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Short communication

Estimation of genetic parameters and genetic trends for biometric traits in Moghani sheep breed

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ABSTRACT

The present study aimed to estimate the genetic parameters as well as genetic trends for biometric traits in Iranian Moghani-sheep breeds. The data set consisted of 15115 biometric records from 3702 individual progenies of 499 sires and 3203 dams, which involved a period of 15 years of time (1996–2011). The records were extracted from Moghani sheep breeding and raising station. The studied traits were: height at withers (HW), height at rump (HR), body length (BL), heart girth (HG) and leg circumference (LC). variance components and genetic parameters were estimated with single and five-trait analysis using restricted maximum likelihood (REML)-methods and WOMBAT software. Six different animal models were fitted to the traits, with the best model for each trait determined by Akaike Information Criterion (AIC). All traits were significantly influenced by year of birth, month of birth, sex of the lamb and birth type ($P < 0.01$). The breeding values were compared across years of birth with respect to the genetic trends. Direct heritabilities using single trait analysis were estimated 0.10 for HW, 0.11 for HR, 0.16 for BL, 0.11 for HG and 0.23 for LC. Using bivariate analysis, the estimates of additive genetic correlations were ranged from −0.55 (between BL and LC) to 0.99 (between HW and HR). Estimates of breeding value by year of birth for all traits were fluctuated throughout the period of study. Estimates of genetic parameters as well as the estimates of breeding values suggested that the genetic selection can lead to a significant genetic improvement of the Moghani sheep.

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1. Introduction

Moghani sheep is known as one of the Iranian native sheep breeds to produce mutton and lambs with high growth performance. Its' population is approximately 5.5 million (Hossein-Zadeh and Ardalan, 2010). This sheep is medium-sized (ewe = 60–63, ram = 63–66 kg) which mostly can be found in the plain Moghan, Ardabil province, Iran. The main characteristic of the breed is: intermediate and muscular neck, commensurate growth, medium shoulder, straight back muscles and pea white body color (Saadatnoori and Siahmansoor, 1986). Moghani sheep breeding and raising station (MSBRS) as the oldest sheep breeding station of Iran was established in 1952. The purpose was improving of the performance in the breed.

Estimating genetic parameters of local breeds is important not only for conservation purposes, but also for defining breeding objectives and programs. Body measurements are influenced by the individual direct genetics and the environment under which the animal is raised as well as by the maternal genetics and the maternal environment effects (Mandal et al., 2010; Jafari and Hashemi, 2014). Then, implementing a full model that includes all of these effects may provide an accurate estimate of genetic parameters for the trait.

As a part of the environmental effects the fixed effects such as year of birth, month of birth, sex and birth type of the lamb play a notable role in the phenotypic variation of the biometric traits (Jafari et al., 2011). Biometric characters or linear body measurements can be used as an indirect criteria in many domestic animal species to help meat-yield improvement. It seems an individual can be described more effective by body and weight measurement than conventional methods (Salako, 2006; Jafari and Hashemi, 2014).

Early and late maturing animals can be detected by using the body measurements as the reliable factors of body size (Brown et al., 1973). Breeders can use linear body measurements as a criterion in

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Table 1
Pedigree structure of Moghani sheep breed.

Item			Number
Individuals in total			13047
Inbreds in total			1200
Sires in total			499
Dams in total			3203
Individuals with progeny			3702
Individuals with no progeny			9345
Founders	Progeny		9014
	Sires	Progeny	7209
	Dams	Progeny	8410
	With no progeny		0
Non-founders	Sires	Progeny	1210
	Dams	Progeny	1586
	Only with known sire		5
	Only with known dam		1582
	With known sire and dam		8414
Full-sib groups	Average family size	Maximum	6
		Minimum	2

assessing growth rate, feed utilization and weight characteristics in farm animals (Brown et al., 1973). Using measurement methods, breeders are able to identify early and late maturing animals with different sizes (Brown et al., 1973). This method will be effective to diagnosis appropriate animals at an earlier growth stage for selection and prediction of mature ranking (Jafari and Hashemi, 2014). As a result, biometric traits can be used as an index in the selection programs. The predications of the breeding values of the studied traits can be used as a functional indicator in selection programs and animal production (Hanford et al., 2006). Also the genetic trend of the flock can be recognized over years (Hanford et al., 2006). In other side the prediction of the breeding values is essential to genetic improvement of the traits and evaluation of breeding success (Kovac and Groenveld, 1990). To the best of our knowledge there is no report for genetic parameter and genetic changes of the biometric traits of Moghani sheep. So the present study focused on the estimates of genetic parameter and genetic trend of biometric traits of the Moghani sheep breed over 15 years (1996–2011).

2. Materials and methods

The number of 15115 body measurement records from 3702 individual progenies of 499 sires and 3203 dams over 15 years (1996–2011) were used at the present study (Table 1). The records were extracted from Moghani sheep breeding and raising station (MSBRS). The traits were: height at withers (HW), height at rump (HR), body length (BL), heart girth (HG) and leg circumference (LC). The significance of the fixed effects for inclusion in the final model was tested using the GLM procedure of the SAS software (SAS, 2005). The considered fixed effects were sex of lambs in two classes (male and female), type of birth in three classes (single, twin and triplet), year of lambing in 15 classes (1996–2011), month of lambing in 5 classes (July–September, December, February).

(Co) variance components and genetic parameters along with genetic trend were estimated using restricted maximum likelihood (REML) method fitting an animal model using WOMBAT software (Meyer, 2007). The following six univariate animal models were tested for each trait.

The statistical model used were on:

$$(\text{Model 1})\, y = \mathrm{Xb} + Z_{\mathrm{a}}a + e$$

$$(\text{Model 2})\, y = \mathrm{Xb} + Z_{\mathrm{a}}a + Z_{\mathrm{pe}}\mathrm{pe} + e$$

$$(\text{Model 3})\, y = \mathrm{Xb} + Z_{\mathrm{a}}a + Z_{\mathrm{m}}m + e \quad \mathrm{Cov}(a, m) = 0$$

$$(\text{Model 4})\, y = \mathrm{Xb} + Z_{\mathrm{a}}a + Z_{\mathrm{m}}m + e \quad \mathrm{Cov}(a, m) \neq 0$$

$$(\text{Model 5})\, y = \mathrm{Xb} + Z_{\mathrm{a}}a + Z_{\mathrm{m}}m + Z_{\mathrm{pe}}\mathrm{pe} + e \quad \mathrm{Cov}(a, m) = 0$$

$$(\text{Model 6})\, y = \mathrm{Xb} + Z_{\mathrm{a}}a + Z_{\mathrm{m}}m + Z_{\mathrm{pe}}\mathrm{pe} + e \quad \mathrm{Cov}(a, m) \neq 0$$

Where y is a vector of records on the considered traits; b, a, m, pe and e are vectors of fixed effects, direct additive genetic effects, maternal genetic effects, permanent environment effects and the residual effects, respectively. X, Z_{a}, Z_{m} and Z_{pe} are corresponding design matrices relating the fixed effect, direct additive genetic effects, maternal additive genetic effects and permanent environmental effects due to ewe to vector of y.

The (co) variance structure for random effects was:

$$\mathrm{var} = \left[\begin{array}{c} a \\ m \\ \mathrm{pe} \\ e \end{array}\right] = \left[\begin{array}{cccc} A\sigma^2_{\mathrm{a}} & A\sigma_{\mathrm{am}} & 0 & 0 \\ A\sigma_{\mathrm{am}} & A\sigma^2_{\mathrm{m}} & 0 & 0 \\ 0 & 0 & I_{\mathrm{d}}\sigma^2_{\mathrm{pe}} & 0 \\ 0 & 0 & 0 & I_{\mathrm{n}}\sigma^2_{\mathrm{e}} \end{array}\right]$$

Also $\sigma^2{}_{\mathrm{a}}$, $\sigma^2{}_{\mathrm{m}}$, $\sigma^2{}_{\mathrm{pe}}$ and $\sigma^2{}_{\mathrm{e}}$ are direct additive genetic variance, maternal additive genetic variance, maternal permanent environmental variance and residual variance, respectively. A is the additive numerator relationship matrix, I_{d} and I_{n} are identity matrices with order equal to the number of ewes and records, respectively. Total heritability ($h^2{}_{\mathrm{t}}$) was estimated using the formula $\sigma^2{}_{\mathrm{a}} + 0.5\sigma^2{}_{\mathrm{m}} + 1.5\sigma_{\mathrm{am}}/\sigma^2{}_{\mathrm{p}}$ (Willham, 1972). Akaike's Information Criterion (AIC) (Akaike, 1974) was used to choose the best model. The genetic trends of the traits were estimated using the regression of breeding values on year of birth. The diagram of the genetic trends was charted using SAS software (SAS, 2005).

Estimation of genetic and phenotypic correlations was accomplished using multi-trait analysis applying the most appropriate model which was determined in univariate analysis.

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