds, are reared in Iran. Sheep meat production contributes more than 45% of total meat production in Iran per year (Atefi et al., 2012). In Iran, there are three well-known breeds of sheep for pelt production (Zandi, Gray-Shiraz and Karakul). The Karakul sheep is a fat-tailed breed, and very common to the Asian and African continents. This breed is very resistant to harsh condition and raised mostly under the semi nomadic system of management. Iranian Karakul breed is mainly found in the plain of Sarakhs in the province of North Khorasan neighboring Turkmenistan. The Karakul is a medium-sized sheep, but it differs from many other breeds with regard to body conformation. Pelt from Karakul lambs is historically referred as "Persian lamb"; this breed is also a source of milk, meat, and fiber. The Karakul has an extended breeding season, with three lamb crops in two years. Single lambs are the rule, though twins are not uncommon (Sefidbakht et al., 1978; Nsoso and Madimabe, 2003). At present, the lamb is not raised due to the high market demand for newborn curly pelt and the increasing demand for red meat (Monem et al., 2004).

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The growth potential of lambs is one of the most important factors in genetic improvement schemes. Particularly in small ruminants, fast growth rate determines their meat producing capability up to marketing age, therefore, it affects economic success of producing system (Abbasi et al., 2012). Mutton is the most important source of red meat in Iran. However, it fails to satisfy the consumer's increasing demand. Thus, to promote the growth potential of lambs and to improve breeding efficiency are possible alternatives to increase meat (Miraei-Ashtiani et al., 2007; Mohammadi et al., 2013). Results of previous published reports indicate that growth traits in sheep are influenced not only by animal genetic potential but also by maternal effects, genetic and permanent environmental effects (Hossein-Zadeh and Ardalan, 2010a; Prince et al., 2010; Di et al., 2011; Mandal et al., 2011; Ghafouri-Kesbi and Baneh, 2012). The estimates of heritability and genetic relationships between productive traits are needed for planning an efficient breeding system and to develop an effective genetic evaluation. To date, the estimates of genetic parameters for growth traits and pelt production in Karakul sheep are scarce in the available literature. Therefore, the objective of this study is to estimate the genetic parameters for body weight traits and pelt quality score in Iranian Karakul sheep breed. Furthermore, correlations among the considered traits were also estimated.

2. Material and methods

2.1. Description of the dataset

The dataset and pedigree information used in this study were obtained from Breeding Station of Karakul sheep located in North Khorasan province in Iran from 1994 to 2009. The climate of this region is cold semi-arid; the drought period is for five months of year and wet season from November to May. The Breeding Station was established in 1955 in order to improve the performance of Karakul sheep through identifying the best rams and their distribution into the commercial flocks. Mating system was controlled to ensure that the identity of the sire and dam of each lamb was known. Ewe lambs and ram lambs were bred for the first time at 18 months of age. In order to reduce variability, only lambs born from 20th January to 15th February were considered. The flock was allowed to graze during the daytime on rangeland and housed at night. During winter (November–February), the animals were fed manually with commercial complete pelleted diet. Dams were weighed approximately 2 h after lambing. Lambs were ear-tagged and weighed immediately after lambing. The average weaning age was 90 days. The considered traits were: birth weight (BW), weight at 3 months of age (3MW), weight at 6 months of age (6MW), weight at 9 months of age (9MW), yearling weight (YW) and pelt quality score (PELT). Data concerning pelt quality were obtained from Breeding Station where newborn lambs were subjectively judged and a score ranging from 50 to 100 was assigned to their pelt based on curl type, pattern score, and shade of fleece according to Hassani et al. (2010). The structure of the dataset is described in Table 1.

Table 1
Description of dataset and pedigree information of Iranian Karakul lambs.

Item	Trait					
	BW	3MW	6MW	9MW	YW	PELT
Number of records	5437	4760	3108	2562	2321	4551
Number of sires	193	191	186	179	171	191
Number of dams	1886	1805	1509	1410	1274	1780
Mean	5.20	24.37	33.23	39.68	47.32	83.08
SD	0.80	4.71	5.34	6.07	7.77	7.55
CV (%)	15.38	19.33	16.07	15.30	16.42	9.09

BW, birth weight (kg); 3MW, weight at 3 months of age (kg); 6MW, weight at 6 months of age (kg); 9MW, weight at 9 months of age (kg); YW, yearling weight (kg). PELT, pelt quality score.
SD, standard deviation.
CV, coefficient of variation.

2.2. Statistical analysis

Variance components and genetic parameters were estimated for each trait using restricted maximum likelihood procedure of the Wombat program (Meyer, 2006) by fitting six single-trait animal models that ignore or include additive maternal or permanent environmental effects. The models used to estimate genetic parameters included random effects and fixed effects that were found significant in the general model analyses. Firstly, the GLM procedure (Sas, 2008) was used for determining the fixed effects that have significant influence on the traits investigated, assuming interactions negligible. Level of significance for the inclusion of effects into the model of analysis was declared at $P < 0.05$. The final model of analysis for weight traits and pelt quality score included the fixed effects of year of lambing (1–15), sex of lamb (male, female), birth type (single, twin), and the linear covariate effect of body weight of dam at lambing. The models used were as follows:

Model 1: $\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Za} + \boldsymbol{e}$
Model 2: $\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Z_a a} + \boldsymbol{Z_c c} + \boldsymbol{e}$
Model 3: $\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Z_a a} + \boldsymbol{Z_m m} + \boldsymbol{e}$ with $Cov(\boldsymbol{a}, \boldsymbol{m}) = 0$
Model 4: $\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Z_a a} + \boldsymbol{Z_m m} + \boldsymbol{e}$ with $Cov(\boldsymbol{a}, \boldsymbol{m}) = \boldsymbol{A\sigma_{am}}$
Model 5: $\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Z_a a} + \boldsymbol{Z_m m} + \boldsymbol{Z_c c} + \boldsymbol{e}$ with $Cov(\boldsymbol{a}, \boldsymbol{m}) = 0$
Model 6: $\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Z_a a} + \boldsymbol{Z_m m} + \boldsymbol{Z_c c} + \boldsymbol{e}$ with $Cov(\boldsymbol{a}, \boldsymbol{m}) = \boldsymbol{A\sigma_{am}}$ where **y** is a vector of observations, **b** is a vector of fixed effects with incidence matrix **X**, $\boldsymbol{a}{\sim}N(0, A\sigma_a^2)$ and $\boldsymbol{m}{\sim}N(0, A\sigma_m^2)$ are vectors of direct and maternal genetic effects with incidence matrices $\mathbf{Z}_a$ and $\mathbf{Z}_m$, respectively, $\boldsymbol{c}{\sim}N(0, \boldsymbol{I_c}\sigma_c^2)$ is a vector of random maternal permanent environmental effects with incidence matrix $\mathbf{Z}_c$, and $\boldsymbol{e}{\sim}N(0, \boldsymbol{I}_n\sigma_e^2)$ is a vector of random residual effects. Also, σ_a^2 is the direct genetic variance, σ_m^2 is the maternal genetic variance, $\sigma_c^2$is the maternal permanent environmental variance, σ_e^2 is the residual variance, **A** the additive genetic relationship matrix, and $\mathbf{I}_c$ and $\mathbf{I}_n$ are the identity matrices of order equal to the number of maternal permanent environmental effects and the number of records, respectively.

A simplex algorithm is used to search for variance components to minimize the function −2log likelihood (L). Convergence was assumed when the variance of the function values (−2logL) of the simplex was less than 10^{-8}. For all models, to ensure that a global maximum was reached, analyses were restarted. A log likelihood ratio test was used to choose the most suitable random effects model for each trait. The reduction in −2logL when a random effect was added to the model was calculated. If this reduction was greater than the value of the chi-square distribution with one degree of freedom ($P < 0.05$), the additional random effect fitted was considered significant. When log likelihoods did not differ significantly ($P > 0.05$), the model that had the fewer number of parameters was selected as the most appropriate (Meyer, 1992).

Total heritability was estimated as $h^2{}_T = \sigma^2{}_a + 0.5\sigma^2{}_m + 1.5\sigma_{am}/\sigma^2{}_p$ (Willham, 1972).

A six-trait analysis was carried out among the considered traits to estimate the genetic and phenotypic correlations.

3. Results and discussion

3.1. Choice of analysis models

Estimates of log-likelihood values obtained under different models are shown in Table 2. Fitting either maternal permanent environmental effect or maternal genetic effect as second random effect or covariance between direct and maternal genetic effects